

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

Met	Glu	Leu	Tyr	Ala	Asn	Glu	Val	Pro	Lys	Thr	Ala	Glu	Asn	Phe	Arg
1				5					10				15		
Ala	Leu	Cys	Thr	Gly	Glu	Lys	Gly	Val	Gly	Lys	Ser	Gly	Lys	Pro	Leu
				20				25					30		
His	Tyr	Lys	Gly	Ser	Thr	Phe	His	Arg	Val	Ile	Pro	Xaa	Phe	Met	Cys
				35			40					45			
Gln	Gly	Gly	Asp	Phe											
				50											

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

acgatattaa	ccgaccacaaa	taagctagtg	gtagcagttg	gaggggtaac	agcacttgct	60
gcagggatat	acacacaaag	ggagggtgca	agagtagtct	ggggctatgt	tgatcgattt	120
ctgggtcagc	catcactgat	aaggggagtc	tcacgtggga	aatatccctg	gtctggtttc	180
ctctcacgtg	ctacaaagtc	cctgactagc	aaactgaaga	atggaagcaa	cctaggggaag	240
gacagaaatg	ggtttggtga	tgttattcta	aatccttctc	tccagaagag	agtgaagcag	300
cttgctaagt	ccacagccaa	tacaaaactt	catcaagctc	ctttcaggaa	catgcttttc	360
tatgggcttc	ctggcacagg	gaaaaccatg	gcagcacgag	aacttgctcg	caattctgga	420
ttagattatg	cactaatgac	tggtggagat	gttgcaccat	tgggatcaca	agcagtcacc	480
aagattcatc	agttgtttga	ctgggctg				

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

Thr	Ile	Leu	Thr	Asp	Gln	Asn	Lys	Leu	Val	Val	Ala	Val	Gly	Gly	Val
1					5				10				15		
Thr	Ala	Leu	Ala	Ala	Gly	Ile	Tyr	Thr	Thr	Arg	Glu	Gly	Ala	Arg	Val
					20			25					30		
Val	Trp	Gly	Tyr	Val	Asp	Arg	Ile	Leu	Gly	Gln	Pro	Ser	Leu	Ile	Arg
					35		40				45				
Glu	Ser	Ser	Arg	Gly	Lys	Tyr	Pro	Trp	Ser	Gly	Phe	Leu	Ser	Arg	Ala
					50		55				60				

Thr	Ser	Thr	Leu	Thr	Ser	Lys	Leu	Lys	Asn	Gly	Ser	Asn	Leu	Gly	Lys
65					70				75					80	
Asp	Arg	Asn	Gly	Phe	Gly	Asp	Val	Ile	Leu	Asn	Pro	Ser	Leu	Gln	Lys
			85						90					95	
Arg	Val	Lys	Gln	Leu	Ala	Asn	Ala	Thr	Ala	Asn	Thr	Lys	Leu	His	Gln
			100					105					110		
Ala	Pro	Phe	Arg	Asn	Met	Leu	Phe	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys
			115				120					125			
Thr	Met	Ala	Ala	Arg	Glu	Leu	Ala	Arg	Asn	Ser	Gly	Leu	Asp	Tyr	Ala
	130					135					140				
Leu	Met	Thr	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ser	Gln	Ala	Val	Thr
	145				150					155				160	
Lys	Ile	His	Gln	Leu	Phe	Asp	Trp	Ala							
				165											

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

aaaagccagg	attcctctgc	tcttctctgtt	tagggtttcc	ccctctctct	gcctctgcgc	60
gatgggatgg	cgattccgcc	gcggactcct	tccecgccgc	catcgtggct	gcgctctgta	120
accgagaccg	tctgggggtc	ccaccagttc	acgcacggg	gctaactccct	cgccaagggc	180
atgggccccg	cgcgctacct	cgccagcgac	gtcttcggcg	tcggaggata	ccactggggc	240
gtctacctct	accgccagcg	caagaacgcc	gaggacaact	ccaactacgt	ctccgttttc	300
gtcgccctcg	cttcgcagcg	catcgacgtc	cgagccctct	tcgagctcac	cctcctcgac	360
cagtycgggc	gcggctgcma	caaggttcac	tcgcactttg	accgctcgct	caagtcgggc	420
ccatacacc	tcaagtacag	ggggtccatg	tgggtttaca	agcgcttcta	caaaagaaca	480
ctcttggaag	aactgtgatt	cttaaagaat	gattgcctag	tgatgaactg	cacagt	

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

Lys	Pro	Gly	Phe	Leu	Cys	Ser	Ser	Cys	Leu	Gly	Phe	Pro	Pro	Leu	Ser
1				5				10						15	
Ala	Pro	Ala	Gly	Cys	Asp	Gly	Asp	Ser	Ala	Ala	Asp	Ser	Phe	Pro	Ala
			20					25					30		
Ala	Ile	Val	Val	Ala	Leu	Cys	Asn	Arg	Asp	Arg	Ser	Gly	Val	Pro	Pro
			35				40					45			
Val	His	Arg	Thr	Gly	Leu	Leu	Pro	Arg	Gln	Gly	His	Gly	Pro	Arg	Pro
			50			55				60					
Leu	Pro	Arg	Gln	Arg	Arg	Leu	Arg	Arg	Arg	Arg	Ile	Pro	Leu	Gly	Arg
			65			70			75					80	
Leu	Pro	Leu	Pro	Arg	Arg	Gln	Glu	Arg	Arg	Gly	Gln	Leu	Gln	Leu	Arg
				85				90					95		
Leu	Arg	Phe	Arg	Arg	Pro	Arg	Phe	Arg	Arg	His	Arg	Arg	Pro	Ser	Pro
			100					105					110		

Leu Arg Ala His Pro Pro Arg Pro Xaa Arg Xaa Arg Leu Xaa Gln Gly  
115 120 125  
Ser Leu Ala Leu  
130

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

Met Ala Ile Pro Pro Arg Thr Pro Ser Pro Pro Pro Ser Trp Ser Arg  
1 5 10 15  
Ser Val Thr Glu Thr Val Arg Gly Ser His Gln Phe Thr Val Arg Gly  
20 25 30  
Tyr Ser Leu Ala Lys Gly Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp  
35 40 45  
Val Phe Ala Val Gly Gly Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp  
50 55 60  
Gly Lys Asn Ala Glu Asp Asn Ser Asn Tyr Val Ser Val Phe Val Ala  
65 70 75 80  
Leu Ala Ser Asp Gly Ile Asp Val Arg Ala Leu Phe Glu Leu Thr Leu  
85 90 95  
Leu Asp Gln Xaa Gly Xaa Gly Cys Xaa Lys Val His Ser His Phe Asp  
100 105 110  
Arg Ser Leu Lys Phe Gly Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met  
115 120 125  
Trp Gly Tyr Lys Arg Phe Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp  
130 135 140  
Phe Leu Lys Asn Asp Cys Leu Val Met Asn Cys Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp Val Phe Ala Val Gly Gly  
1 5 10 15  
Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp Gly Lys Asn Ala Glu Asp  
20 25 30  
Asn Ser Asn Tyr Val Ser Val Phe Val Ala Leu Ala Ser Asp Gly Ile  
35 40 45  
Asp Val Arg Ala Leu Phe Glu Leu Thr Leu Leu Asp Gln Xaa Gly Xaa  
50 55 60  
Gly Cys Xaa Lys Val His Ser His Phe Asp Arg Ser Leu Lys Phe Gly  
65 70 75 80  
Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met Trp Gly Tyr Lys Arg Phe  
85 90 95  
Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp Phe Leu Lys Asn Asp Cys

100 105 110

Leu Val Met Asn Cys Thr  
115

(2) INFORMATION FOR SEQ ID NO:1405:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 540 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..540  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500186  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:  
ggcccaacct tcgctccccc ggctcccgct cgctcgcgcg cccgcctgtc cctgtctgtc 60  
tctctctctc ctgcctgagt cgcgcgccgc catgaacaac ctctcacgg attcctttga 120  
gtctcccccg cgggactctc caagagatgc agacattgaa atgggaatgc atcaagctga 180  
tgcttcagac aactttaaag atttcttgaa gaaggtcgat acaattgaga gtttaattgc 240  
aaagctgaca aaacttattga ataagtacaa gactgcgaat gaggaatcca aagcagttac 300  
aaaagcaagt tccatgaaag caattaagca gcggatggag aaagatatgt atgaagtggg 360  
gaaaattgct cgtcaggcga agacaaaaag tgaatgaatt gaaaaagaca acttatcaaa 420  
taggcaaaaa cctggatgtg gaaaagggtc tgccgtggag cgatcaagag agcaaaamtac 480  
tggagcagtg aaaaagaaat tgaaggagcg gatggatgac ttccagacct tgagagaagg 540

(2) INFORMATION FOR SEQ ID NO:1406:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 179 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..179  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500187  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:  
Ala Thr Pro Ser Val Pro Arg Pro Pro Leu Ala Ser Pro Pro Ala Cys  
1 5 10 15  
Pro Cys Leu Ser Leu Ser Leu Leu Ala Glu Ser Pro Pro Ala Met Asn  
20 25 30  
Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser Ser Arg  
35 40 45  
Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser Asp Asn  
50 55 60  
Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala  
65 70 75  
Lys Leu Thr Asn Leu Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser  
85 90 95  
Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met  
100 105 110  
Glu Lys Asp Ile Asp Glu Val Gly Lys Lys Ile Ala Arg Gln Ala Lys Thr  
115 120 125  
Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro  
130 135 140  
Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr  
145 150 155  
Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr  
165 170 175  
Leu Arg Glu

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1500188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

Met	Asn	Asn	Leu	Leu	Thr	Asp	Ser	Phe	Glu	Leu	Pro	Arg	Arg	Asp	Ser
1			5						10					15	
Ser	Arg	Arg	Asp	Ala	Asp	Ile	Glu	Met	Gly	Met	His	Gln	Ala	Asp	Ala
			20						25					30	
Asp	Asn	Leu	Lys	Asp	Phe	Leu	Lys	Lys	Val	Asp	Thr	Ile	Glu	Ser	Leu
			35					40				45			
Ile	Ala	Lys	Leu	Thr	Asn	Leu	Leu	Asn	Lys	Leu	Gln	Thr	Ala	Asn	Glu
			50					55				60			
Glu	Ser	Lys	Ala	Val	Thr	Lys	Ala	Ser	Ser	Met	Lys	Ala	Ile	Lys	Gln
			65					70				75		80	
Arg	Met	Glu	Lys	Asp	Ile	Asp	Glu	Val	Gly	Lys	Ile	Ala	Arg	Gln	Ala
			85					90						95	
Lys	Thr	Lys	Val	Asp	Glu	Leu	Glu	Lys	Asp	Asn	Leu	Ser	Asn	Arg	Gln
			100					105						110	
Lys	Pro	Gly	Cys	Gly	Lys	Gly	Ser	Ala	Val	Asp	Arg	Ser	Arg	Glu	Gln
			115					120						125	
Xaa	Thr	Gly	Ala	Val	Lys	Lys	Lys	Leu	Lys	Glu	Arg	Met	Asp	Asp	Phe
			130					135						140	
Gln	Thr	Leu	Arg	Glu											
															145

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1500189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

Met	Gly	Met	His	Gln	Ala	Asp	Ala	Ser	Asp	Asn	Leu	Lys	Asp	Phe	Leu
1				5					10					15	
Lys	Lys	Val	Asp	Thr	Ile	Glu	Ser	Leu	Ile	Ala	Lys	Leu	Thr	Asn	Leu
			20					25						30	
Leu	Asn	Lys	Leu	Gln	Thr	Ala	Asn	Glu	Glu	Ser	Lys	Ala	Val	Thr	Lys
			35					40						45	
Ala	Ser	Ser	Met	Lys	Ala	Ile	Lys	Gln	Arg	Met	Glu	Lys	Asp	Ile	Asp
			50					55				60			
Glu	Val	Gly	Lys	Ile	Ala	Arg	Gln	Ala	Lys	Thr	Lys	Val	Asp	Glu	Leu
			65					70				75		80	
Glu	Lys	Asp	Asn	Leu	Ser	Asn	Arg	Gln	Lys	Pro	Gly	Cys	Gly	Lys	Gly
			85					90						95	
Ser	Ala	Val	Asp	Arg	Ser	Arg	Glu	Gln	Xaa	Thr	Gly	Ala	Val	Lys	Lys
			100					105						110	
Lys	Leu	Lys	Glu	Arg	Met	Asp	Asp	Phe	Gln	Thr	Leu	Arg	Glu		
			115					120						125	

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1473  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
agaaagaaga agataacaca atgctcttct tcttattctt cttctactta ctcttatctt 60
catccctcga tctagttctt gccgaccgtc gtgtactcca cgaaccatto ttccctatag 120
attcgcacac accgtcacca ccataccacc caccacttcc taaactacca ttctcttcaa 180
ccactctcc atcttcatca gacccaaatg cttctccttt cttcccttta tacccttcat 240
ctccaccacc acccttccca gctctccttc cttcttttcc ggcgaaatct tcactctcaa 300
tcgtccctca cgccactaaa tcccacccta actccaaaaa actccttato gtgcctatct 360
ccgcgcgttc ctccgtgtgt ttagtgcgtc taattatcgc tttactctat tggcgaagaa 420
gcaaacgtta ccaagatctt aaacttctcg atgatagcaa aacatacacc accgacagta 480
gcgcgcgtgt ctaccctctc cctccggcaa cgcgcgctcc aacacgacgc aatcgcgagg 540
ctagaagtaa acagaggacc accacgagct ccaccaataa caacagctct gagtttcttt 600
acttaggaac aatggtgaaat caaagaggaa tggatgaaca atctcttagt aataatggat 660
caagctcaa gaaaactgaa tctccagatc tccaaccact tcctccatgt atgaacgaa 720
gtttccgttt aaatccagat gttgggtcaa tcggagaaga agatgaagaa gatgagttt 780
actctccacg tgggtcacaa agcgggcgag aaccgttaaa ccgggctcga ctctccgggtc 840
aaaaacttag atctgttaac atgacacacta tctctgtctc atcttcaagc ctctgggtcac 900
caggaagact aacatttatt agtatctctc cttcaatgag tcctaagaga tctgaaccaa 960
aacgcgcggt tatctccaca ccagaaccgg cggagttaac cgatattaga tttgttcggt 1020
ctcctgtcact gtctgttagt tctttatctg cgggagttaa aaactccgat gaagttaggt 1080
tgaatcaaat ctttagatct ccgacgggta catctctaac aacttcaccg gagaataaca 1140
aaaaagagaa ctctccatta tcactctact caacttcacc ggaacgacga ccaaatgata 1200
caccagaagc ttacttgaga tctccgtcgc attcttctgc tctcatatca ccgatagat 1260
gttttcagaa atctccggag gtcttaccgg cgtttatgag taatctcccg caagggtttgc 1320
aatctcagtt actatcttct ccttctaact ctcatggagg acaaggtttc cttaagcagt 1380
tagatgcatt acgtttctgt tcaccgtcgt cgtctctctc ttctgtttgt tcttcaccgg 1440
```

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..490  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

```
Lys Glu Glu Asp Asn Thr Met Leu Phe Phe Leu Phe Phe Phe Tyr Leu
1      5      10      15
Leu Leu Ser Ser Ser Ser Asp Leu Val Phe Ala Asp Arg Arg Val Leu
      20      25      30
His Glu Pro Phe Phe Pro Ile Asp Ser Pro Pro Pro Ser Pro Pro Ser
      35      40      45
Pro Pro Pro Leu Pro Lys Leu Pro Phe Ser Ser Thr Thr Pro Pro Ser
      50      55      60
Ser Ser Asp Pro Asn Ala Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser
      65      70      75      80
Pro Pro Pro Pro Ser Pro Ala Ser Phe Ala Ser Phe Pro Ala Asn Ile
      85      90      95
Ser Ser Leu Ile Val Pro His Ala Thr Lys Ser Pro Pro Asn Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:1411:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: per

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1500192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

Met Leu Phe Phe Leu Phe Phe Phe Tyr Leu Leu Leu Ser Ser Ser Ser  
1 5 10 15  
Asp Leu Val Phe Ala Asp Arg Arg Val Leu His Glu Pro Phe Phe Pro  
20 25 30  
Ile Asp Ser Pro Pro Pro Ser Pro Pro Pro Pro Pro Lys  
35 40 45  
Leu Pro Phe Ser Ser Thr Thr Pro Ser Ser Ser Ser Asp Pro Asn Ala  
50 55 60  
Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser Pro Pro Pro Ser Pro  
65 70 75  
Ala Ser Phe Ala Ser Phe Pro Ala Asn Ile Ser Ser Leu Ile Val Pro  
85 90 95  
His Ala Thr Lys Ser Pro Pro Asn Ser Lys Lys Leu Leu Ile Val Ala  
100 105 110  
Ile Ser Ala Val Ser Ser Ala Ala Leu Val Ala Leu Leu Ile Ala Leu  
115 120 125  
Leu Tyr Trp Arg Arg Ser Lys Arg Asn Gln Asp Leu Asn Phe Ser Asp  
130 135 140  
Asp Ser Lys Thr Tyr Thr Thr Asp Ser Ser Arg Arg Val Tyr Pro Pro  
145 150 155  
Pro Pro Ala Thr Ala Pro Pro Thr Arg Arg Asn Ala Glu Ala Arg Ser  
165 170 175  
Lys Gln Arg Thr Thr Thr Ser Ser Thr Asn Asn Asn Ser Ser Glu Phe  
180 185 190  
Leu Tyr Leu Gly Thr Met Val Asn Gln Arg Gly Ile Asp Glu Gln Ser  
195 200 205  
Leu Ser Asn Asn Gly Ser Ser Ser Arg Lys Leu Glu Ser Pro Asp Leu  
210 215 220  
Gln Pro Leu Pro Pro Leu Met Lys Arg Ser Phe Arg Leu Asn Pro Asp  
225 230 235  
Val Gly Ser Ile Gly Glu Glu Asp Glu Glu Asp Glu Phe Tyr Ser Pro  
245 250 255  
Arg Gly Ser Gln Ser Gly Arg Glu Pro Leu Asn Arg Val Gly Leu Pro  
260 265 270  
Gly Gln Asn Pro Arg Ser Val Asn Asn Asp Thr Ile Ser Cys Ser Ser  
275 280 285  
Ser Ser Ser Gly Ser Pro Gly Arg Ser Thr Phe Ile Ser Ile Ser Pro  
290 295 300  
Ser Met Ser Pro Lys Arg Ser Glu Pro Lys Pro Pro Val Ile Ser Thr  
305 310 315  
Pro Glu Pro Ala Glu Leu Thr Asp Tyr Arg Phe Val Arg Ser Pro Ser  
325 330 335  
Leu Ser Leu Ala Ser Leu Ser Ser Gly Leu Lys Asn Ser Asp Glu Val  
340 345 350  
Gly Leu Asn Gln Ile Phe Arg Ser Pro Thr Val Thr Ser Leu Thr Thr  
355 360 365  
Ser Pro Glu Asn Asn Lys Lys Glu Asn Ser Pro Leu Ser Ser Thr Ser  
370 375 380  
Thr Ser Pro Glu Arg Arg Pro Asn Asp Thr Pro Glu Ala Tyr Leu Arg  
385 390 395  
Ser Pro Ser His Ser Ser Ala Ser Thr Ser Pro Tyr Arg Cys Phe Gln  
405 410 415  
Lys Ser Pro Glu Val Leu Pro Ala Phe Met Ser Asn Leu Arg Gln Gly  
420 425 430  
Leu Gln Ser Gln Leu Leu Ser Ser Pro Ser Asn Ser His Gly Gly Gln  
435 440 445  
Gly Phe Leu Lys Gln Leu Asp Ala Leu Arg Ser Arg Ser Pro Ser Ser  
450 455 460  
Ser Ser Ser Ser Val Cys Ser Ser Pro Glu Lys Ala Ser His Lys Ser  
465 470 475 480  
Pro Val Thr Ser

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1500193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met	Val	Asn	Gln	Arg	Gly	Ile	Asp	Glu	Gln	Ser	Leu	Ser	Asn	Asn	Gly
1			5						10					15	
Ser	Ser	Ser	Arg	Lys	Leu	Glu	Ser	Pro	Asp	Leu	Gln	Pro	Leu	Pro	Pro
			20					25					30		
Leu	Met	Lys	Arg	Ser	Phe	Arg	Leu	Asn	Pro	Asp	Val	Gly	Ser	Ile	Gly
		35					40				45				
Glu	Glu	Asp	Glu	Glu	Asp	Glu	Phe	Tyr	Ser	Pro	Arg	Gly	Ser	Gln	Ser
	50				55					60					
Gly	Arg	Glu	Pro	Leu	Asn	Arg	Val	Gly	Leu	Pro	Gly	Gln	Asn	Pro	Arg
65				70					75					80	
Ser	Val	Asn	Asn	Asp	Thr	Ile	Ser	Cys	Ser	Ser	Ser	Ser	Ser	Gly	Ser
			85					90						95	
Pro	Gly	Arg	Ser	Thr	Phe	Ile	Ser	Ile	Ser	Pro	Ser	Met	Ser	Pro	Lys
			100					105					110		
Arg	Ser	Glu	Pro	Lys	Pro	Pro	Val	Ile	Ser	Thr	Pro	Glu	Pro	Ala	Glu
			115				120					125			
Leu	Thr	Asp	Tyr	Arg	Phe	Val	Arg	Ser	Pro	Ser	Leu	Ser	Leu	Ala	Ser
			130				135				140				
Leu	Ser	Ser	Gly	Leu	Lys	Asn	Ser	Asp	Glu	Val	Gly	Leu	Asn	Gln	Ile
			145			150				155				160	
Phe	Arg	Ser	Pro	Thr	Val	Thr	Ser	Leu	Thr	Ser	Pro	Glu	Asn	Asn	
			165						170				175		
Lys	Lys	Glu	Asn	Ser	Pro	Leu	Ser	Ser	Thr	Ser	Thr	Ser	Pro	Glu	Arg
			180					185					190		
Arg	Pro	Asn	Asp	Thr	Pro	Glu	Ala	Tyr	Leu	Arg	Ser	Pro	Ser	His	Ser
			195				200					205			
Ser	Ala	Ser	Thr	Ser	Pro	Tyr	Arg	Cys	Phe	Gln	Lys	Ser	Pro	Glu	Val
			210				215				220				
Leu	Pro	Ala	Phe	Met	Ser	Asn	Leu	Arg	Gln	Gly	Leu	Gln	Ser	Gln	Leu
			225			230				235				240	
Leu	Ser	Ser	Pro	Ser	Asn	Ser	His	Gly	Gly	Gln	Gly	Phe	Leu	Lys	Gln
			245					250					255		
Leu	Asp	Ala	Leu	Arg	Ser	Arg	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Val
			260				265						270		
Cys	Ser	Ser	Pro	Glu	Lys	Ala	Ser	His	Lys	Ser	Pro	Val	Thr	Ser	
			275				280						285		

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

gccatttttr gtgartgccc cctttccctt cctccccaga tccccgtccc cgttttccac 60  
ttttgcctcc gccccaattc ggataacaaa cccctccgcc tcgtcgcgtc tcctcccagc 120  
cgagccgcatc cggtagagag agggagargg agggactgar ggaggaggag ctgggttccg 180  
gtccccggcgc cccggccgnc ntgcgcgatt cgattgcagc tctcgtcccc gggcggcgtc 240  
caggatgggt cggggcaaga cgcagatgaa gcgcatagag aaccggacca gccgccaggt 300  
caccttctcc aagcgccgca acggcctgct caagaaggcg ttcgarctct ccgtcctctg 360  
cramgcccag gtgcacctcg tmtgtctctc cmcgcgcggc aagctctacg aatcgccag 420  
cggaagtrcg cagaaaacga ttgaacgtta tagaacatac acaaaggata atgtcagcaa 480  
caagacagtg cagcaggata ttg

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

Ala Ile Phe Xaa Xaa Cys Ala Leu Ser Leu Pro Pro Gln Ile Pro Val  
1 5 10 15  
Pro Val Phe His Phe Cys Leu Arg Pro Asn Ser Asp Asn Lys Pro Leu  
20 25 30  
Arg Leu Val Ala Ser Pro Pro Ser Arg Ala Asp Pro Val Glu Arg Gly  
35 40 45  
Arg Xaa Arg Asp  
50

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Pro Thr Ser  
1 5 10 15  
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala  
20 25 30  
Phe Xaa Leu Ser Val Leu Cys Xaa Ala Glu Val Ala Leu Xaa Val Phe  
35 40 45  
Ser Xaa Arg Gly Lys Leu Tyr Glu Phe Ala Ser Gly Ser Xaa Gln Lys  
50 55 60  
Thr Ile Glu Arg Tyr Arg Thr Tyr Thr Lys Asp Asn Val Ser Asn Lys  
65 70 75 80  
Thr Val Gln Gln Asp Ile  
85

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500201  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:  
Met Lys Arg Ile Glu Asn Pro Thr Ser Arg Gln Val Thr Phe Ser Lys  
1 5 10 15  
Arg Arg Asn Gly Leu Leu Lys Lys Ala Phe Xaa Leu Ser Val Leu Cys  
20 25 30  
Xaa Ala Glu Val Ala Leu Xaa Val Phe Ser Xaa Arg Gly Lys Leu Tyr  
35 40 45  
Glu Phe Ala Ser Gly Ser Xaa Gln Lys Thr Ile Glu Arg Tyr Arg Thr  
50 55 60  
Tyr Thr Lys Asp Asn Val Ser Asn Lys Thr Val Gln Gln Asp Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 892 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..892

(D) OTHER INFORMATION: / Ceres Seq. ID 1500202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

atcctcggca tcggtccgc ttgtcccttg tttaatccca aaggtttcat tttctgcagg 60  
gataacattt gtvggggtgt gtgagccggc cgccctata gaatcctgct cctgtctccg 120  
cgcccgcccc cttttcatgt tgctttccct ttctctctct tcttctctct cactctacgg 180  
gtctacctcc tatttagcgg tcggaattgc ttgtcagcat ctccccagct tcttcttctt 240  
cttccaaaccg cgtctacgctc tcttgtcccc ggtgtcgtct tggattcttc tcttctcata 300  
ggaagggaagg attggctacc gagatattcc tactagtcca gggctgtagt gcattcctgg 360  
cgcttggttt attctgcagc cataaaccagt accagttacc ccagcctgav ccggtgagga 420  
gaggagatag agagagcgag cgggagcggg gagcagagga ggagggccat ggaaggcgac 480  
agcttytccg gcggcgccat ggccaacggc ggccggcgcg gcggcagcgg cggcgggcag 540  
gtgggtggacg ggaagctgat ccacacgttc cacaggagct tctgtcaggt gcagagcctg 600  
ctggaccaga accggatgct catcagcgag atcaaacaga accacgagtc ccgcgcgcgt 660  
gntmstccgc tgctgttgct gcgggataga tatagcgctt ccacttaatt tcttctgtct 720  
ttttcggttt ctcttctctc tctggttccc gctgcttgta ttgtattgta tctagtatat 780  
atcgctgcc ctcctccgg cgggctctga gatgtacct caticctct cgtgtaccgg 840  
tctcgatgca gatgataccg gggcatgtga atgaacagag ctggtttccga cc

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1500203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

Ser Ser Ala Ser Val Pro Leu Cys Pro Cys Leu Ile Pro Lys Val Ser  
1 5 10 15  
Phe Ser Ala Gly Ile Thr Phe Xaa Gly Gly Glu Pro Ala Gly Pro  
20 25 30  
Ile Glu Ser Cys Ser Cys Ser Cys Ala Arg Pro Leu Phe Met Leu Leu  
35 40 45  
Ser Leu Ser Ser Ser Ser Ser Ser Pro His Arg Leu Thr Ser Tyr  
50 55 60

Leu Ala Val Arg Ile Ala Cys Gln His Leu Pro Ser Phe Phe Phe Phe  
65 70 75 80  
Phe Gln Pro Arg Tyr Ala Leu Leu Ser Pro Val Leu Ala Trp Ile Leu  
85 90 95  
Leu Ser Ser

(2) INFORMATION FOR SEQ ID NO:1419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

Met Glu Gly Asp Ser Xaa Ser Gly Gly Ala Met Ala Asn Gly Gly Gly  
1 5 10 15  
Gly Gly Gly Ser Gly Gly Gly Gln Val Val Asp Gly Lys Leu Ile His  
20 25 30  
Thr Phe His Arg Ser Phe Val Gln Val Gln Ser Leu Leu Asp Gln Asn  
35 40 45  
Arg Met Leu Ile Ser Glu Ile Asn Gln Asn His Glu Ser Arg Ala Arg  
50 55 60  
Xaa Xaa Pro Leu Leu Leu Arg Asp Arg Tyr Ser Ala Ser Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

Met Ala Asn Gly Gly Gly Gly Gly Ser Gly Gly Gly Gln Val Val  
1 5 10 15  
Asp Gly Lys Leu Ile His Thr Phe His Arg Ser Phe Val Gln Val Gln  
20 25 30  
Ser Leu Leu Asp Gln Asn Arg Met Leu Ile Ser Glu Ile Asn Gln Asn  
35 40 45  
His Glu Ser Arg Ala Arg Xaa Xaa Pro Leu Leu Leu Leu Arg Asp Arg  
50 55 60  
Tyr Ser Ala Ser Thr  
65

(2) INFORMATION FOR SEQ ID NO:1421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..756
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:  
ataggggtctt aagcctcggc cgttttcttc tctccacagc tcccgcgcgc gcggaaccagc 60  
gcgtcaactct accgggttcc ggcgctctcc cgtacccgta gcgcggcatc catggcggas 120  
agacggaaaag ggcctttcttg aagcagccca aggtgtttct ctgttccaag aaggccacca 180  
aggtaaacaa acctggcaag ggaggaaaca gattctggaa gaacattggc cttggtttca 240  
agacacccag ggaagccatt gaaggaacct acattgataa gaagtgtcca ttcaccggca 300  
ctgtgtctat caggggtcgc atcatcgccg gaacatgcca cagtgtcaag atgaatagg 360  
ccatcatctt tcgtaggaat tatcttcaat tcgtcaagaa gtaccagagg tatgagaaga 420  
gacactccaa catccctgcg cacattccac catgcttccg gtccaaggaa ggaagatcatg 480  
tgatcattgt ccaattcgag ccaagtgcga agactgntaa gggttcaatg ggctcaaatg 540  
attcctcgag gttcgaagag aagaaagctt tcactgccgc ttaagatcat 600  
gacgagttca tcatccatgg ccgcgaaaag ctctgtgtta taactgtttg atgctgccta 660  
ttagcctttt tcccgtaac tactatatgt gtacttggaa ttggacttga attacatcca 720  
gaacttgaaa tctgaaaaa aaatcataac cctttg

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:  
Met Asn Arg Thr Ile Ile Val Arg Arg Asn Tyr Leu His Phe Val Lys  
1 5 10  
Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His Ile  
20 25  
Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Val Ile Ile Gly Gln  
35 40  
Cys Arg Pro Val Ser Lys Thr Xaa Lys Val Gln Cys Gly Gln Ser Tyr  
50 55 60  
Ser Cys Arg Phe Glu Glu Trp Ser Ser Glu Glu Ser Phe His Cys Arg  
65 70 75 80  
Leu Arg Ser

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:  
gtgtctctta ttcttttgtg tgtttgggtg ctggaaaggg agtggaactt tacaacttct 60  
catgtcccta ttgttgggag ggttcggagt ccggtatcgg atttgccaca accagattgt 120  
tcaacactcg gaaggctcac caaatcgctc tacgcttctg ctctcctctc cagcaggtga 180  
ggaaacccta gatcgtagcc atggcggttg ccgacgggtc gcgtctcttg 240  
ctaccccgcg gtgcgtactc gcgcgcgcgc ctgcggggcg ctccccgacc tccccagcgc 300  
catacggggg ccgcgcccca ccgcgatgt cgaagaggnc cgagtctcgt gttcccaagg 360  
ttgatgcact gatgaactgg gcgcgtaagg gtcgatttg gcccatgacc ttggggctcg 420  
cctgctgcrc ggtcgagatg atgcacgcgc gcgcgtcccg ctacagactc gaccgggttc 480  
ggcgtcatct tccgtccctc gcgcgcgcmg tccgattgca tgatcgtcgc cgccagcgtc 540  
accacacaaa ttgctccagc cctcccgacc gtttatgacc aaatgcctga ccctagatgg 600  
gtttatttcaa tgggcagctg tgccaacggt ggtggatact accattactc ctactctgtt 660

gtacgtggat gtgaccgtat agtccccgtg gacatctacg tccctgggtg cccaccaact 720  
gctgaggcac tgctgtacgg tgttcttcag ctccaaaaga agatcaacag gcgtaaggat 780  
ttccttcact ggtggaccacaa gtgaagcatg cttctgctgt tgctcgcttg ctacgtttct 840  
ttgcactcga cctacctgtc ttatctgaaa taaggacgga ctttgctcgg attcacaagt 900  
ttgtttgtcc tggaaggatg tatgcccagg ttgtgacgaa catataact gtgtacttgg 960  
agtcagttcg cctgtaattg acaccagacc tgctgtgaat ctgtttttaa gcttcattg 1020  
taatacagca atac

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1500235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu  
1 5 10  
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile  
20 25 30  
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn  
35 40  
Arg Pro Thr Leu Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala  
50 55 60  
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu  
65 70 75  
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp  
85 90 95  
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu  
100 105 110  
Xaa Arg Val Arg Gly Leu Gln Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

Met Ser Leu Leu Leu Gly Gly Phe Val Arg Ile Gly Ile Cys His  
1 5 10  
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu  
20 25 30  
Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly  
35 40 45  
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val  
50 55 60  
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala  
65 70 75  
Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Xaa Arg Val Arg  
85 90 95  
Gly Leu Gln Gly  
100

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

Met	Ala	Leu	Leu	Pro	Arg	Thr	Ala	Arg	Leu	Ala	Phe	Leu	Ser	Thr	Pro	
				5					10					15		
Arg	Ser	Tyr	Ser	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Ser	Pro	Thr	Ser	Pro	
				20				25					30			
Ala	Pro	Tyr	Gly	Gly	Ala	Pro	Pro	Pro	Ala	Met	Ser	Lys	Arg	Xaa	Glu	
				35				40					45			
Phe	Val	Val	Ser	Lys	Val	Asp	Asp	Leu	Met	Asn	Trp	Ala	Arg	Lys	Gly	
				50			55						60			
Ser	Ile	Trp	Pro	Met	Thr	Phe	Gly	Leu	Ala	Cys	Cys	Xaa	Val	Glu	Met	
				65			70			75				80		
Met	His	Ala	Gly	Ala	Ser	Arg	Tyr	Asp	Phe	Asp	Arg	Val	Arg	Arg	His	
				85				90						95		
Leu	Pro	Ser	Leu	Ala	Ala	Xaa	Val	Arg	Leu	His	Asp	Arg	Arg	Arg	His	
				100				105						110		
Xaa	His	Gln	Gln	Asn	Gly	Ser	Ser	Pro	Pro	Gln	Gly	Leu				
				115			120						125			

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

aaccacacca	ctcgavcgcg	cgcgacggcc	caccgctcgc	ccgctgcccgc	cccgccgcga	60
tcgcagggat	ctctctctct	tcctccgcgtc	tcctccggcg	agccggcgcc	cagctctcgc	120
gcacggactg	cagtagcccc	tcagcgctcg	cgacctctcc	tcctccggcg	tcctctcttc	180
agaatgggaa	aagagacaca	ttttgttcgc	tttggttcaa	aggtcgcttcg	gtatcaacca	240
cgagtgatat	gcagtttagac	tatgagagtg	atccccctct	tgacgataca	aaagctattg	300
agaaggagtc	atcacttaat	gttgctgttt	ctcaactcgc	aattgacttc	gatagagact	360
ctaatttatg	tgtggagcga	ttttcccggt	caaggaaagc	atctgtagtc	tctactgggt	420
ctcttaagct	tgamctcgct	ctcggcggtg	gaggattacc	gaaggtagaa	tggtggaagt	480
atatgggaaa	gaagcatctg	ggaagacaac	actcgcgctt	catgttatta	aggaagctc	

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Pro His His Ser Xaa Ala Arg Asp Gly Pro Pro Leu Arg Arg Cys Pro  
1 5 10 15  
Pro Ala Ala Met Arg Gly Ile Leu Ser Ser Ser Ser Ala Leu Arg  
20 25 30  
Arg Ala Gly Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala  
35 40 45  
Ser Ala Thr Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg  
50 55 60  
Asp Thr Phe Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr  
65 70 75 80  
Val Asp Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr  
85 90 95  
Lys Ala Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu  
100 105 110  
Ala Ile Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser  
115 120 125  
Arg Ala Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa  
130 135 140  
Leu Ala Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr  
145 150 155 160  
Met Gly Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu  
165 170 175  
Arg Lys Leu

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

Met Arg Gly Ile Leu Ser Ser Ser Ser Ala Leu Leu Arg Arg Ala Gly  
1 5 10 15  
Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala Ser Ala Thr  
20 25 30  
Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg Asp Thr Phe  
35 40 45  
Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr Val Asp Met  
50 55 60  
Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala Ile  
65 70 75 80  
Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile Asp  
85 90 95  
Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala Arg  
100 105 110  
Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala Leu  
115 120 125  
Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly Lys  
130 135 140  
Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys Leu  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500249  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:  
Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala  
1 5 10 15  
Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile  
20 25 30  
Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala  
35 40  
Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala  
50 55 60  
Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly  
65 70 75 80  
Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys  
85 90 95  
Leu

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 749 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..749  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500250  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:  
agccgactgg gactgagaag aaacctccaa acacctacct cctacgaac tacctgccgc 60  
cggaaaaccc tagagcgctc gaccatggat ccgcagcagc cggagcctgt cagttacctc 120  
tgccgagatt gcggactgag aacaccctga agcccggaga tgcctccag tgccgtgaat 180  
gtggctaccg catcctctac aagaagcggg agccacattc acggcactgg aagacctctg 240  
aggggtgaact gcggggccacc gccacctaga gatggatccg caccacaagagc accaaggggt 300  
gggtgtgtgt gcggcgccgg cagcagcttt gtgcattcag ggaacaagggt atactgtgggg 360  
aaaccttgcatt ggggcgttga caactcgact ctggagaacc tattcagtga gcaaggacag 420  
gtgctgggat ctaagggtcat ctacgacagg gatagcgcca gggtcaagggg gtttggtttc 480  
gtcacctatg gctctgccga ggaggtcaac aatgccatat caaaccttga tggcatagac 540  
ttggaatgta gacagatccg agtcacggtt gcagaatcaa agcccaggcg tgaattttga 600  
gattttgtta aggtgggtta gagggtcaata gcgtgtgttc acaagttcta gttgtagcg 660  
tctattcttt ctctcgatg agtaacaaga agatgtgat atagagagac tggaaagtga 720  
actgctgcc acaggaagat attttccc

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500251  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:  
Met Ser Ser Ser Ala Val Asn Val Ala Thr Ala Ser Ser Thr Arg Ser

1	5	10	15
Gly Ser His Ile His Gly Thr Gly Arg Pro Leu Arg Val Asn Cys Gly	20	25	30
Pro Pro Pro Pro Arg Asp Gly Ser Ala Pro Arg Ala Pro Arg Gly Gly	35	40	45
Gly Gly Gly Gly Gly Gly Ser Ser Phe Val Asp Ser Gly Asn Lys Val	50	55	60
Tyr Val Gly Asn Leu Ala Trp Gly Val Asp Asn Ser Thr Leu Glu Asn	65	70	75
Leu Phe Ser Glu Gln Gly Gln Val Leu Asp Ala Lys Val Ile Tyr Asp	85	90	95
Arg Asp Ser Gly Arg Ser Arg Gly Phe Gly Phe Val Thr Tyr Gly Ser	100	105	110
Ala Glu Glu Val Asn Asn Ala Ile Ser Asn Leu Asp Gly Ile Asp Leu	115	120	125
Asp Gly Arg Gln Ile Arg Val Thr Val Ala Glu Ser Lys Pro Arg Arg	130	135	140
Glu Phe			
145			

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Asp Pro His Gln Glu His Gln Gly Val Val Val Ala Ala Ala	5	10	15
Ala Ala Ala Leu Ser Ile Gln Gly Thr Arg Tyr Thr Trp Gly Thr Leu	20	25	30
His Gly Ala Leu Thr Thr Arg Leu Trp Arg Thr Tyr Ser Val Ser Lys	35	40	45
Asp Arg Cys Trp Met Leu Arg Ser Ser Thr Thr Gly Ile Ala Ala Gly	50	55	60
Gln Gly Gly Leu Val Ser Ser Pro Met Ala Leu Pro Arg Arg Ser Thr	65	70	75
Met Pro Tyr Gln Thr Leu Met Ala	85		

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

ctctctctct	ctctctcttc	tcgcttctct	tctctctctc	gatctctctct	gtgacctctt	60
ctctctctcg	ttctcttttg	gtttcttctc	cgaatcgccg	gagaaaaaaa	cccttctttg	120
aatctaaaag	gactgttttt	ttgaagctat	tgactgattg	attgataaag	aagaataaag	180
attgatcgat	ctgaattttg	gttacaagat	gtcagagattc	agagacagga	cggaggattt	240
caaggattct	gttcggaagt	ccgctgtttc	gataggttat	aatgagtcta	aagtggcatc	300
acaataggcg	ctcttttatta	tacataagcc	aaaggagaga	tcgcctttca	cgaagactgc	360

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tttcaaaacg cttgatagca tcaaggagtt ggaactgttt atgttgaagc atcgaaagga 420
ttatgttgat ctgcaccgga ctacagaaca gaaaaaggat agtattgaac aagaagttgc 480
tgctttttatt aaagcttgca aagaacagat cgatatcttc ataacacgta ttagaaatga 540
agaagcaaac tccaaaggat ggcttggcct ccccgagat aacttcaatg ctgattctat 600
agcacacaaa catggagtggt ttttgattct gagtgaagaa cttcattcag tcaactgccca 660
gtttgatcag cttagagcta ctgttttcca agatattata aacagagcta tgcggagaag 720
aaaacctaaq agggctcataa aggaagctac cccaattaat acaactctgg gaaattcggg 780
gtccatagaa ccggatgaaa tccaggccca accctgtaga ttacaacaac acaactctt 840
agacagttaa acacaagccc ttcaggtaga gctaagtaat cttttagatg gtgctaggca 900
gcagaaaaat aaagtgtggg agatgtctgc attaaaccac ttgatggcaa ctcatgttct 960
gcagcaagcc caacagatag agtttcttta tgaccagcca gttgagggcaa caaagaacgt 1020
ggagcttgga aacaagagc tttctcaagc aatccaagca aacagcagca gcagaacctt 1080
tctcttactg tttttcttcg tcttacttt ctccgtcttg tcttggatt ggtacagtta 1140
aaaaaccatt ctccaacaac aacttcacac agtttttgta gattttgatt gtttaactata 1200
aattatgaaa aattggaaat gggtttaaat gttaaaacaa aaataatgag

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(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..310
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

```

Met Ser Arg Phe Arg Asp Arg Thr Glu Asp Phe Lys Asp Ser Val Arg
1      5      10      15
Lys Ser Ala Val Ser Ile Gly Tyr Asn Glu Ser Lys Val Ala Ser Thr
20      25      30
Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr
35      40      45
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe
50      55      60
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
65      70      75      80
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
85      90      95
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
100     105     110
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
115     120     125
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
130     135     140
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
145     150     155     160
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
165     170     175
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
180     185     190
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
195     200     205
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
210     215     220
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
225     230     235
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
240     245     250     255
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
260     265     270

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Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser  
275 280 285  
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu  
290 295 300  
Phe Leu Asp Trp Tyr Ser  
305 310

(2) INFORMATION FOR SEQ ID NO:1436:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 278 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1500265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr  
1 5 10 15  
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe  
20 25 30  
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu  
35 40 45  
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala  
50 55 60  
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu  
65 70 75 80  
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala  
85 90 95  
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys  
100 105 110  
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe  
115 120 125  
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val  
130 135 140  
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser  
145 150 155 160  
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln  
165 170 175  
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn  
180 185 190  
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser  
195 200 205  
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln  
210 215 220  
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu  
225 230 235 240  
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser  
245 250 255  
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu  
260 265 270  
Phe Leu Asp Trp Tyr Ser  
275

(2) INFORMATION FOR SEQ ID NO:1437:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1500266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu  
1 5 10 15  
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala  
20 25  
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu  
35 40 45  
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala  
50 55 60  
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys  
65 70 75 80  
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe  
85 90 95  
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val  
100 105 110  
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser  
115 120 125  
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln  
130 135 140  
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn  
145 150 155 160  
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser  
165 170 175  
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln  
180 185 190  
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu  
195 200 205  
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser  
210 215 220  
Arg Thr Phe Leu Leu Leu Phe Phe Val Leu Thr Phe Ser Val Leu  
225 230 235 240  
Phe Leu Asp Trp Tyr Ser  
245

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1500283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

agagtccag cgacctgtag cctctctct cgtctcgcc tcgccgcctc 60  
cgaccgcag cagcgctcc attgctctct ctccagagtc cggcggttc agtggggggc 120  
attcatggcg gggcagtcg acccgaccc ctccatcttc tcgccctccg agtgaggagt 180  
cgtggctgag gatgagatt tcgaaatcgt ccccaacatc cgcatggagc cctcacaatc 240  
gatctgcggg gatttcgggc ccttcttccc ccagattccc accaaggtgc ctctctggct 300  
cgctgtcgcg ctcaagaagc gtasaagtgc accatccgca ccccgagctg gatgactgtt 360  
gaccgcttga cacaggtatt ggaagcggaa agagagtcgc cagcagaatt cagaccatta 420  
cattccact atattgaaat ttctaagctt ctgtttgac atgtctgtga tgacatctca 480  
gatgcatacc tggtaagatc tctaattgag gatcatagag atgtcagat

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500284  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:  
Arg Val Pro Ala Thr Cys Ser Leu Leu Ser Pro Ser Thr Ser Leu Ser  
1 5 10 15  
Pro Arg Arg Leu Arg Pro Ala Ala Ala Pro Pro Leu Leu Ser Leu Thr  
20 25 30  
Ser Pro Gly Val Pro Val Gly Gly Ile His Gly Gly Ala Val Arg Pro  
35 40 45  
Ala Pro Leu His Leu Leu Ala Leu Arg Gly Gly Val Arg Gly  
50 55 60  
(2) INFORMATION FOR SEQ ID NO:1440:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500285  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:  
Glu Ser Gln Arg Pro Val Ala Ser Ser Leu Arg Arg Pro Arg Ser Arg  
1 5 10 15  
Leu Ala Ala Ser Asp Pro Gln Gln Arg Leu His Cys Ser Leu Ser Arg  
20 25 30  
Val Pro Ala Phe Gln Trp Gly Ala Phe Met Ala Gly Gln Ser Asp Pro  
35 40 45  
His Leu Ser Ile Phe Ser Pro Ser Glu Val Glu Phe Val Ala Glu Asp  
50 55 60  
Glu Ile Val Glu Ile Val Pro Asn Ile Arg Met Asp Ala Leu Asn Met  
65 70 75 80  
Ile Cys Gly Asp Phe Gly Pro Phe Phe Pro Gln Ile Pro Thr Lys Val  
85 90 95  
Pro Leu Trp Leu Ala Val Ala Leu Lys Lys Arg Xaa Ser Ala Pro Ser  
100 105 110  
Ala Pro Arg Thr Gly  
115  
(2) INFORMATION FOR SEQ ID NO:1441:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..76  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500286  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:  
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu  
1 5 10 15  
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile  
20 25 30

Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe  
35 40 45  
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys  
50 55 60  
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

tactacatgc	aatttgggaa	atgtaaattt	caatcagctt	gtatatccaa	tcattcaaaa	60
gacatacttt	caagtvgrrt	gcattccagca	gaatgccccat	tctacatgaa	aactaggaca	120
tgccaatttg	gattcagcttg	tgagttttat	caccctaaag	atcggvgctc	cttcaagang	180
rtcggaaca	ggcaggcgcc	ctaccagccg	cgaabgccc	tgacgctgcg	tgccasacga	240
catgtaccct	gcrrntgcgcg	cagargcgcc	ggcgccggga	gggtctcgcc	gctcgaracg	300
ggcaccgaag	tctacatctc	caacctggac	tttrgggttt	cgaacgacga	tatcaaggag	360
ctgttctctg	agctaggtga	tctgaagcgt	ttttcgataa	tatatgadcg	aagtrggagg	420
tctaagggaa	cagctgaagt	tg				

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Tyr	Tyr	Met	Gln	Phe	Gly	Lys	Cys	Lys	Phe	Gln	Ser	Ala	Cys	Ile	Phe
1			5					10					15		
Asn	His	Ser	Lys	Asp	Ile	Leu	Ser	Ser	Xaa	Trp	His	Pro	Ala	Glu	Cys
			20					25					30		
Pro	Phe	Tyr	Met	Lys	Thr	Arg	Thr	Cys	Gln	Phe	Gly	Ser	Ala	Cys	Glu
			35				40					45			
Phe	Tyr	His	Pro	Lys	Asp	Arg	Xaa	Ser	Phe	Lys	Xaa	Xaa	Gly	Asn	Arg
	50					55					60				
Gln	Ala	Pro	Tyr	Gln	Pro	Pro	Xaa	Ala	Leu	Thr	Leu	Arg	Gly	Xaa	Arg
	65				70					75				80	
His	Val	Pro	Cys	Xaa	Arg	Arg	Arg	Xaa	Gly	Gly	Gly	Gly	Arg	Val	Ser
			85						90				95		
Ala	Leu	Xaa	Thr	Gly	Thr	Lys	Leu	Tyr	Ile	Ser	Asn	Leu	Asp	Phe	Xaa
			100					105					110		
Val	Ser	Asn	Asp	Asp	Ile	Lys	Glu	Leu	Phe	Ser	Glu	Leu	Gly	Asp	Leu
			115				120					125			
Lys	Arg	Phe	Ser	Ile	Ile	Tyr	Xaa	Arg	Ser	Xaa	Arg	Ser	Lys	Gly	Thr
			130				135					140			
Ala	Glu	Val													
145															

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500300  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

Met	Gln	Phe	Gly	Lys	Cys	Lys	Phe	Gln	Ser	Ala	Cys	Ile	Phe	Asn	His
1				5				10				15			
Ser	Lys	Asp	Ile	Leu	Ser	Ser	Xaa	Trp	His	Pro	Ala	Glu	Cys	Pro	Phe
		20						25				30			
Tyr	Met	Lys	Thr	Arg	Thr	Cys	Gln	Phe	Gly	Ser	Ala	Cys	Glu	Phe	Tyr
		35					40					45			
His	Pro	Lys	Asp	Arg	Xaa	Ser	Phe	Lys	Xaa	Xaa	Gly	Asn	Arg	Gln	Ala
	50					55					60				
Pro	Tyr	Gln	Pro	Pro	Xaa	Ala	Leu	Thr	Leu	Arg	Gly	Xaa	Arg	His	Val
65				70						75				80	
Pro	Cys	Xaa	Arg	Arg	Arg	Xaa	Gly	Gly	Gly	Gly	Arg	Val	Ser	Ala	Leu
			85					90						95	
Xaa	Thr	Gly	Thr	Lys	Leu	Tyr	Ile	Ser	Asn	Leu	Asp	Phe	Xaa	Val	Ser
			100					105					110		
Asn	Asp	Asp	Ile	Lys	Glu	Leu	Phe	Ser	Glu	Leu	Gly	Asp	Leu	Lys	Arg
		115					120					125			
Phe	Ser	Ile	Ile	Tyr	Xaa	Arg	Ser	Xaa	Arg	Ser	Lys	Gly	Thr	Ala	Glu
		130				135						140			
Val															
145															

(2) INFORMATION FOR SEQ ID NO:1445:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

Met	Lys	Thr	Arg	Thr	Cys	Gln	Phe	Gly	Ser	Ala	Cys	Glu	Phe	Tyr	His
1				5				10				15			
Pro	Lys	Asp	Arg	Arg	Xaa	Ser	Phe	Lys	Xaa	Xaa	Gly	Asn	Arg	Gln	Ala
		20						25				30			
Tyr	Gln	Pro	Pro	Xaa	Ala	Leu	Thr	Leu	Arg	Gly	Xaa	Arg	His	Val	Pro
		35				40						45			
Cys	Xaa	Arg	Arg	Arg	Xaa	Gly	Gly	Gly	Arg	Val	Ser	Ala	Leu	Xaa	
	50					55				60					
Thr	Gly	Thr	Lys	Leu	Tyr	Ile	Ser	Asn	Leu	Asp	Phe	Xaa	Val	Ser	Asn
65				70					75					80	
Asp	Asp	Ile	Lys	Glu	Leu	Phe	Ser	Glu	Leu	Gly	Asp	Leu	Lys	Arg	Phe
			85					90					95		
Ser	Ile	Ile	Tyr	Xaa	Arg	Ser	Xaa	Arg	Ser	Lys	Gly	Thr	Ala	Glu	Val
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:1446:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 501 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1500305

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

aacttggccc	caaatcgtagg	agtggaaacc	ctactcgtcc	ccttccgcat	cgccgccc	aa	60
ttccccacc	caattcccac	tctccgctcg	acagatccat	acatgatggg	agaggccaa	g	120
gagaacgacg	ttatgagg	ggagctcctg	gactacgagg	aggacgacga	caagacggtc		180
gatggctccg	ctgctaagcc	caccggagag	gtcgcaaga	agggctacgt	cgggatccac		240
agttccgggt	tcagagactt	cctgctcaag	ccagagctgc	tccgtgctat	ccaggattgt		300
ggttttragc	atccttccga	agtgcaacac	gagtgatcc	ctcaagccat	tcttggaaatg		360
gatgtcatct	gtcaagctaa	atctgggatg	gggaaaaactg	ctgtttttgtg	cctttcatcc		420
ctccaacaaa	ttgacctgtg	tgcggggtcg	gtagcagcac	ttgtactgtg	ccacacaarg		480
gaactggctt	atcagatatg	c					

- (2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1500306

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Asn	Leu	Ala	Pro	Asn	Arg	Gly	Val	Glu	Thr	Leu	Leu	Val	Pro	Phe	Arg
1				5					10					15	
Ile	Ala	Ala	Gln	Phe	Pro	His	Pro	Ile	Pro	Thr	Leu	Arg	Ser	Thr	Asp
				20					25					30	
Pro	Tyr	Met	Met	Gly	Glu	Ala	Lys	Glu	Asn	Asp	Val	Tyr	Glu	Glu	Glu
				35			40					45			
Leu	Leu	Asp	Tyr	Glu	Glu	Asp	Asp	Asp	Lys	Thr	Val	Asp	Gly	Ser	Ala
				50			55					60			
Ala	Lys	Pro	Thr	Gly	Glu	Val	Ala	Lys	Lys	Gly	Tyr	Val	Gly	Ile	His
				70								75		80	
Ser	Ser	Gly	Phe	Arg	Asp	Phe	Leu	Leu	Lys	Pro	Glu	Leu	Leu	Arg	Ala
				85					90					95	
Ile	Gln	Asp	Cys	Gly	Phe	Xaa	His	Pro	Ser	Glu	Val	Gln	His	Glu	Cys
				100					105					110	
Ile	Pro	Gln	Ala	Ile	Leu	Gly	Met	Asp	Val	Ile	Cys	Gln	Ala	Lys	Ser
				115			120					125			
Gly	Met	Gly	Lys	Thr	Ala	Val	Phe	Val	Leu	Ser	Ser	Leu	Gln	Gln	Ile
				130			135					140			
Asp	Pro	Val	Ala	Gly	Gln	Val	Ala	Ala	Leu	Val	Leu	Cys	His	Thr	Xaa
				145			150			155				160	
Glu	Leu	Ala	Tyr	Gln	Ile	Cys									
				165											

- (2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Met Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu  
1 5 10 15  
Asp Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys  
20 25 30  
Pro Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser  
35 40 45  
Gly Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln  
50 55 60  
Asp Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro  
65 70 75 80  
Gln Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met  
85 90 95  
Gly Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro  
100 105 110  
Val Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu  
115 120 125  
Ala Tyr Gln Ile Cys  
130

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu Asp  
1 5 10 15  
Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys Pro  
20 25 30  
Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser Gly  
35 40 45  
Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln Asp  
50 55 60  
Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln  
65 70 75 80  
Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met Gly  
85 90 95  
Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro Val  
100 105 110  
Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu Ala  
115 120 125  
Tyr Gln Ile Cys  
130

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1500313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

atcatcatcg	tattcaccgt	tgtcctttct	ttcattgaca	cttgccagtt	tacatcgaca	60
aacaaaagaa	atcagaatgg	attttccagg	gagattcttt	gtcatcttcg	ttaccttctt	120
ctttctccct	ctctctgtctt	cagctggggag	ctacgattct	ggttcggggtc	tcgagtcact	180
cgctcgccgg	atgctctcatt	cagccaagga	tcttgagttc	tctgagtgga	tgagaggaat	240
taggagaaa	attcatgaga	acccagagac	agggtttcag	gagttcaaaa	cgagtcact	300
cgctcgagac	gagcttgact	cgcttgaggt	gaagtataag	tatcctgtgg	ccaagactgg	360
cgctcgtcct	tggtacggat	cctgttcgaa	acctgttttc	ggacttagag	ccgacatgga	420
cgcaacttgc	gttacaggga	atttgaggaa	tgggaatcga	aaagataagt	agatggaaag	480
atgcatgtgt	gttggtatga	tactcatggt	gctatgcttc	tgtgtgctgc	taagcttctt	540
caaacacaaa	aaacactcat	caagggggaca	gtaaaaactg	tgtttcaacc	agccgaggaa	600
ggttatgcag	gtgcttatga	aatgctaaaa	gacgagatcc	tagacgactt	msatgggata	660
ctcagtggtc	atgtctttcc	atcgatccca	tcaggtggta	tgtgttctag	gcctggggac	720
gtctctgcag	gtgcaggatt	gtttacagtc	acgggttcacg	gtcaaggtag	ccacgcgagc	780
acaccgcact	tcctctaara	cccggttctt	gcagcttctt	ccgctgtgtt	tgccttgcaa	840
acagattggtt	acagatgggc	ggatccactc	gaagctgggtg	tggttacagt	tggaatattt	900
gaaggaggtc	atgctcaaaa	cgtaataccg	cagagtgcgga	aatttggagg	tactttcaga	960
magcttaagc	aacgatgggc	ttctatttat	ccaaagacgg	atcaaaagaga	tttcagaggc	1020
acaagcatcg	gtataccgat	gcaaaagcaga	agtaaaactc	gaagagaaaa	agccgctcgt	1080
tcacmccggg	aatgaataac	gacgagggct	tatacbgagc	acggtaaaaa	agtagcggaa	1140
cgcatgattg	gaaagaataa	cttccatgat	ttccccggta	caatggggag	agagagatttc	1200
agctttcttc	actcaaaaaga	cntaaaggctg	cgattttcgt	gctgggggag	aaagaatgaga	1260
cgctagggcg	tggttaagccg	cttcaactcg	cttacttctt	tgttgatgaa	gaagctctctc	1320
ctgttggggc	tgctcttcac	gcagctatgg	ccgtttctta	tttgagacga	catgscycta	1380
ggcatgaaga	agaggttaag	agtgaattat	agaaggtgtt	gggagaaaa	cagcttatat	1440
tagtcatcat	ctatttgat	ttgaacttga	aagttaggtg	aggttaggtt	tcggggtggg	1500
agaatgtttt	gttaatagtc	acagaaaaac	aaccactttc			

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

Met	His	Ala	Cys	Gly	His	Asp	Thr	His	Val	Ala	Met	Leu	Leu	Gly	Ala
1			5						10					15	
Ala	Lys	Leu	Leu	Gln	Thr	Thr	Lys	His	Leu	Ile	Lys	Gly	Thr	Val	Lys
			20					25					30		
Leu	Val	Phe	Gln	Pro	Gly	Glu	Glu	Gly	Tyr	Ala	Gly	Ala	Tyr	Glu	Met
			35				40					45			
Leu	Lys	Asp	Glu	Ile	Leu	Asp	Asp	Xaa	Xaa	Gly	Ile	Leu	Ser	Val	His
			50			55					60				
Val	Phe	Pro	Ser	Ile	Pro	Ser	Gly	Gly	Ile	Gly	Ser	Arg	Pro	Gly	Thr
			65		70			75					80		
Val	Leu	Ala	Gly	Ala	Gly	Leu	Phe	Thr	Val	Thr	Val	His	Gly	Gln	Gly
			85					90					95		
Ser	His	Ala	Ala	Thr	Pro	His	Phe	Ser	Lys	Xaa	Pro	Val	Leu	Ala	Ala
			100				105						110		
Ser	Ser	Ala	Val	Val	Ala	Leu	Gln	Gln	Ile	Val	Ser	Arg	Glu	Leu	Asp
			115			120						125			
Pro	Leu	Glu	Ala	Gly	Val	Val	Thr	Val	Gly	Tyr	Ile	Glu	Gly	Gly	His
			130			135					140				
Ala	Gln	Asn	Val	Ile	Pro	Gln	Ser	Ala	Lys	Phe	Gly	Gly	Thr	Phe	Arg
			145		150				155					160	
Xaa	Leu	Lys	Gln	Arg	Trp	Ala	Ser	Ile	Tyr	Pro	Lys	Thr	Asp	Gln	Arg
			165					170						175	

Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser Lys  
180 185 190  
Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg  
195 200

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

Met Leu Leu Gly Ala Ala Lys Leu Leu Gln Thr Thr Lys His Leu Ile  
1 5 10 15  
Lys Gly Thr Val Lys Leu Val Phe Gln Pro Gly Glu Gly Tyr Ala  
20 25 30  
Gly Ala Tyr Glu Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly  
35 40 45  
Ile Leu Ser Val His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly  
50 55 60  
Ser Arg Pro Gly Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr  
65 70 75 80  
Val His Gly Gln Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa  
85 90 95  
Pro Val Leu Ala Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val  
100 105 110  
Ser Arg Glu Leu Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr  
115 120 125  
Ile Glu Gly Gly His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe  
130 135 140  
Gly Gly Thr Phe Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro  
145 150 155 160  
Lys Thr Asp Gln Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met  
165 170 175  
Gln Ser Arg Ser Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg  
180 185 190

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly Ile Leu Ser Val  
1 5 10 15  
His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly Ser Arg Pro Gly  
20 25 30  
Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr Val His Gly Gln  
35 40 45  
Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa Pro Val Leu Ala

50	55	60
Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val Ser Arg Glu Leu		
65	70	75
Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr Ile Glu Gly Gly		80
	85	90
His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe Gly Gly Thr Phe		95
	100	105
Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro Lys Thr Asp Gln		110
	115	120
Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser		125
	130	135
Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

gcttgctgcg	taacaatcag	tgaactgaac	accttcgcgc	tcccgggtctc	ctccctgcgc	60
gggtgctgaag	aaccttcgcca	tcccgcggaac	tggatcgatc	tgccgcgcaac	tctgaaaatc	120
catccgatcc	atctctgtcg	tcacaagtcta	ctcccgcgatg	gacattattt	accaggacag	180
cagttgtctt	gccttagagc	aggcgctaca	tgatgaagcg	gtgggaccaa	tcgacctacc	240
tttcatgctt	ctcaggcgcca	tcacaaaaga	ttctctgat	actcaactaa	ttggcagggg	300
tgggttcgga	gaggtttaca	aggtatgcat	ggggatttg	gcacctgaat	ttctgagcac	360
caatgcaatc	acattcaagg	cggacatata	cagtctargt	gttataatca	ctgagattct	420
gacgggggca	taargratgc	accartgttg	acaaaggkcg	ttgaaarctg	gacggacatg	480
tttcagacat	taggaagc					

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Ala Cys Ser Leu Thr Ile Ser Glu Leu Asn Thr Phe Arg Leu Pro Val		
1	5	10
Ser Ser Leu Pro Gly Ala Glu Glu Pro Cys His Pro Arg Asn Trp Ile		15
	20	25
Asp Leu Pro Pro Thr Leu Lys Ile His Pro Ile His Leu Cys Arg Pro		30
	35	40
Ser Leu Leu Pro Asp Gly His Tyr Leu Pro Gly Gln Gln Leu Ser Cys		45
	50	55
Pro Arg Ala Gly Ala Thr		60
65	70	

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500323  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:  
Met Asp Ile Ile Tyr Gln Asp Ser Ser Cys Leu Ala Leu Glu Gln Ala  
1 5 10 15  
Leu His Asp Glu Gly Val Gly Pro Ile Asp Leu Pro Phe Met Leu Leu  
20 25 30  
Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile Gly Arg Gly  
35 40 45  
Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu Ala Pro Glu  
50 55 60  
Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile Tyr Ser Leu  
65 70 75 80  
Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500324  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:  
Met Leu Leu Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile  
1 5 10 15  
Gly Arg Gly Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu  
20 25 30  
Ala Pro Glu Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile  
35 40 45  
Tyr Ser Leu Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 368 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..368  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500367  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:  
tcacactctg cccagctaag ctaagctccc tccgtccatc ggcatggcga ctaccactac 60  
taccatctct ctctctctcc tcgtcgcagc cacagccgtc tcggcgggccg acctctccgt 120  
gtaccacaac gtgcacccgc cgtccccgtc cccgctcgag tccatcatcg cgtcgcgccg 180  
cgccgacgac gcgcgggtcc tcttctctct atccaaaggc gcctcgtccg gcggcgctcac 240  
ctccgctccc gtcgcctcgc gccagactcc gcmctcgtag gtmgtccgcg cggggctcgg 300  
caccgccgtc cagcagctgc tctcgcgcct cgacaccagg gccgaagcca cctggctcga 360  
ctgcgcgc

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..122
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1500368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

Thr Leu Cys Pro Ala Lys Leu Ser Ser Leu Arg Pro Ser Ala Trp Arg  
1 5 10 15  
Leu Pro Leu Leu Pro Ser Ser Ser Ser Ser Ser Gln Pro Gln Pro  
20 25 30  
Ser Arg Arg Pro Thr Ser Pro Cys Thr Thr Thr Cys Thr Arg Arg Pro  
35 40 45  
Arg Pro Arg Ser Ser Pro Ser Ser Arg Ser Pro Ala Pro Thr Thr Arg  
50 55 60  
Gly Ser Ser Ser Ser His Pro Arg Arg Pro Arg Pro Ala Ala Ser Pro  
65 70 75 80  
Pro Leu Pro Ser Pro Pro Ala Arg Leu Arg Xaa Arg Thr Xaa Ser Ala  
85 90 95  
Arg Gly Ser Ala Pro Arg Ser Ser Ser Cys Ser Ser Arg Ser Thr Pro  
100 105 110  
Ala Pro Thr Pro Pro Gly Arg Thr Ala Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..108
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1500369
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

Met Ala Thr Thr Thr Thr Ile Leu Leu Leu Leu Leu Val Ala Ala  
1 5 10 15  
Thr Ala Val Ser Ala Ala Asp Leu Ser Val Tyr His Asn Val His Pro  
20 25 30  
Pro Ser Pro Ser Pro Leu Glu Ser Ile Ile Ala Leu Ala Arg Ala Asp  
35 40 45  
Asp Ala Arg Leu Leu Phe Leu Ser Ser Lys Ala Ala Ser Ser Gly Gly  
50 55 60  
Val Thr Ser Ala Pro Val Ala Ser Gly Gln Thr Pro Xaa Ser Tyr Xaa  
65 70 75 80  
Val Arg Ala Gly Leu Gly Thr Pro Val Gln Gln Leu Leu Leu Ala Leu  
85 90 95  
Asp Thr Ser Ala Asp Ala Thr Trp Ser His Cys Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 921 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1500370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

atcctctagc	tctctctctc	tctctctctc	cacacacaca	cacagtcaca	gacaccacct	60
tcacttagac	tgtgtctagta	ggtagcgccg	gcgtaatgga	gcagagagctc	agccttgagc	120
tcaccctctc	ccaccctctg	gcctcgccgc	cggagccacc	gggctacttc	gtctgcatgt	180
actgcgacgc	caagtctctc	agctcgccag	ctctcggtgg	ccaccagaac	gcgcacaagt	240
acgagcgcas	ctggccaagc	gcccagaggga	gtagccgcgc	gccctgcgcg	cgcacggggc	300
ggccgcgccc	gcmacggggc	cyccggaggga	cgacgmcgyc	gcccgcatgg	gctctcgcca	360
tgtcccccgc	agccccaagc	gcacgggtac	cggagtcgtc	gtcgttgaag	atgagagtgc	420
aaccaggatg	atgggacaag	cagaaggctc	ctgctgctga	tgacgasstc	cgcgcaccgc	480
gtcgtcgagc	aacatgaaga	ggctgtcgga	gtacggctac	ggcgtcgagg	agctggatct	540
ctccctcagg	ctttgatggg	ttctctcttc	tcctccacyn	nnanataaaa	ttcgcgccctg	600
tngtcnagat	aattcgatct	ttgtggtcag	tgcgaatcat	tggttcgcgt	gcgtgggtatc	660
tcagtgtctg	atccgtcact	ttcttctcca	tgtagttgtt	gtgcagttat	attcttccat	720
ccgtagtcgg	aaectatcgg	caagaactat	tgtcggccca	tcctgctatc	caaaagggcgt	780
gggtatttgt	gtgctctttt	cggttttctg	ccttgagctc	tcittgtgcg	atctaaaattc	840
gcagcttgtt	ttttccaaaa	cggcggaaac	agttttgcgc	caatttcggt	tggacctttt	900
tcaagtgact	ctaaattggg	c				

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

Met	Glu	Gln	Glu	Leu	Ser	Leu	Glu	Leu	Thr	Leu	Leu	His	Pro	Ser	Ala
1			5						10					15	
Ser	Pro	Pro	Glu	Pro	Pro	Gly	Tyr	Phe	Val	Cys	Met	Tyr	Cys	Asp	Arg
			20						25				30		
Lys	Phe	Phe	Ser	Ser	Gln	Ala	Leu	Gly	Gly	His	Gln	Asn	Ala	His	Lys
			35					40				45			
Tyr	Glu	Arg	Xaa	Trp	Pro	Ser	Ser	Ala	Ala	Gly	Arg				
			50				55								

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1500372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

Met	Gly	Ser	Arg	Asp	Val	Pro	Ala	Arg	Pro	Gln	Gly	Thr	Gly	Thr	Gly
1				5					10					15	
Val	Val	Val	Val	Glu	Asp	Glu	Ser	Ala	Thr	Arg	Met	Met	Gly	Gln	Ala
				20				25					30		
Glu	Gly	Ser	Cys	Cys											
				35											

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..50  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500373  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:  
Met Thr Xaa Ser Arg Asp Arg Val Val Glu Gln His Glu Glu Val Val  
1          5          10          15  
Gly Val Arg Leu Arg Arg Arg Gly Ala Gly Ser Leu Pro Gln Ala Leu  
          20          25          30  
Ile Gly Ser Ser Ser Ser Ser Xaa Xaa Xaa Tyr Asn Ser Pro Arg Xaa  
          35          40          45  
Xaa Arg  
50

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 380 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..380  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500374  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

aaaatagagt tcacacgcac aaccgccgcg cgacgcgg gatctcgata gactctggct 60  
gccgcggaaa gcggaaagaa gccaggggatc gtggccaaga tgcagatctt cgtgaagacg 120  
ctgtcgtcga caaggacgat cacgtggag gttgagcctt cggacacggt gccggacgtr 180  
aaggccaagg tgtacagatc ggaggcgctc ccgtacacct tggccttcca gaactagagc 240  
gcggcagata gctaggtcgc ttggtactcc cccatttgc aatgacaaa cgttttacc 300  
ttcttagata tgcacttatg tctagatata tagattatct tatacttttd wcgttctkkt 360  
ttatttatcg tgttttagtt

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 50 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..50  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500375  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

Asn Arg Val His Thr His Asn Pro Pro Pro His Ala Gly Ile Ser Ile  
1          5          10          15  
Asp Ser Gly Cys Arg Gly Lys Arg Lys Glu Gly Arg Asp Arg Gly Gln  
          20          25          30  
Asp Ala Asp Leu Arg Glu Asp Ala Val Val Asp Lys Asp Asp His Ala  
          35          40          45  
Gly Gly  
50

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 45 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..45  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Ser	Ser	Thr	Arg	Thr	Ile	Thr	Leu
1															
				5					10					15	
Glu	Val	Glu	Pro	Ser	Asp	Thr	Val	Ala	Asp	Xaa	Lys	Ala	Lys	Val	Tyr
				20					25				30		
Glu	Ser	Glu	Gly	Val	Pro	Tyr	Thr	Leu	Ala	Phe	Gln	Asn			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:1468:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..33  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

Met	Thr	Lys	Arg	Phe	Tyr	Leu	Ser	Arg	Tyr	Ala	Leu	Met	Ser	Arg	Tyr
1															
				5					10					15	
Ile	Asp	Tyr	Leu	Ile	Leu	Xaa	Xaa	Phe	Xaa	Phe	Ile	Tyr	Arg	Val	Leu
				20				25				30			
Val															

(2) INFORMATION FOR SEQ ID NO:1469:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1326 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1326  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

aaaaaaccaa	atcgaagatc	tttgaagtt	tccttttttc	cgaatctga	gcttgggtat	60
tggttgataa	gctcttcgga	gattgagatt	gaggattttg	ataggtgagg	agattgaaa	120
atttggattt	ttgggcgcca	aaaatgggtga	tgcagacgga	agctaggggt	ggtgtgagct	180
caggacatgg	cgtagctctg	tcttctctac	gtttaacgca	ggaccagaga	tcacatatcg	240
aatcgcgctg	gcagctctta	gccggaggac	tcgctggtgc	ttttagcaag	actgttactg	300
ctctctctac	tcgtctcacc	attctcttcc	aggtgcgaag	tatgcacaca	aatgtctgac	360
ctttaagaaa	gcccaagcata	ttacacgagg	cttcacggat	attgaatgaa	gaaggattga	420
aagctttttg	gaaaggggat	ctagtactta	ttgtctcacc	gcttccatat	tcttctgtta	480
atttctacgc	atatgaacac	tacaagaagt	tcattgtatat	ggttactggg	atggaataatc	540
acaagggagag	tataagttca	aacctttttg	tacatttttg	agccggtgtg	ttggctggaa	600
tcacagctgc	tctctgccact	tatccacttg	attcttgttag	aactcgtctt	gctgctcaga	660
caaaagtaat	ctactactcg	ggatctctggc	atactctcgc	ctctattaca	accgatgaag	720
gtatctttggg	ctcttcaaga	gcctataggaa	caacgcttgt	gggtgttggg	cttagtattg	780
ccattagcct	tctctgtgat	gaatcattga	gatcttattg	gaggtcaact	agggcccatg	840
atttccccat	catggctcagt	tctgtttgtg	gaagctcttc	aggaatagca	tcttcaacag	900
ctacgtttcc	attggtactg	gtgagaagaa	cgaagcagct	ggaaggaata	ggcgggagg	960
cggtagtgta	caagacaggt	ttgttagcca	cattaaagcg	tattgttcaa	acggaaggag	1020
cgagaggcct	gtacagagga	attcttccag	agtactacaa	agtggtacct	ggtgtaggga	1080
tttgcttcac	gaacctacag	gaactcaagc	tttacttcaa	ggatctttct	tcgaattctat	1140
aacgggtttaa	aaggttggtga	gatttggtta	ggtctatttt	tggtgagagg	aaaaaaactg	1200

taaaaaccaa acagcggaata atgataatgt atacgaaatg tagaattata tatgtagttg 1260  
ttggtatgtag cttatcacgag attaacattt gtattggtac aatccttttc catgtttaca 1320  
tggctt

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..332

(D) OTHER INFORMATION: / Ceres Seq. ID 1500388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Met Val Met Gln Thr Glu Ala Arg Val Gly Val Ser Ser Gly His Gly  
1 5 10 15  
Val Ala Ser Ser Ser His Arg Leu Thr Gln Asp Gln Arg Ser His Ile  
20 25 30  
Glu Ser Ala Ser Gln Leu Leu Ala Gly Gly Leu Ala Gly Ala Phe Ser  
35 40 45  
Lys Thr Cys Thr Ala Pro Leu Ser Arg Leu Thr Ile Leu Phe Gln Val  
50 55 60  
Gln Gly Met His Thr Asn Ala Ala Ala Leu Arg Lys Pro Ser Ile Leu  
65 70 75  
His Glu Ala Ser Arg Ile Leu Asn Glu Gly Gly Leu Lys Ala Phe Trp  
85 90 95  
Lys Gly Asn Leu Val Thr Ile Ala His Arg Leu Pro Tyr Ser Ser Val  
100 105 110  
Asn Phe Tyr Ala Tyr Glu His Tyr Lys Lys Phe Met Tyr Met Val Thr  
115 120 125  
Gly Met Glu Asn His Lys Glu Ser Ile Ser Ser Asn Leu Phe Val His  
130 135 140  
Phe Val Ala Gly Gly Leu Ala Gly Ile Thr Ala Ala Ser Ala Thr Tyr  
145 150 155  
Pro Leu Asp Leu Val Arg Thr Arg Leu Ala Ala Gln Thr Lys Val Ile  
165 170 175  
Tyr Tyr Ser Gly Ile Trp His Thr Leu Arg Ser Ile Thr Thr Asp Glu  
180 185 190  
Gly Ile Leu Gly Leu Tyr Lys Gly Leu Gly Thr Thr Leu Val Gly Val  
195 200 205  
Gly Pro Ser Ile Ala Ile Ser Phe Ser Val Tyr Glu Ser Leu Arg Ser  
210 215 220  
Tyr Trp Arg Ser Thr Arg Pro His Asp Ser Pro Ile Met Val Ser Leu  
225 230 235  
Ala Cys Gly Ser Leu Ser Gly Ile Ala Ser Ser Thr Ala Thr Phe Pro  
245 250 255  
Leu Asp Leu Val Arg Arg Thr Lys Gln Leu Glu Gly Ile Gly Gly Arg  
260 265 270  
Ala Val Val Tyr Lys Thr Gly Leu Leu Gly Thr Leu Lys Arg Ile Val  
275 280 285  
Gln Thr Glu Gly Ala Arg Gly Leu Tyr Arg Gly Ile Leu Pro Glu Tyr  
290 295 300  
Tyr Lys Val Val Pro Gly Val Gly Ile Cys Phe Met Thr Tyr Glu Thr  
305 310 315 320  
Leu Lys Leu Tyr Phe Lys Asp Leu Ser Ser Asn Leu  
325 330

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..330  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500389  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly	Val	Ala
1				5				10						15	
Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile	Glu	Ser
			20					25					30		
Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser	Lys	Thr
		35				40					45				
Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val	Gln	Gly
	50					55				60					
Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu	His	Glu
65			70						75					80	
Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp	Lys	Gly
		85						90						95	
Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val	Asn	Phe
		100						105					110		
Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr	Gly	Met
	115							120				125			
Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His	Phe	Val
	130					135					140				
Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr	Pro	Leu
145			150						155					160	
Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile	Tyr	Tyr
		165						170						175	
Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu	Gly	Ile
	180							185					190		
Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val	Gly	Pro
	195					200						205			
Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser	Tyr	Trp
	210					215					220				
Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu	Ala	Cys
225					230					235					
Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro	Leu	Asp
		245						250					255		
Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg	Ala	Val
	260							265					270		
Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val	Gln	Thr
	275							280					285		
Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr	Tyr	Lys
	290					295					300				
Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr	Leu	Lys
305					310					315				320	
Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu						
		325						330							

(2) INFORMATION FOR SEQ ID NO:1472:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 266 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..266  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

Met His Thr Asn Ala Ala Leu Arg Lys Pro Ser Ile Leu His Glu  
1 5 10 15  
Ala Ser Arg Ile Leu Asn Glu Gly Leu Lys Ala Phe Trp Lys Gly  
20 25 30  
Asn Leu Val Thr Ile Ala His Arg Leu Pro Tyr Ser Ser Val Asn Phe  
35 40 45  
Tyr Ala Tyr Glu His Tyr Lys Lys Phe Met Tyr Met Val Thr Gly Met  
50 55 60  
Glu Asn His Lys Glu Ser Ile Ser Ser Asn Leu Phe Val His Phe Val  
65 70 75 80  
Ala Gly Gly Leu Ala Gly Ile Thr Ala Ala Ser Ala Thr Tyr Pro Leu  
85 90 95  
Asp Leu Val Arg Thr Arg Leu Ala Ala Gln Thr Lys Val Ile Tyr Tyr  
100 105 110  
Ser Gly Ile Trp His Thr Leu Arg Ser Ile Thr Thr Asp Glu Gly Ile  
115 120 125  
Leu Gly Leu Tyr Lys Gly Leu Gly Thr Thr Leu Val Gly Val Gly Pro  
130 135 140  
Ser Ile Ala Ile Ser Phe Ser Val Tyr Glu Ser Leu Arg Ser Tyr Trp  
145 150 155 160  
Arg Ser Thr Arg Pro His Asp Ser Pro Ile Met Val Ser Leu Ala Cys  
165 170 175  
Gly Ser Leu Ser Gly Ile Ala Ser Ser Thr Ala Thr Phe Pro Leu Asp  
180 185 190  
Leu Val Arg Arg Thr Lys Gln Leu Glu Gly Ile Gly Gly Arg Ala Val  
195 200 205  
Val Tyr Lys Thr Gly Leu Leu Gly Thr Leu Lys Arg Ile Val Gln Thr  
210 215 220  
Glu Gly Ala Arg Gly Leu Tyr Arg Gly Ile Leu Pro Glu Tyr Tyr Lys  
225 230 235 240  
Val Val Pro Gly Val Gly Ile Cys Phe Met Thr Tyr Glu Thr Leu Lys  
245 250 255  
Leu Tyr Phe Lys Asp Leu Ser Ser Asn Leu  
260 265

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686

(D) OTHER INFORMATION: / Ceres Seq. ID 1500391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

tcccaagtga taatgcaagt aatgaaatgg aaaggcgctc accccggaag cgaaagtgttc 60  
aggaaacttcc agctgattgt aagggttccag aaaaagacaa acagcaatcg gagttagcaa 120  
tgacagggtga tgttactcca tcagcaaaata gactgcggtc gccgccttca ccaagatctg 180  
taatgccttcc tcttccacca aagaccatcg caccaccgctc tcttaagacc atgtctcttc 240  
catcatcaaa aagcatgctt cctccaccac cagttcttaa gaccatgtct cctctaacat 300  
caaaaagcat gcttcttcca ccaccgcgat ttactatgac aactcaacct tcaagattac 360  
aggacaacca catcagtgta aagaaaccaa atccagttcc agatacgtta ataaagtctga 420  
tggaatatgg agacgatgaa gacgatgatg acgatcctga tgagccattg acaactagat 480  
cgtgacagtg tattagatta cagaaccttc ttatctggca acaaaatgtc aatttgtgtt 540  
tgtaacaata gaaagaatgg ttggtctctt actgatttgg aacttcattg cctaaggcta 600  
ttagttaaata attaaagaca ttactacttt gttttgcaag gcactgctcg ttttgttgta 660  
ttctctatca ttaatacata atggtt

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..160  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500392  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:  
Pro Ser Asp Asn Ala Ser Asn Glu Met Glu Arg Arg Pro Pro Arg Lys  
1 5 10 15  
Arg Lys Phe Gln Glu Leu Pro Ala Asp Cys Lys Val Pro Glu Lys Asp  
20 25 30  
Lys Gln Gln Ser Glu Leu Ala Met Thr Gly Asp Val Thr Pro Ser Ala  
35 40 45  
Asn Arg Val Arg Ser Pro Pro Ser Pro Arg Ser Val Met Pro Pro Pro  
50 55 60  
Pro Pro Lys Thr Ile Ala Pro Pro Pro Ser Lys Thr Met Ser Pro Pro  
65 70 75 80  
Ser Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Ser Lys Thr Met Ser  
85 90 95  
Pro Leu Thr Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Phe Thr Leu  
100 105 110  
Thr Thr Gln Pro Ser Arg Leu Gln Asp Asn His Ile Ser Val Lys Lys  
115 120 125  
Pro Asn Pro Val Pro Asp Thr Leu Ile Lys Leu Met Glu Tyr Gly Asp  
130 135 140  
Asp Glu Asp Asp Asp Asp Asp Pro Asp Glu Pro Leu Thr Thr Arg Ser  
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1475:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..152  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500393  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:  
Met Glu Arg Arg Pro Pro Arg Lys Arg Lys Phe Gln Glu Leu Pro Ala  
1 5 10 15  
Asp Cys Lys Val Pro Glu Lys Asp Lys Gln Gln Ser Glu Leu Ala Met  
20 25 30  
Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro Ser  
35 40 45  
Pro Arg Ser Val Met Pro Pro Pro Pro Pro Lys Thr Ile Ala Pro Pro  
50 55 60  
Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro Pro  
65 70 75 80  
Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met Leu  
85 90 95  
Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu Gln  
100 105 110  
Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr Leu  
115 120 125  
Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp Pro

130 135 140  
Asp Glu Pro Leu Thr Thr Arg Ser  
145 150  
(2) INFORMATION FOR SEQ ID NO:1476:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..121  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500394  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:  
Met Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro  
1 5 10 15  
Ser Pro Arg Ser Val Met Pro Pro Pro Pro Lys Thr Ile Ala Pro  
20 25 30  
Pro Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro  
35 40 45  
Pro Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met  
50 55 60  
Leu Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu  
65 70 75 80  
Gln Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr  
85 90 95  
Leu Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp  
100 105 110  
Pro Asp Glu Pro Leu Thr Thr Arg Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:1477:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 441 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..441  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500395  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:  
ccagacttta ttcccaaaaa accaaaaataa tcgccaccgc tctccgcacg gaaccgaagc 60  
ggcggcgatg gcggcgagaga agccggctcc cgtgcgcgtg ctctactgcg gcgtctgcgg 120  
ctctccggcc gagtactgcg agttcggccc cgacttcgag cgctgcaagc cctggctgcg 180  
cgcgatgns ccggcgtcta ccccgacgaa ctgtcgcgcg cmtctctctc ctcatccggm 240  
ggcggcgaca aggacgtcga cagggtcggg gatcgctccc agggcgctcg gatctccgac 300  
ggctccacca gcgcgcgagg gatgcttcgc cgtetaagcc ccaagaggcg aaacgcctgc 360  
mtgggtgtaa gctcaagaaa aaggagaagc aagaagtggc catlgagaag attgtccgta 420  
acaagcgcaa atgtgttact g

(2) INFORMATION FOR SEQ ID NO:1478:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1500396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

Gln Thr Leu Phe Pro Lys Asn Gln Asn Arg His Arg Ser Pro His  
1 5 10 15  
Gly Thr Glu Ala Ala Ala Met Ala Ala Glu Lys Pro Ala Pro Val Arg  
20 25 30  
Val Leu Tyr Cys Gly Val Cys Gly Leu Pro Ala Glu Tyr Cys Glu Phe  
35 40 45  
Gly Pro Asp Phe Glu Arg Cys Lys Pro Trp Leu Arg Ala His Xaa Pro  
50 55 60  
Ala Ser Thr Pro Thr Asn Leu Ser Pro Xaa Pro Pro His Pro Xaa  
65 70 75 80  
Ala Ala Thr Arg Thr Ser Thr Gly Ser Gly Ile Ala Ser Arg Ala Ser  
85 90 95  
Gly Ser Pro Thr Ala Pro Pro Ala Pro Gln Gly Cys Phe Arg Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

Arg Leu Tyr Ser Pro Lys Thr Lys Ile Ala Thr Ala Leu Arg Thr  
1 5 10 15  
Glu Pro Lys Arg Arg Arg Trp Arg Arg Arg Ser Arg Leu Pro Cys Ala  
20 25 30  
Cys Ser Thr Ala Ala Ser Ala Ala Ser Arg Pro Ser Thr Ala Ser Ser  
35 40 45  
Ala Pro Thr Ser Ser Ala Ala Ser Pro Gly Cys Ala Arg Met Xaa Arg  
50 55 60  
Arg Leu Pro Arg Arg Thr Cys Arg Arg Xaa Leu Leu Ile Arg Xaa  
65 70 75 80  
Arg Arg Gln Gly Arg Arg Gln Gly Arg Gly Ser Pro Pro Gly Arg Arg  
85 90 95  
Asp Leu Arg Arg Leu His Gln Arg Arg Arg Asp Ala Ser Ala Ser Lys  
100 105 110  
Pro Gln Glu Ala Lys Arg Leu Xaa Gly Gly Lys Leu Lys Lys Glu  
115 120 125  
Lys Gln Glu Val Val Ile Glu Lys Ile Val Arg Asn Lys Arg Lys Cys  
130 135 140  
Val Thr  
145

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1500398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

Met Ala Ala Glu Lys Pro Ala Pro Val Arg Val Leu Tyr Cys Gly Val

1 5 10 15  
Cys Gly Leu Pro Ala Glu Tyr Cys Glu Phe Gly Pro Asp Phe Glu Arg  
20 25 30  
Cys Lys Pro Trp Leu Arg Ala His Xaa Pro Ala Ser Thr Pro Thr Asn  
35 40 45  
Leu Ser Pro Xaa Pro Pro Pro His Pro Xaa Ala Ala Thr Arg Thr Ser  
50 55 60  
Thr Gly Ser Gly Ile Ala Ser Arg Ala Ser Gly Ser Pro Thr Ala Pro  
65 70 75 80  
Pro Ala Pro Gln Gly Cys Phe Arg Val  
85

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..431  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

atccctccct ccctcatcgc tttttattat tcccgctcctt cttcattcgg cccttcgcgg 60  
ctgctatatatt tcgcggcgccg cttgcctcctt aataatagcm gccgcggcag tggataccgc 120  
caccgcgatg ggaagcgtcg aggaaggccca cctcgcggccc gccgcgtgcg cgtgcgagga 180  
ggaaggaggaa agcagactaca tcggcctcct cgcagggggaa gcggcgccgcg gcgacgcccgt 240  
ggaagcggccc gtgcgcgccc tgctgctggg gctcgggtgag gacgacccgcc gcgargccct 300  
gtcccggaag cccaagcgcg tcgccaaaggc cttccgcgac gccaccccgag gctacaggga 360  
aaaagtaaaa gacatagtgc aaggtgctct gttccarag gttgggtgtgg ataaaaggac 420  
tggatctgct g

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1500408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

Ile Pro Pro Ser Leu Ile Ala Phe Tyr Tyr Ser Arg Pro Ser Ser Phe  
1 5 10 15  
Gly Pro Ser Pro Leu Leu Tyr Phe Ala Ala Ala Leu Pro Pro Asn Asn  
20 25 30  
Ser Xaa Arg Gly Ser Gly Tyr Arg His Arg His Gly Ser Ala Arg Gly  
35 40 45  
Gly Pro Pro Arg Gly Arg Arg Val Arg Val Arg Gly Gly Gly Lys  
50 55 60  
Arg Leu His Arg Pro Pro Arg Arg Gly Ser Gly Gly Gly Arg Arg Arg  
65 70 75 80  
Gly Ala Gly Arg Ala Arg Pro Ala Ala Gly Ala Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..143  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500409  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:  
Ser Leu Pro Pro Ser Ser Arg Phe Ile Ile Pro Val Leu Leu His Ser  
1                  5                  10                  15  
Ala Leu Arg Arg Cys Tyr Ile Ser Arg Pro Pro Cys Leu Leu Ile Ile  
                  20                  25                  30  
Xaa Ala Ala Val Asp Thr Ala Thr Ala Met Gly Ala Leu Glu Glu  
                  35                  40                  45  
Ala His Leu Ala Ala Ala Cys Ala Cys Glu Glu Glu Glu Ser  
                  50                  55                  60  
Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala Ala Gly Asp Ala Val  
65                  70                  75                  80  
Glu Pro Ala Val Arg Ala Leu Leu Leu Gly Leu Gly Asp Asp Arg  
                  85                  90                  95  
Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg Val Ala Lys Ala Phe Arg  
                  100                 105                 110  
Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val Lys Asp Ile Val Gln Gly  
                 115                 120                 125  
Ala Leu Phe Pro Xaa Val Gly Val Asp Lys Arg Thr Gly Ser Ala  
130                 135                 140

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 101 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..101  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500410  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:  
Met Gly Ala Leu Glu Glu Ala His Leu Ala Ala Ala Cys Ala Cys  
1                  5                  10                  15  
Glu Glu Glu Glu Glu Ser Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala  
                  20                  25                  30  
Ala Ala Gly Asp Ala Val Glu Pro Ala Val Arg Ala Leu Leu Leu Gly  
                  35                  40                  45  
Leu Gly Glu Asp Asp Arg Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg  
                  50                  55                  60  
Val Ala Lys Ala Phe Arg Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val  
65                  70                  75                  80  
Lys Asp Ile Val Gln Gly Ala Leu Phe Pro Xaa Val Gly Val Asp Lys  
                  85                  90                  95  
Arg Thr Gly Ser Ala  
                  100

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 470 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..470  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:  
agcaaacccct agcgcanncce anccaccaccac ccaactcgctt cagccgcctc cgccgcgcgt 60  
acaagcaggt ggagacagga tgccggctgg ccacggcctg cgctcgcgga cgcgcgacct 120  
cttcgcgcgc cccctccgca agaagggcta catccgcctc accacctacc tccgcacct 180  
caagatcggc gattacgtcg atgtcaaggt gaacggcgcc gtcacaaggt ggatgcgcga 240  
caagtcttac cagggccgca cggctcgctg ctggaacgtc accaagcgcg ccacgcgcgt 300  
cgaggtcaac aagcaggtag acaacgcgga tccctttttc gcagagggca ttacgattag 360  
tgcgctggcg catcttctga tcgtttcatt ctaggaaatg taacgsttta atatagaatg 420  
gsgcgtattt gctgacgggt ttgtttgatt tggatttata gaatttgtac

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Ala Asn Pro Ser Ala Xaa Xaa Pro Pro Thr His Ser Leu Gln Pro Pro  
1 5 10 15  
Pro Pro Arg Val Gln Ala Gly Gly Asp Arg Met Pro Ala Gly His Gly  
20 25 30  
Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala Arg Pro Phe Arg Lys Lys  
35 40 45  
Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg Thr Tyr Lys Ile Gly Asp  
50 55 60  
Tyr Val Asp Val Lys Val Asn Gly Ala Val His Lys Gly Met Pro His  
65 70 75 80  
Lys Phe Tyr His Gly Arg Thr Gly Arg Val Trp Asn Val Thr Lys Arg  
85 90 95  
Ala Ile Gly Val Glu Val Asn Lys Gln Val Asp Asn Ala Asp Pro Phe  
100 105 110  
Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu Ala His Leu Leu Ile Val  
115 120 125  
Ser Phe  
130

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1500424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

Gln Thr Leu Ala Xaa Xaa Xaa His Pro Pro Thr Arg Phe Ser Arg Leu  
1 5 10 15  
Arg Arg Ala Tyr Lys Gln Val Glu Thr Gly Cys Arg Leu Ala Thr Ala  
20 25 30  
Cys Ala Arg Gly Arg Ala Thr Ser Ser Arg Ala Pro Ser Ala Arg Arg  
35 40 45  
Ala Thr Ser Arg Ser Pro Pro Thr Ser Ala Pro Thr Arg Ser Ala Ile  
50 55 60  
Thr Ser Met Ser Arg  
65

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

Met Pro Ala Gly His Gly Leu Arg Ser Arg Thr Arg Asp Leu Phe Ala  
1 5 10 15  
Arg Pro Phe Arg Lys Lys Gly Tyr Ile Pro Leu Thr Thr Tyr Leu Arg  
20 25 30  
Thr Tyr Lys Ile Gly Asp Tyr Val Asp Val Lys Val Asn Gly Ala Val  
35 40 45  
His Lys Gly Met Pro His Lys Phe Tyr His Gly Arg Thr Gly Arg Val  
50 55 60  
Trp Asn Val Thr Lys Arg Ala Ile Gly Val Glu Val Asn Lys Gln Val  
65 70 75 80  
Asp Asn Ala Asp Pro Phe Phe Ala Glu Ala Ile Thr Ile Ser Ala Leu  
85 90 95  
Ala His Leu Leu Ile Val Ser Phe  
100

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..453
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

aatcggaaca attcgcggtt gcccatccat cccggaaaata tccccaagga aaccctcgcc 60  
ccctccttc ccgcgcgcgc gtcgccagat ctccggtcat ggacgacgac ggcggggcct 120  
cccggtgcgc ctgcgcgtcc ccgtcgcgct ctccgtcccc gctccccgtg gccgaccccg 180  
tcacggctgc ntcggcgccgc ccggcccaacg tcgcgctgcg tatccccctc cgaagcaact 240  
cgctctctc cggcgccggcg ggccggcgcg gcggccggna ggacgattg ggacgacgg 300  
cgccacctc acgctctatcg acgctgggg ggagcgcttc gtggcgctgg gccggggcag 360  
ctctcgccac ccgcagtgcc aggaggtcgc cgaggtcgtc tcctctcgcg acagytactc 420  
caaggcgccc caaatccgac gtcccgatgc aag

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

Asn Arg Asn Asn Ser Ala Leu Pro Ile His Pro Gly Asn Ile Pro Lys  
1 5 10 15  
Glu Thr Leu Ala Pro Leu Leu Pro Arg Arg Arg Ser Pro Asp Leu Arg

	20		25		30										
Ser	Trp	Thr	Thr	Ala	Gly	Pro	Pro	Gly	Arg	Pro	Arg	Arg	Pro	Arg	
	35					40				45					
Arg	Ala	Leu	Arg	Pro	Arg	Ser	Pro	Trp	Pro	Thr	Pro	Ser	Arg	Ser	Xaa
	50					55						60			
Arg	Arg	Arg	Pro	Ala	Thr	Ser	Pro	Ser	Leu	Ser	Pro	Ser	Ala	Ser	Thr
	65				70					75					80
Arg	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Xaa	Arg	Asp	Asp	
				85					90				95		
Trp	Glu	Arg	Arg	Arg	His	Leu	His	Ala	His	Arg	Arg	Leu	Gly	Gly	Ala
				100					105				110		
Leu	Arg	Gly	Ala	Gly	Pro	Gly	Gln	Pro	Pro	Pro	Pro	Ala	Val	Ala	Gly
		115					120						125		
Gly	Arg	Arg	Gly	Arg	Leu	Leu	Ser	Arg	Gln	Xaa	Leu	Gln	Gly	Ala	Pro
	130						135					140			
Asn	Pro	Thr	Ser	Gln	Cys	Lys									
	145				150										

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

Ile	Gly	Thr	Ile	Pro	Arg	Cys	Pro	Ser	Ile	Pro	Glu	Ile	Ser	Pro	Arg
	1			5					10					15	
Lys	Pro	Ser	Pro	Pro	Ser	Phe	Pro	Ala	Ala	Gly	Arg	Gln	Ile	Ser	Gly
			20					25					30		
His	Gly	Arg	Arg	Arg	Arg	Gly	Leu	Pro	Val	Ala	Leu	Ala	Val	Pro	Val
		35				40					45				
Ala	Leu	Ser	Val	Pro	Ala	Pro	Arg	Gly	Arg	Pro	Arg	His	Gly	Arg	Xaa
	50				55						60				
Gly	Ala	Ala	Arg	Pro	Arg	Arg	Arg	Arg	Tyr	Pro	Pro	Gln	Ala	Leu	
	65				70				75					80	
Ala	Phe	Leu	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Pro	Xaa	Gly	Thr	Ile	
			85					90					95		
Gly	Ser	Asp	Gly	Ala	Thr	Ser	Thr	Leu	Ile	Asp	Ala	Trp	Gly	Glu	Arg
			100					105					110		
Phe	Val	Ala	Leu	Gly	Arg	Gly	Ser	Leu	Arg	His	Pro	Gln	Trp	Gln	Glu
		115					120						125		
Val	Ala	Glu	Val	Val	Ser	Ser	Arg	Asp	Xaa	Tyr	Ser	Lys	Ala	Pro	Gln
	130						135					140			
Ile	Arg	Arg	Pro	Ser	Ala										
	145				150										

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

Ser Glu Gln Phe Arg Val Ala His Pro Ser Arg Lys Tyr Pro Gln Gly  
1 5 10 15  
Asn Pro Arg Pro Pro Ser Pro Pro Pro Val Ala Arg Ser Pro Val  
20 25 30  
Met Asp Asp Asp Gly Gly Ala Ser Arg Ser Pro Ser Pro Ser  
35 40 45  
Arg Ser Pro Ser Pro Leu Pro Val Ala Asp Pro Val Thr Val Xaa Ala  
50 55 60  
Ala Pro Pro Gly His Val Ala Val Ala Ile Pro Leu Arg Lys His Ser  
65 70 75 80  
Pro Ser Ser Gly Gly Gly Gly Gly Gly Gly Arg Xaa Gly Arg Leu  
85 90 95  
Gly Ala Thr Ala Pro Pro Pro Arg Ser Ser Thr Pro Gly Gly Ser Ala  
100 105 110  
Ser Trp Arg Trp Ala Gly Ala Ala Ser Ala Thr Arg Ser Gly Arg Arg  
115 120 125  
Ser Pro Arg Ser Ser Pro Leu Ala Thr Xaa Thr Pro Arg Arg Pro Lys  
130 135 140  
Ser Asp Val Pro Val Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..654  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

ggacctttct atcgcgcgca ttttctttcc gaccagccga vcgccgccgc cctccggcag 60  
gtctttcttc cgcccaacgac caccacgccc aggtcttccc ggcccgaac gcgagcacc 120  
agccctcttc caggtcttcc ccggcgacga gcgcgtagaa gaggggatcc tttagacaa 180  
ggaagaagga gcaccagggc cgtcgcaagc catcccgat tctggagaca cgtaccgcaa 240  
cagctccacc gcgcccgtgg gcagcagctc accgtctgtc gcgaagctcc ggaagctgct 300  
gttcggcggg atgtctcatcg gcgtcaacga cggccgctac ttccacggcc tgttccactg 360  
catcgacaag cagggcaaca tcatctcca ggacgcgcta gattaccgca gcgcccgcga 420  
ctgtctgcct ccgacggagc agcgggtgcct ggggctcacc ctgattccgg ccgctgcgg 480  
gtcgtcgtgc caggtcgatt gctccgttga agagaagatg tcgtccctgt gttttgagtg 540  
aatcgtgtct caaaggggat acactacgca tgtactaagt tactggggct catctctgct 600  
atctgaaact gagagggcatg attgtgtttt cctatttttg aaggattggt tatt

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..179  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

Asp Leu Ser Ile Ala Arg Ile Phe Phe Pro Thr Ser Arg Xaa Pro Pro  
1 5 10 15  
Pro Ser Gly Arg Ser Ser Ser Arg Pro Arg Pro Pro Thr Pro Gly Leu  
20 25 30  
Pro Gly Pro Glu Arg Glu His Pro Ala Leu Leu Gln Val Phe Pro Gly  
35 40 45

Asp Glu Arg Val Glu Glu Gly Ile Leu Ser Thr Met Glu Glu Gly Ala  
50 55 60  
Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly Asp Thr Tyr Arg Asn  
65 70 75 80  
Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro Ser Val Ala Lys Leu  
85 90 95  
Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly Val Asn Asp Gly Arg  
100 105 110  
Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys Gln Gly Asn Ile Ile  
115 120 125  
Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg His Cys Ser Pro Pro  
130 135 140  
Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile Pro Ala Ala Cys Arg  
145 150 155 160  
Ser Ser Cys Gln Val Asp Cys Ser Val Glu Lys Met Ser Leu Leu  
165 170 175  
Cys Phe Glu

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1500470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly  
1 5 10 15  
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro  
20 25 30  
Ser Val Ala Lys Leu Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly  
35 40 45  
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys  
50 55 60  
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg  
65 70 75 80  
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile  
85 90 95  
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu  
100 105 110  
Lys Met Ser Leu Leu Cys Phe Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1500474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

gtgcttcaag aattgatccg ttccgcggtgc gacctccagc tccaggagca gcaccaatcc 60  
cccaagccgc catggccgcg gaccccaagc tgctgcttct cgtaccttc ctcgccatcc 120  
ccctctactt ctctctgtgcc accagacgta ggacgccacg cgggggcgcg cggtcccgcc 180

cggggcccgtg ggcgcgtgcc gtggtcgggc acctgcacaa cctagcccg ggcctccgcg 240  
accgcgtcat ggcgcamctg gcgargcgcc acggcccgcct catgatgctc cggttcggcg 300  
aggtcccggt ggtggtggcc tcctcgccgg cmgcrgcgcg cgaggtgatg cggaccacg 360  
acgcggcggtt cgcgtcgggg cccatcggtc ccgtgtmccg gctctggttc

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1500475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Val Leu Gln Glu Leu Ile Arg Ser Arg Cys Asp Leu Gln Leu Gln Glu  
1 5 10 15  
Gln His Gln Ser Pro Lys Pro Pro Trp Pro Pro Thr Pro Arg Cys Cys  
20 25 30  
Phe Ser Tyr Leu Ser Ser Pro Ser Pro Ser Thr Ser Ser Trp Pro Pro  
35 40 45  
Asp Val Gly Arg His Ala Gly Ala Arg Gly Ser Arg Arg Gly Arg Gly  
50 55 60  
Arg Cys Pro Trp Ser Gly Thr Cys Ile Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1500476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

Ala Ser Arg Ile Asp Pro Phe Ala Val Arg Pro Pro Ala Pro Gly Ala  
1 5 10 15  
Ala Pro Ile Pro Gln Ala Ala Met Ala Ala Asp Pro Thr Leu Leu Leu  
20 25 30  
Leu Val Pro Phe Leu Ala Ile Pro Leu Tyr Phe Phe Leu Ala Thr Arg  
35 40 45  
Arg Arg Thr Pro Arg Gly Gly Ala Arg Leu Pro Pro Gly Pro Trp Ala  
50 55 60  
Leu Pro Val Val Gly His Leu His His Leu Ala Arg Gly Leu Pro His  
65 70 75 80  
Arg Val Met Arg Xaa Leu Ala Xaa Arg His Gly Pro Leu Met Met Leu  
85 90 95  
Arg Phe Gly Glu Val Pro Val Val Ala Ser Ser Pro Xaa Xaa Ala  
100 105 110  
Arg Glu Val Met Arg Thr His Asp Ala Ala Phe Xaa Ser Arg Pro Ile  
115 120 125  
Gly Pro Val Xaa Arg Leu Trp Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

Met	Ala	Ala	Asp	Pro	Thr	Leu	Leu	Leu	Leu	Val	Pro	Phe	Leu	Ala	Ile	
1			5						10				15			
Pro	Leu	Tyr	Phe	Phe	Leu	Ala	Thr	Arg	Arg	Arg	Thr	Pro	Arg	Gly	Gly	
		20						25				30				
Ala	Arg	Leu	Pro	Pro	Gly	Pro	Trp	Ala	Leu	Pro	Val	Val	Gly	His	Leu	
		35					40					45				
His	His	Leu	Ala	Arg	Gly	Leu	Pro	His	Arg	Val	Met	Arg	Xaa	Leu	Ala	
		50					55				60					
Xaa	Arg	His	Gly	Pro	Leu	Met	Met	Leu	Arg	Phe	Gly	Glu	Val	Pro	Val	
		65					70				75			80		
Val	Val	Ala	Ser	Ser	Pro	Xaa	Xaa	Ala	Arg	Glu	Val	Met	Arg	Thr	His	
							85				90			95		
Asp	Ala	Ala	Phe	Xaa	Ser	Arg	Pro	Ile	Gly	Pro	Val	Xaa	Arg	Leu	Trp	
			100					105					110			
Phe																

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 328 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..328  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

cagatcttat	ccctccagt	tccaggcagc	atccccagcc	tgacgaagga	attgaggacg	60
ctcgagctcg	agctacgtca	ggrtccaaca	ccascatggt	tacgggaaca	agaggacggt	120
cgtgctctac	ccgtcgctgg	gcgtgggccca	cctgatcccg	atgggtggagc	tggccaagca	180
cctcttgcgc	cacggccacg	gcgcgctcat	cgccgtggtc	aaccgcgccg	acascgacgc	240
cgtgcggccc	gcmgcggtkg	agcgctckc	ggcgggcaac	ccgggccatcg	cgttccgect	300
cgctgccggtc	cgggccagcc	cggaagcc				

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

Gln	Ile	Leu	Ser	Leu	Pro	Val	Pro	Gly	Ser	Ile	Pro	Ser	Leu	Thr	Lys	
1			5						10				15			
Glu	Leu	Arg	Thr	Leu	Glu	Leu	Glu	Leu	Arg	Gln	Xaa	Pro	Thr	Pro	Xaa	
			20					25				30				
Trp	Leu	Arg	Glu	Gln	Glu	Asp	Val	Arg	Ala	Leu	Pro	Val	Ala	Gly	Arg	
			35				40					45				
Gly	Pro	Pro	Asp	Pro	Asp	Gly	Gly	Ala	Gly	Gln	Ala	Pro	Leu	Ala	Pro	
			50			55					60					

Arg Pro Arg Arg Ala His Arg Arg Gly Gln Pro Ala Arg Xaa Arg Arg  
65 70 75 80  
Arg Val Gly Arg Xaa Gly Xaa Ala Pro Xaa Gly Xaa Gln Pro Gly His  
85 90 95  
Arg Val Pro Pro Pro Ala Gly Pro Gly Gln Pro Gly Arg  
100 105

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

Met Val Glu Leu Ala Lys His Leu Leu Arg His Gly His Gly Ala Leu  
1 5 10 15  
Ile Ala Val Val Asn Pro Pro Asp Xaa Asp Ala Val Ser Ala Xaa Ala  
20 25 30  
Xaa Glu Arg Leu Xaa Ala Xaa Asn Pro Ala Ile Ala Phe Arg Leu Leu  
35 40 45  
Pro Val Pro Ala Ser Pro Asp Ala  
50 55

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..531
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

atcaaaactgc acagcttctc ctgcattgccc cttccaggaa tatccacctg gaataacact 60  
tgtacctatg aagagttagga cactagcgccc attccgtaca actaatcttg tgtagtagc 120  
atcaaccaat ggtgctggtg gatctacatg ttctgatttt ttgtcttcgg gggaaagctct 180  
gcttatagat cctgggatgca gctctcagggt tcatgcagag cttgcagatc tcattgattc 240  
ccttccaaaa aggttattag ttcttgttac acatcatcat caggatcaca ttgagggtct 300  
ttcagtcggt cagagatgca atcctgatgc tgttcttctg acacacccaa gtacaatgga 360  
tcgcattggg aaaggaaactt ggcagattga ctacacttca gtaactgggt gtgaaaagat 420  
atgcattaggt gaccaagaac tacaagttgt ttttgacctt ggctcatcac atggtcatat 480  
ggggcttctc catgtaata ccaatacatt ggttggttga gatcattgtg t

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

Ser Asn Cys Thr Ala Ser Pro Ala Leu Pro Phe Gln Glu Tyr Pro Pro  
1 5 10 15

Gly	Ile	Thr	Leu	Val	Pro	Met	Lys	Ser	Arg	Thr	Leu	Ala	Pro	Phe	Arg	
			20					25					30			
Thr	Thr	Asn	Leu	Val	Val	Val	Arg	Ser	Thr	Asn	Gly	Ala	Gly	Gly	Ser	
		35					40					45				
Thr	Cys	Ser	Asp	Phe	Phe	Ala	Ser	Gly	Glu	Ala	Leu	Leu	Ile	Asp	Pro	
	50					55					60					
Gly	Cys	Ser	Ser	Gln	Val	His	Ala	Glu	Leu	Ala	Asp	Leu	Ile	Asp	Ser	
	65				70					75				80		
Leu	Pro	Lys	Arg	Leu	Leu	Val	Leu	Val	Thr	His	His	His	Gln	Asp	His	
			85						90					95		
Ile	Glu	Gly	Leu	Ser	Val	Val	Gln	Arg	Cys	Asn	Pro	Asp	Ala	Val	Leu	
		100					105						110			
Leu	Thr	His	Gln	Ser	Thr	Met	Asp	Arg	Ile	Gly	Lys	Gly	Thr	Trp	Gln	
		115					120					125				
Ile	Asp	Tyr	Thr	Ser	Val	Thr	Gly	Gly	Glu	Lys	Ile	Cys	Ile	Gly	Asp	
	130					135					140					
Gln	Glu	Leu	Gln	Val	Val	Phe	Ala	Pro	Gly	His	Thr	Asp	Gly	His	Met	
	145				150					155				160		
Gly	Leu	Leu	His	Val	Asn	Thr	Asn	Thr	Leu	Val	Val	Gly	Asp	His	Cys	
			165						170					175		

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

Met	Lys	Ser	Arg	Thr	Leu	Ala	Pro	Phe	Arg	Thr	Thr	Asn	Leu	Val	Val	
				5					10					15		
Val	Arg	Ser	Thr	Asn	Gly	Ala	Gly	Gly	Ser	Thr	Cys	Ser	Asp	Phe	Phe	
			20				25						30			
Ala	Ser	Gly	Glu	Ala	Leu	Leu	Ile	Asp	Pro	Gly	Cys	Ser	Ser	Gln	Val	
		35				40					45					
His	Ala	Glu	Leu	Ala	Asp	Leu	Ile	Asp	Ser	Leu	Pro	Lys	Arg	Leu	Leu	
	50				55						60					
Val	Leu	Val	Thr	His	His	His	Gln	Asp	His	Ile	Glu	Gly	Leu	Ser	Val	
	65				70					75				80		
Val	Gln	Arg	Cys	Asn	Pro	Asp	Ala	Val	Leu	Leu	Thr	His	Gln	Ser	Thr	
			85						90					95		
Met	Asp	Arg	Ile	Gly	Lys	Gly	Thr	Trp	Gln	Ile	Asp	Tyr	Thr	Ser	Val	
			100				105						110			
Thr	Gly	Gly	Glu	Lys	Ile	Cys	Ile	Gly	Asp	Gln	Glu	Leu	Gln	Val	Val	
		115				120						125				
Phe	Ala	Pro	Gly	His	Thr	Asp	Gly	His	Met	Gly	Leu	Leu	His	Val	Asn	
	130				135							140				
Thr	Asn	Thr	Leu	Val	Val	Gly	Asp	His	Cys							
	145				150											

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..555  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

gactccacgc	cgccagtcac	gaccacgccg	cgctccgcc	tggaaccctt	tagccgagcg	60
gasaaggga	gaaatggga	agggtaggg	cagcttcggc	aagcgccgga	acaagacgca	120
cacgtcttgc	atccgtctgc	gcggccggcg	tgagcgggcg	gcgtcaagaa	ccccgattca	180
aatcgggcgc	ccagcccgga	gaqctccgac	gccgagtgac	atgagaagcg	agcgagcagc	240
agcagcagca	gccaccgcaa	aggtccaacg	acgacgagct	ccgtgtttgc	gacggcgccc	300
agcgagcat	cgcgctgtcg	tcttctttcg	tatccacgta	cgtacgacgc	cccagctgac	360
ccgcttgctt	accgctccgt	tctgtgcgac	tgagtggtcg	gtcgcgggcg	gtcgcgggcg	420
gggctttcgg	tacgtctggg	ataagcacga	ggggagggcg	ggcagcgcg	aacggagcg	480
gagcgggcg	ccccagtg	cggtctttcc	aatgtcaaaa	aaggacagct	gtaacagtga	540
taagaaaaac	aagtc					

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

Asp	Ser	Thr	Pro	Pro	Val	Thr	Thr	Thr	Pro	Arg	Leu	Arg	Leu	Glu	Pro
1			5					10						15	
Phe	Ser	Arg	Ala	Xaa	Lys	Gly	Arg	Asn	Gly	Glu	Gly	Tyr	Gly	Gln	Leu
			20					25					30		
Arg	Gln	Ala	Pro	Glu	Gln	Asp	Ala	His	Ala	Leu	His	Pro	Leu	Arg	Arg
			35				40					45			
Pro	Ala	Trp	Ser	Gly	Arg	Val	Lys	Asn	Pro	Asp	Leu	Asn	Arg	Ala	Pro
			50				55				60				
Ser	Pro	Glu	Ser	Ser	Asp	Ala	Glu								
65			70												

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

Thr	Pro	Arg	Arg	Gln	Ser	Arg	Pro	Arg	Arg	Ala	Ser	Ala	Trp	Asn	Pro
1				5						10				15	
Leu	Ala	Glu	Arg	Xaa	Arg	Glu	Glu	Met	Gly	Lys	Gly	Thr	Gly	Ser	Phe
			20					25					30		
Gly	Lys	Arg	Arg	Asn	Lys	Thr	His	Thr	Leu	Cys	Ile	Arg	Cys	Gly	Gly
			35				40					45			
Arg	Arg	Gly	Ala	Gly	Ala	Ser	Arg	Thr	Arg	Ile					
			50				55								

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500490  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:  
Met Arg Ser Glu Arg Ala Ala Ala Ala Ala Thr Ala Lys Ala Gln  
1 5 10 15  
Arg Arg Arg Arg Pro Leu Leu Arg Arg Pro Ala Gln His Ala Ala  
20 25 30  
Val Val Phe Val Arg Ile His Val Arg Thr Thr Ala Gln Leu Thr Arg  
35 40 45  
Leu Pro Thr Arg Pro Phe Cys Ala Thr Gly Trp Ser Val Gly Gly Arg  
50 55 60  
Arg Gly Glu Gly Phe Arg Tyr Val Val Asp Lys His Glu Gly Arg Ala  
65 70 75 80  
Gly Arg Arg Glu Arg Arg Arg Arg Arg Pro Gln Val Ala Val Phe  
85 90 95  
Pro Asn Val Lys Lys Asp Ser Cys Asn Ser Asp Lys Lys Asn Lys  
100 105 110  
(2) INFORMATION FOR SEQ ID NO:1510:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 825 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..825  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500491  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:  
attaaaaaac taatatggct actaggggaag agagagataa gtatagatca gtccttgaag 60  
atgcatgaca ggttcaatgg aggtatgata accctccaga cttcaatagt gtgaaccagc 120  
tcctttgaaga aggcagacct aaggtgtggc cagaagggtc gttagaagag acagtgcaaa 180  
acgcgatcaa gtcatgggag atggagttct cacataagat ccgtttacag gacttcaaga 240  
ctataaaccc tgagaagttt aagctctttg tcaatgtggt atcagctgaa gagacgtcta 300  
ggcttgggag ttacaatgct ttgctcaaga actccttggc tgaagagttt cagtactata 360  
agcccgagga agagagcttt gagtcatcac atgacgcctt tagatctgct ttaccacgcg 420  
ggtttgcgtg gaaataactc tctgtgtact cggggccgcc tgttatagcc ttcaaattta 480  
gacactgggg atactttgaa ggaactttca aaggtcatgc tcctactggg gaaatgggtc 540  
aattcctggg ctaggagttt ctaaaagttg acgaatcact tagagcagag gagattgaga 600  
ttactatga tccaggagag ctgttcgggg gactactcaa gggacctcct atatcagaga 660  
ccaaaaccac agacagtggg gacaaacactg cagagaaaca aagctgcccc ttcacacact 720  
aagataataa gaaaagcaga agtgatttt accctttaaa gaatatattg taacagtctc 780  
ttggttattg atgcatggaa taaattataa gtatgttag gcgcc  
(2) INFORMATION FOR SEQ ID NO:1511:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..173  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500492  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:  
Met Glu Phe Ser His Lys Ile Arg Leu Gln Asp Phe Lys Thr Ile Asn

1	5	10	15												
Pro	Glu	Lys	Phe	Lys	Leu	Phe	Val	Asn	Gly	Leu	Ser	Ala	Glu	Glu	Thr
	20							25					30		
Leu	Arg	Leu	Gly	Ser	Tyr	Asn	Ala	Leu	Lys	Asn	Ser	Leu	Pro	Glu	
	35					40				45					
Glu	Phe	Gln	Tyr	Tyr	Lys	Pro	Glu	Glu	Ser	Phe	Glu	Ser	Ser	His	
	50				55					60					
Asp	Ala	Phe	Arg	Ser	Ala	Leu	Pro	Arg	Gly	Phe	Ala	Trp	Glu	Ile	Leu
65					70				75					80	
Ser	Val	Tyr	Ser	Gly	Pro	Pro	Val	Ile	Ala	Phe	Lys	Phe	Arg	His	Trp
			85						90					95	
Gly	Tyr	Phe	Glu	Gly	Thr	Phe	Lys	Gly	His	Ala	Pro	Thr	Gly	Glu	Met
			100					105					110		
Val	Gln	Phe	Leu	Gly	Leu	Gly	Val	Leu	Lys	Val	Asp	Glu	Ser	Leu	Arg
			115				120					125			
Ala	Glu	Glu	Ile	Glu	Ile	Tyr	Asp	Pro	Gly	Glu	Leu	Phe	Gly	Gly	
	130					135				140					
Leu	Leu	Lys	Gly	Pro	Pro	Ile	Ser	Glu	Thr	Lys	Thr	Thr	Asp	Ser	Gly
145					150				155					160	
Asp	Asn	Thr	Ala	Glu	Lys	Gln	Ser	Cys	Pro	Phe	Thr	His			
			165					170							

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

agtacttact	cactctcccc	ccaccgcgc	caggccagac	agactaactg	agcaccgcgt	60
gcaaggagtc	cgcgcccatg	gcgagcacca	acatggcgct	ggccacctcg	cggttcattg	120
tgcccgccgg	cgtgccccacc	ggcagcagcg	gcggccgcgt	caacttcgcc	tcggcgccca	180
accggcttgg	caggaggctc	gtggcccggg	ccgacaacga	ggccgcgcga	gctgaggcgg	240
cggaagggga	gggtgccctg	gccaccaagc	ccaaggccga	gaagcccgcc	ccgatcgggc	300
ccaataggcg	cgccaagggt	aagatcctta	ggaggggagt	ctacttggtc	aacgggatcg	360
gcaacgtctg	caccgtcgat	caggatccca	acaccgccta	cccgttggtt	gtgcggttca	420
acaaggtgaa	ctacgcgcgc	gtgtccacca	acaactacgc	cttgagcag	gtcttagagg	480
tgaatgagtc	ggggccggcc	ggctcaagg	tcgcgcgctg	ctaccgtgtg	attgatttgt	540
agtagttgtg	aaatgaggtc	gtgaagctgc	atgctgtgct	ggctagcgtg	acaacatcga	600
tcctatgtgt	aatagcataa	tccacataat	catatcatgt	aattgcttgc	tttattcacc	660

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

Met	Ala	Ser	Thr	Asn	Met	Ala	Ser	Ala	Thr	Ser	Arg	Phe	Met	Leu	Ala
1			5						10				15		
Ala	Gly	Val	Pro	Thr	Gly	Ser	Ser	Gly	Gly	Arg	Val	Asn	Phe	Ala	Ser
	20				25							30			

Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu  
35 40 45  
Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys  
50 55 60  
Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys  
65 70 75 80  
Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn  
85 90 95  
Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val  
100 105 110  
Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala  
115 120 125  
Leu Asp Glu Val Leu Glu Val Lys  
130 135

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1500497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

Met Ala Ser Ala Thr Ser Arg Phe Met Leu Ala Ala Gly Val Pro Thr  
1 5 10 15  
Gly Ser Ser Gly Gly Arg Val Asn Phe Ala Ser Ala Pro Asn Arg Leu  
20 25 30  
Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu Ala Ala Ala Glu  
35 40 45  
Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys Pro Lys Ala Glu Lys  
50 55 60  
Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys Val Lys Ile Leu Arg  
65 70 75 80  
Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn Val Val Thr Val Asp  
85 90 95  
Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val Arg Phe Asn Lys Val  
100 105 110  
Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala Leu Asp Glu Val Leu  
115 120 125  
Glu Val Lys  
130

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Met Leu Ala Ala Gly Val Pro Thr Gly Ser Ser Gly Gly Arg Val Asn  
1 5 10 15  
Phe Ala Ser Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala  
20 25 30  
Asp Asn Glu Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val

	35		40		45	
Ala Thr Lys Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg						
50		55		60		
Gly Ala Lys Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly						
65		70		75		80
Ile Gly Asn Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro						
	85		90			95
Val Val Val Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn						
	100		105			110
Asn Tyr Ala Leu Asp Glu Val Leu Glu Val Lys						
	115		120			

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

gacaacaccg cgcgcgcaat acacgggaca cacacgcaga tccgagctaa ccaccatcga	60
cgagcgccas cgcgagcagc cgagcgggac cgaccttttc ttttttttt tacacagcgg	120
gacggagaaa ggagtcaatc agccaaagcc acccaccgct ttaccaccac gatcgcgctt	180
gcgcgcgcta gcattgtcgg cttaagctcc atccaaatcc accgccagca agcaagcaag	240
caagccggcg ccattgggtct gccgatgagg agggagaggg acgcggaggg ggagctgaac	300
ctgcgcgcgg ggttcgcggtt ccacccaccg gacgacgagc tgggtggagca ctacctgttc	360
cgcaaggggc ggggcagcgc ctcccgtgc ccatcatcgc cgaggtggac ctgtacaggt	420
tcgac	

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Asp Asn Thr Ala Arg Ala Ile His Gly Thr His Thr Gln Ile Arg Ala	
1	15
Asn His His Arg Arg Ala Pro Xaa Pro Ala Ala Glu Pro Asp Arg Pro	
20	25
Phe Leu Phe Ser Phe Thr Gln Arg Asp Gly Glu Arg Ser Gln Ser Ala	
35	40
Lys Ala Thr His Arg Phe Tyr Pro Pro Ile Gly Val Ala Ala Ala Ser	
50	55
Ile Val Gly Phe Ser Ser Ile Gln Ile His Arg Gln Gln Ala Ser Lys	
65	70
Gln Ala Gly Ala Met Gly Leu Pro Met Arg Arg Glu Arg Asp Ala Glu	
	85
Ala Glu Leu Asn Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Asp	
	100
Glu Leu Val Glu His Tyr Leu Xaa Arg Lys Gly Arg Gly Ser Ala Ser	
	115
Pro Cys Pro Ser Ser Pro Arg Trp Thr Cys Thr Gly Ser	
130	135
	140

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

Thr	Thr	Pro	Arg	Ala	Gln	Tyr	Thr	Gly	His	Thr	Arg	Arg	Ser	Glu	Leu	
1				5					10					15		
Thr	Thr	Ile	Asp	Glu	Arg	Xaa	Arg	Gln	Pro	Ser	Arg	Thr	Asp	Leu		
			20					25					30			
Phe	Phe	Phe	Leu	Leu	His	Ser	Gly	Thr	Glu	Lys	Gly	Val	Asn	Gln	Pro	
		35					40					45				
Lys	Pro	Pro	Thr	Ala	Phe	Thr	His	Arg	Ser	Ala	Leu	Pro	Pro	Leu	Ala	
		50					55				60					
Leu	Ser	Ala	Ser	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Ser	Lys	Gln	Ala	Ser	
		65			70				75					80		
Lys	Pro	Ala	Pro	Trp	Val	Cys	Arg									
					85											

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

attcttcttg	ctctctccct	ccaccagcat	ccctgagctc	gccatgggca	actgctgggg	60
aaccaagatt	agctctgaca	ccgccgcctc	cccttccaca	tcaccgttcc	ctcgacagca	120
gggtgagatt	ctccggtgtg	ccaatgtcag	gagcttcacc	ttgacggagc	tgatgacctc	180
cacccgggaa	ttccggcccg	acagcgtctc	cgccgaggga	ggcttcggct	ccgtcttcaa	240
gggggtgatc	gacgagacca	ccctcggccc	ggccaggccc	ggcacaggga	tggtcatcgc	300
gttcaagaag	ctcaaccagc	agggattgca	ggggcacagg	gagtggtctg	ctgaagtcac	360
ctacctgggc	cagttgtctc	amcccagctc	cgtaargctc	gtagggtact	gcctccaaga	420
cgagcagcgc	cttctcgtct	acgagttcat	gcgcgarga	agcttkgaga	accatctttt	480
caggacctca	cgt					

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Phe	Phe	Leu	Pro	Pro	Pro	Ser	Thr	Ser	Ile	Pro	Glu	Ser	Ala	Met	Gly	
1				5					10					15		
Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	Pro	Ser	
			20					25					30			

Thr	Ser	Pro	Phe	Pro	Arg	Ser	Glu	Gly	Glu	Ile	Leu	Arg	Cys	Ala	Asn	
		35					40					45				
Val	Arg	Ser	Phe	Thr	Leu	Thr	Glu	Leu	Met	Thr	Ser	Thr	Arg	Asn	Phe	
		50					55					60				
Arg	Pro	Asp	Ser	Val	Leu	Gly	Glu	Gly	Gly	Phe	Gly	Ser	Val	Phe	Lys	
		65				70				75					80	
Gly	Trp	Ile	Asp	Glu	Thr	Thr	Phe	Ala	Pro	Ala	Arg	Pro	Gly	Thr	Gly	
			85							90					95	
Met	Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Gln	Gly	Leu	Gln	Gly	His	
			100					105						110		
Arg	Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Leu	Ser	Xaa	Pro	
		115					120					125				
Ser	Leu	Val	Xaa	Leu	Val	Gly	Tyr	Cys	Leu	Gln	Asp	Glu	Gln	Arg	Leu	
		130					135					140				
Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Xaa	Ser	Xaa	Glu	Asn	His	Leu	Phe	
		145			150					155					160	
Arg	Thr	Ser	Arg													

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met	Gly	Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	
			5						10						15	
Pro	Ser	Thr	Ser	Pro	Phe	Pro	Arg	Ser	Glu	Gly	Glu	Ile	Leu	Arg	Cys	
			20					25						30		
Ala	Asn	Val	Arg	Ser	Phe	Thr	Leu	Thr	Glu	Leu	Met	Thr	Ser	Thr	Arg	
		35					40					45				
Asn	Phe	Arg	Pro	Asp	Ser	Val	Leu	Gly	Glu	Gly	Gly	Phe	Gly	Ser	Val	
		50					55					60				
Phe	Lys	Gly	Trp	Ile	Asp	Glu	Thr	Thr	Phe	Ala	Pro	Ala	Arg	Pro	Gly	
		65				70				75					80	
Thr	Gly	Met	Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Gln	Gly	Leu	Gln	
			85					90							95	
Gly	His	Arg	Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Leu	Ser	
			100				105						110			
Xaa	Pro	Ser	Leu	Val	Xaa	Leu	Val	Gly	Tyr	Cys	Leu	Gln	Asp	Glu	Gln	
		115					120					125				
Arg	Glu	Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Xaa	Ser	Xaa	Glu	Asn	His	
		130				135						140				
Leu	Phe	Arg	Thr	Ser	Arg											
		145			150											

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1500507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

Met	Thr	Ser	Thr	Arg	Asn	Phe	Arg	Pro	Asp	Ser	Val	Leu	Gly	Glu	Gly
1			5					10						15	
Gly	Phe	Gly	Ser	Val	Phe	Lys	Gly	Trp	Ile	Asp	Glu	Thr	Thr	Phe	Ala
			20					25					30		
Pro	Ala	Arg	Pro	Gly	Thr	Gly	Met	Val	Ile	Ala	Val	Lys	Lys	Leu	Asn
			35				40					45			
Gln	Gln	Gly	Leu	Gln	Gly	His	Arg	Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr
			50				55				60				
Leu	Gly	Gln	Leu	Ser	Xaa	Pro	Ser	Leu	Val	Xaa	Leu	Val	Gly	Tyr	Cys
65					70				75					80	
Leu	Gln	Asp	Glu	Gln	Arg	Leu	Leu	Val	Tyr	Glu	Phe	Met	Pro	Arg	Xaa
				85					90					95	
Ser	Xaa	Glu	Asn	His	Leu	Phe	Arg	Thr	Ser	Arg					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

acgaacccaa	ccacgtcgaa	ccacctcgcc	agtgagcgcc	cccccccggt	cctctttccc	60
tgctggccag	aactcgcgaat	gaatcgctg	ctccaccagc	tttctttacc	ttcagcaagc	120
gagccggtag	actcaageta	gatcgcgagg	aagctctctg	tttcccccat	cgccgctgtg	180
ctggcgggga	gaagcgtctc	ctcacggcgg	ccgggaagac	caatccgcgc	cgccagtcgc	240
tgccggcggt	tccgtgaggt	ggctctgggt	ctggggcgcg	cgtgtgtctg	gcggccggcg	300
agatgagcag	ccacgcgggt	ggaacaagca	acggcggtac	cggtgatgcg	gcccgcgggg	360
gcgcggccag	gaggaacacc	aggatgccca	aatattccaa	gttcacacag	caggagctgc	420
ccgcttkcaa	gcccgtctct	actccaaaat	gggttgctct	tgt		

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

Thr	Asn	Pro	Thr	Gln	Ser	Asn	His	Leu	Ala	Ser	Glu	Arg	Pro	Pro	Pro
1			5					10					15		
Val	Leu	Phe	Pro	Cys	Trp	Pro	Glu	Leu	Arg	Met	Lys	Ser	Leu	Leu	His
			20					25					30		
Gln	Leu	Ser	Leu	Pro	Ser	Ala	Ser	Glu	Pro	Val	Ala	Ser	Ser		
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500518  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:  
Met Ser Ser His Ala Val Gly Thr Ser Asn Gly Gly Ser Gly Asp Ala  
1 5 10 15  
Ala Ala Gly Gly Ala Ala Arg Arg Asn Thr Arg Met Pro Lys Tyr Ser  
20 25 30  
Lys Phe Thr Gln Gln Glu Leu Pro Ala Xaa Lys Pro Ile Leu Thr Pro  
35 40 45  
Lys Trp Val Val Ser  
50

(2) INFORMATION FOR SEQ ID NO:1526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..39  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:

Met Arg Pro Pro Gly Ala Arg Pro Gly Gly Thr Pro Gly Cys Pro Asn  
1 5 10 15  
Ile Pro Ser Ser His Ser Arg Ser Cys Pro Leu Xaa Ser Arg Phe Leu  
20 25 30  
Leu Gln Asn Gly Leu Ser Leu  
35

(2) INFORMATION FOR SEQ ID NO:1527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..535  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:

tgggatgaag ccgtgggttat gttaccgtga ctacgactgt aacttcaact ccgacatatt 60  
cgttgagttt gctaccgata tcgcatacgaa aatgggtggat ggtccacgac gccatgccac 120  
aggaaacttca ccaattctgt tactttgcga ccaagcaaaa ggcacagctg gaatatgac 180  
gccggcaagc agaggccgca aattatgccg acggtcattg gaaaataaga gtaaaaggacc 240  
cgagattcaa aatttgcac gacaaattat gtaattggaa aagtatgctg cggcattggg 300  
gcgaatcaaa ttggactgac tacgagtctt ttgtccccc cccaccagcc attaccgtag 360  
accggagatc atcaacttccc ggccataaact tgtgacgcaa taattataca tactatttaa 420  
tggatttcac gagttttttg gtttgaattg ttgtcgcgag attaggtgaa tatcagttgt 480  
gtaactatat ctttttcccta tagtttggtc aaattgaata aaacattttt ttgcy

(2) INFORMATION FOR SEQ ID NO:1528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

Gly	Met	Lys	Pro	Trp	Leu	Cys	Tyr	Arg	Asp	Tyr	Asp	Cys	Asn	Phe	Asn
1				5					10					15	
Ser	Asp	Ile	Phe	Val	Glu	Phe	Ala	Thr	Asp	Ile	Ala	Ser	Lys	Met	Val
			20					25					30		
Asp	Gly	Pro	Arg	Arg	His	Ala	Thr	Gly	Thr	Ser	Pro	Ile	Leu	Leu	
			35				40					45			
Ala	Ile	Gln	Ala	Lys	Gly	Thr	Ala	Gly	Ile						

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1500541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

Met	Val	His	Asp	Ala	Met	Pro	Gln	Glu	Leu	His	Gln	Phe	Cys	Tyr	Leu
1				5				10					15		
Arg	Ser	Lys	Gln	Lys	Ala	Gln	Leu	Glu	Tyr	Asp	Arg	Arg	Gln	Ala	Glu
			20					25					30		
Ala	Ala	Asn	Tyr	Ala	Asp	Gly	His	Trp	Lys	Ile	Arg	Val	Lys	Asp	Pro
			35				40					45			
Arg	Phe	Lys	Ile	Cys	Ile	Asp	Lys	Leu	Cys	Asn	Trp	Lys	Ser	Met	Leu
			50				55					60			
Arg	His	Trp	Gly	Glu	Ser	Asn	Trp	Thr	Asp	Tyr	Glu	Ser	Phe	Val	Pro
			65			70				75				80	
Thr	Pro	Pro	Ala	Ile	Thr	Val	Asp	Arg	Arg	Ser	Ser	Leu	Pro	Gly	His
				85				90					95		
Asn	Leu														

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1500542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Met	Pro	Gln	Glu	Leu	His	Gln	Phe	Cys	Tyr	Leu	Arg	Ser	Lys	Gln	Lys
1				5					10					15	
Ala	Gln	Leu	Glu	Tyr	Asp	Arg	Arg	Gln	Ala	Glu	Ala	Ala	Asn	Tyr	Ala
			20					25					30		
Asp	Gly	His	Trp	Lys	Ile	Arg	Val	Lys	Asp	Pro	Arg	Phe	Lys	Ile	Cys
			35				40					45			
Ile	Asp	Lys	Leu	Cys	Asn	Trp	Lys	Ser	Met	Leu	Arg	His	Trp	Gly	Glu
			50				55					60			
Ser	Asn	Trp	Thr	Asp	Tyr	Glu	Ser	Phe	Val	Pro	Thr	Pro	Pro	Ala	Ile
			65			70				75				80	
Thr	Val	Asp	Arg	Arg	Ser	Ser	Leu	Pro	Gly	His	Asn	Leu			
				85				90							

(2) INFORMATION FOR SEQ ID NO:1531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1530  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

tctgtcgctc	tctatttttt	cttctttttt	cgattttcata	ccaaaacaag	aactctctgt	60
ttcgacacaa	gaacaaacct	tgagactcat	ttttagtgac	ttttaagaac	gagagagact	120
ttcttttgaa	ggtttgttgt	cgctgccatt	gaagaatccg	ggtttgtctt	tcgaaattca	180
gagagaaaaa	gggttgatgag	cgagagatca	aggaatacct	aaagccacaa	gcttcactgt	240
aaacaaatga	caagaaacat	aatgtgaag	ggaaagagtt	atggcagaaa	gtcaagatca	300
aatttggtgga	tcttctatca	ttgctcgctt	atttaagagta	acatgagtc	atcatttgctc	360
attaccgatc	cgaattggcgc	atcacaacga	tttctctcag	catctttacc	attcataatg	420
agactttgaa	gttttggcgc	caattgatgt	gttttttctc	gtttttggcg	ctcactattt	480
acactcgcaac	gaaaagtacc	agttgtgtgt	attctctatc	gcttcaaac	cgtttaccgc	540
atttgttgag	ataaaacagat	ctccacaaac	tctcatctga	gctcagtgct	cgctctctt	600
ctagtccatc	tatgtggcat	gtgatggacc	tcttttataa	ctgtttgect	gaaagatttt	660
ctcatggcaa	ctcacactga	attgtgtgtc	tgcattctgt	gagggaagat	cttgcgaact	720
tgtatgcttc	tttgatcttc	agggccaata	ctcgaatggc	gtttttatga	tttctagtgt	780
gtgtcatgtt	cttcttatta	cgaaagcaga	ctgcgccact	ctctctctga	catcccgagc	840
gagttctccta	cataatgctt	aggtctttatt	acgcggccat	cgacgctcta	atagcgactt	900
ctcttcaccc	tccggttttt	tactccttca	tgtgtgatcc	tttctctcgc	aacctctact	960
taggattcat	aacctctata	ggaaatgcga	ctgtgcttgt	tctctctctc	cggtttttcc	1020
aaagcccgga	tttccgggtg	gtgaggcgct	ctctgtcttt	tggaaaggga	ttctctgctt	1080
tagctccgat	tcttccaca	ctgataaatc	tttggggaca	acctgaagcc	cttcaacaga	1140
cagggttatga	ttttttgatg	ggtttgtctt	atgggttagg	agctcttggt	tatgcataca	1200
ggatcccaga	gagatagtgt	ccgggttaat	tgcattatga	aggacatagc	catcatttgt	1260
tctcatgttt	gctgttgtct	gtgcgtctac	gcacattaga	gctgggctag	tgatgtttaa	1320
gtggagagat	atygaaagat	gttgaagatg	aagatagaag	atttagatga	atctttgaat	1380
cttgttttga	gtagctttcat	ataaaagttg	gattatgata	agttctatat	gttaatcaac	1440
gttttaattgt	tctctttttt	caacacaagg	tttatattgt	taatccacat	atgtattact	1500
gtttaaagaa	ctctaaagat	tcatattttt				

(2) INFORMATION FOR SEO ID NO:1532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..373  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

Met	Gly	Asp	Glu	Ala	Glu	Ile	Lys	Glu	His	Leu	Lys	Pro	Gln	Ala	Ser
1			5					10					15		
Ser	Glu	Thr	Met	Asp	Lys	Lys	His	Asn	Val	Lys	Gly	Lys	Arg	Leu	Trp
			20					25					30		
Gln	Lys	Val	Lys	Tyr	Gln	Leu	Val	Glu	Phe	His	Ser	Leu	Pro	Ala	Tyr
			35				40					45			
Leu	Arg	Asp	Asn	Glu	Tyr	Ile	Ile	Gly	His	Tyr	Arg	Ser	Glu	Trp	Pro
	50					55					60				
Ile	Lys	Gln	Ile	Leu	Leu	Ser	Ile	Phe	Thr	Ile	His	Asn	Glu	Thr	Leu
65					70					75				80	
Asn	Val	Trp	Thr	His	Leu	Ile	Gly	Phe	Phe	Leu	Phe	Leu	Ala	Leu	Thr
				85					90					95	

Ile	Tyr	Thr	Ala	Thr	Lys	Val	Pro	Ser	Val	Val	Asp	Leu	His	Ser	Leu
		100						105					110		
Gln	His	Arg	Leu	Pro	Asp	Leu	Leu	Arg	Lys	Thr	Asp	Leu	His	Lys	Leu
		115				120					125				
His	Ser	Glu	Leu	Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His
		130				135					140				
Val	Met	Asp	Leu	Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly
		145			150					155					160
Asn	Tyr	Thr	Asp	Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala
			165					170							175
Asn	Leu	Ile	Ala	Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe
		180					185							190	
Tyr	Ala	Phe	Leu	Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr
		195				200						205			
Cys	His	Leu	Leu	Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu
		210				215					220				
Arg	Leu	Tyr	Tyr	Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr
		225			230					235					240
Pro	Pro	Val	Tyr	Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu
			245						250						255
Tyr	Leu	Gly	Phe	Ile	Thr	Ile	Leu	Gly	Ile	Ala	Thr	Val	Leu	Val	Ser
		260					265								270
Leu	Leu	Pro	Val	Phe	Gln	Ser	Pro	Glu	Phe	Arg	Val	Val	Arg	Ala	Ser
		275					280					285			
Leu	Phe	Phe	Gly	Met	Gly	Phe	Ser	Gly	Leu	Ala	Pro	Ile	Leu	His	Lys
		290				295					300				
Leu	Ile	Ile	Phe	Trp	Asp	Gln	Pro	Glu	Ala	Leu	His	Thr	Thr	Gly	Tyr
		305			310					315					320
Glu	Ile	Leu	Met	Gly	Leu	Leu	Tyr	Gly	Leu	Gly	Ala	Leu	Val	Tyr	Ala
			325					330							335
Thr	Arg	Ile	Pro	Glu	Arg	Trp	Met	Pro	Gly	Lys	Phe	Asp	Ile	Ala	Gly
			340				345						350		
His	Ser	His	Gln	Leu	Phe	His	Val	Leu	Val	Val	Leu	Val	Arg	Ser	Arg
		355				360						365			
Thr	Ile	Glu	Leu	Gly											
			370												

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

Met	Asp	Lys	Lys	His	Asn	Val	Lys	Gly	Lys	Arg	Leu	Trp	Gln	Lys	Val
1			5					10					15		
Lys	Tyr	Gln	Leu	Val	Glu	Phe	His	Ser	Leu	Pro	Ala	Tyr	Leu	Arg	Asp
			20					25					30		
Asn	Glu	Tyr	Ile	Ile	Gly	His	Tyr	Arg	Ser	Glu	Trp	Pro	Ile	Lys	Gln
		35					40					45			
Ile	Leu	Leu	Ser	Ile	Phe	Thr	Ile	His	Asn	Glu	Thr	Leu	Asn	Val	Trp
		50				55					60				
Thr	His	Leu	Ile	Gly	Phe	Phe	Leu	Phe	Leu	Ala	Leu	Thr	Ile	Tyr	Thr
		65			70					75					80
Ala	Thr	Lys	Val	Pro	Ser	Val	Val	Asp	Leu	His	Ser	Leu	Gln	His	Arg
			85					90					95		
Leu	Pro	Asp	Leu	Leu	Arg	Lys	Thr	Asp	Leu	His	Lys	Leu	His	Ser	Glu

[illegible]

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 241 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..241  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His	Val	Met	Asp	Leu
1				5				10						15	
Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly	Asn	Tyr	Thr	Asp
		20						25					30		
Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala	Asn	Leu	Ile	Ala
		35					40					45			
Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe	Tyr	Ala	Phe	Leu
	50					55					60				
Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr	Cys	His	Leu	Leu
	65				70					75				80	
Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu	Arg	Leu	Tyr	Tyr
			85						90					95	
Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr	Pro	Pro	Val	Tyr
			100					105					110		
Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu	Tyr	Leu	Gly	Phe
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:1535:

(A) LENGTH: 660 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..660

(D) OTHER INFORMATION: / Ceres Seq. ID 1500558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

tatccattatt	tctatgtagt	catctctctc	actctcttcc	cactcttaac	tctcttaacc	60
tatcccaaaa	tttggaaaaa	gacetttggt	tctttatcca	ttaatgcaga	tgtcgcgaaa	120
atgcaaacaa	actgcgattt	gttctaacaa	gagtatgtgt	cccgctgttg	gagaagcttc	180
accggagctc	aaggcagcga	agcattctca	tgactctttt	acctacgctg	cagtaggaat	240
agtgctctgt	cagctctaga	gttataatcc	tggaggtctt	atggaggtga	gacgaatctt	300
atgatacaac	tctgtaagt	accgtatgaa	attctgcgcc	actctcatgc	gtcgtctctc	360
acgtcacatg	aacttaagccc	tctgaatttt	aggagatcgg	tctgcttatt	gtaaaaaacga	420
tctcgaatgg	gaataataga	agccgcctgc	ctcacaagaac	gtagagagag	gtgagagagc	480
ccgaattatc	ctctgaatca	cattctcata	ctaatgcctg	ctaatgattc	ataaaggatt	540
accgttttct	ctctgaatata	catcaccatt	tactagtgtt	tgagagatta	ccacactgaa	600
			tactagtgtt	ctcccaqatt	tctataacct	660

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1500559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Ser	Asn	Ile	Ser	Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr
1			5					10					15		
Leu	Ser	Tyr	Leu	Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr
			20					25					30		
Pro	Leu	Met	Gln	Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser
		35					40				45				
Asn	Lys	Met	Tyr	Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys
		50				55				60					
Ala	Ala	Lys	His	Leu	His	Asp	Phe	Phe	Thr	Val	Ala	Val	Val	Arg	Ile

65				70				75				80			
Val	Ser	Ala	Gln	Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu
				85				90						95	
Arg	Glu	Phe	Leu	Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys
			100					105					110		
Ala	Thr	Leu	Met	Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg
			115					120					125		
Ile	Leu	Glu	Val	Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp
			130					135				140			
Asn	Met	Lys	Arg	Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg
			145					150				155			160
Leu	Met	Arg	Glu	Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser
				165					170					175	
Asp	Lys														

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr	Leu	Ser	Tyr	Leu
1						5				10					15
Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr	Pro	Leu	Met	Gln
			20					25					30		
Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser	Asn	Lys	Met	Tyr
			35				40					45			
Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys	Ala	Ala	Lys	His
			50				55					60			
Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile	Val	Ser	Ala	Gln
			65				70				75				80
Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu	Arg	Glu	Phe	Leu
				85					90					95	
Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys	Ala	Thr	Leu	Met
			100					105					110		
Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg	Ile	Leu	Glu	Val
			115					120					125		
Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp	Asn	Met	Lys	Arg
			130					135				140			
Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg	Leu	Met	Arg	Glu
			145					150				155			160
Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser	Asp	Lys		
				165					170						

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

Met	Gln	Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser	Asn	Lys
1				5					10					15	
Met	Tyr	Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys	Ala	Ala
			20					25					30		
Lys	His	Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile	Val	Ser
		35					40					45			
Ala	Gln	Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu	Arg	Glu
		50				55					60				
Phe	Leu	Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys	Ala	Thr
				70						75				80	
Leu	Met	Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg	Ile	Leu
				85					90					95	
Glu	Val	Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp	Asn	Met
				100				105					110		
Lys	Arg	Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg	Leu	Met
				115			120					125			
Arg	Glu	Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser	Asp	Lys
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1616

(D) OTHER INFORMATION: / Ceres Seq. ID 1500562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

atcgataacc	aaataaaaaa	tggcgatctc	tttccctctgt	gtttttctca	tcaccttcgt	60
ttcgtaaatc	ttttttgcca	agaaaaatcaa	acgatcaaaa	tggaaatcttc	ctccaagccc	120
tcccaagttt	ccggtcatcg	ggaaacttaca	tcagattgga	gaattgacctc	acagggtcaact	180
tcaacatctc	ccggaagaat	acggacctgt	gatgcttctt	cactttgggt	ttgtccctat	240
aactgtggtc	tcatcgagag	aagccgctga	agaagtgcct	agaactcatg	acctagactg	300
ttgcagcagg	cctaagcttg	tcgggacaag	gttactctcg	gcgggatttt	aaagatatcg	360
gttttaacgc	atacggtaac	gaggtggaag	gcgcggcgta	aggttttgccc	tgcggtgagac	420
ttttctgttt	gaaaaagggtt	cagtctctta	ggcatatccg	agagggaagaa	tgtaaccttct	480
tggtcaagca	actgtcggaa	tccgcgggtg	atcgctctcc	ggctgatattg	agcaaatccc	540
ttttctggct	aaccgctagt	atccttttta	gagttgcctt	aggacagaat	tttcacgaga	600
gcgattttat	cgataaagaa	aagatcgaag	agctcgtgtt	cgaagctgag	actgcccctag	660
caagtcttca	ttgttctgat	tcttccctgt	ttgcgggaact	tggatggctc	gttgatttgtt	720
tttccggaca	acacaagaga	ctcaacgatg	ttttttacaa	gctcgatgct	ctgtttcaat	780
atgtcataga	tgatcatatta	aattcctggaa	gatcaaaaaga	gcacagaagac	atcatcgatt	840
caatgtttgga	tgtgattcat	aaacaaggag	aggatagttc	cttagacagct	acaatagatc	900
atatcaaggg	gtttctcgcg	aatatatttc	ttgcagggat	agacagaggtg	gccatcacca	960
tgatatgggc	agtgcaggag	ctcgttaaaa	acccgaaact	gataaaagaaa	gttcaaggcg	1020
atatcggaga	acaaactggc	agacaataag	agagaatacac	cgagggaagat	atcgagaaag	1080
tctctctact	gaagattgta	atcaaaagaa	cattcagggt	acacccagca	gctcctctta	1140
tacttccaag	ggaaacaagt	gtcatcatca	aagttcaagg	gtatgatatt	cctcccaga	1200
ggaggattct	ggtccaatgt	tcggcaatag	gaagagatcc	caaaactctg	acaaacccga	1260
aagagtttga	ccctcgagag	tttatggata	gctttgttga	ttatagggtg	caacattacg	1320
agctcttaact	atttggtgtc	ggtcgaagga	tatgtcccg	gatgccaatg	gggattgctg	1380
ccgtcgtaatt	gggactcttg	aacttacttt	acttcttcga	ttggaaagttc	cttgatggga	1440
tgacacataa	agatatcgat	actgaagaag	ctgttactct	tacaaatgac	aagaaagtac	1500
ctctcaagct	cgtttcagtt	cgagttcagt	gatcagacca	acctccaagt	cttttgtaata	1560
aatatatcat	gcaaatcatg	taagcttctc	tgatgatga	tgaagtatat	tttttc	

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..229  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500563  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

Met Leu Asp Val Ile His Lys Gln Gly Glu Asp Ser Ser Leu Glu Leu  
1 5 10 15  
Thr Ile Asp His Ile Lys Gly Phe Leu Ala Asn Ile Phe Leu Ala Gly  
20 25 30  
Ile Asp Thr Gly Ala Ile Thr Met Ile Trp Ala Val Thr Glu Leu Val  
35 40 45  
Lys Asn Pro Lys Leu Ile Lys Lys Val Gln Gly Asp Ile Arg Glu Gln  
50 55 60  
Leu Gly Ser Asn Lys Glu Arg Ile Thr Glu Glu Asp Ile Glu Lys Val  
65 70 75 80  
Pro Tyr Leu Lys Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala  
85 90 95  
Ala Pro Leu Ile Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln  
100 105 110  
Gly Tyr Asp Ile Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala  
115 120 125  
Ile Gly Arg Asp Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro  
130 135 140  
Glu Arg Phe Met Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu  
145 150 155 160  
Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met  
165 170 175  
Gly Ile Ala Ala Val Glu Leu Gly Leu Leu Asn Leu Leu Tyr Phe Phe  
180 185 190  
Asp Trp Lys Leu Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu  
195 200 205  
Glu Ala Gly Thr Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val  
210 215 220  
Pro Val Arg Val Gln  
225

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 190 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..190  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500564  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

Met Ile Trp Ala Val Thr Glu Leu Val Lys Asn Pro Lys Leu Ile Lys  
1 5 10 15  
Lys Val Gln Gly Asp Ile Arg Glu Gln Leu Gly Ser Asn Lys Glu Arg  
20 25 30  
Ile Thr Glu Glu Asp Ile Glu Lys Val Pro Tyr Leu Lys Met Val Ile  
35 40 45  
Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile Leu Pro Arg  
50 55 60  
Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile Pro Pro Lys

65	Arg	Arg	Ile	Leu	Val	Asn	Val	Ser	Ala	Ile	Gly	Arg	Asp	Pro	Lys	Leu
					85					90					95	
Trp	Thr	Asn	Pro	Lys	Glu	Phe	Asp	Pro	Glu	Arg	Phe	Met	Asp	Asp	Ser	Phe
			100					105						110		
Val	Asp	Tyr	Arg	Gly	Gln	His	Tyr	Glu	Leu	Leu	Pro	Phe	Gly	Ser	Gly	
		115					120					125				
Arg	Arg	Ile	Cys	Pro	Gly	Met	Pro	Met	Gly	Ile	Ala	Ala	Val	Glu	Leu	
		130				135					140					
Gly	Leu	Leu	Asn	Leu	Leu	Tyr	Phe	Phe	Asp	Trp	Lys	Leu	Pro	Asp	Gly	
145				150					155					160		
Met	Thr	His	Lys	Asp	Ile	Asp	Thr	Glu	Glu	Ala	Gly	Thr	Leu	Thr	Ile	
			165					170						175		
Val	Lys	Lys	Val	Pro	Leu	Lys	Leu	Val	Pro	Val	Arg	Val	Gln			
			180					185								

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1500565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met	Val	Ile	Lys	Glu	Thr	Phe	Arg	Leu	His	Pro	Ala	Ala	Pro	Leu	Ile
1								10						15	
Leu	Pro	Arg	Glu	Thr	Met	Ala	His	Ile	Lys	Val	Gln	Gly	Tyr	Asp	Ile
			20					25						30	
Pro	Pro	Lys	Arg	Arg	Ile	Leu	Val	Asn	Val	Ser	Ala	Ile	Gly	Arg	Asp
		35				40						45			
Pro	Lys	Leu	Trp	Thr	Asn	Pro	Lys	Glu	Phe	Asp	Pro	Glu	Arg	Phe	Met
		50				55					60				
Asp	Ser	Phe	Val	Asp	Tyr	Arg	Gly	Gln	His	Tyr	Glu	Leu	Leu	Pro	Phe
65					70					75				80	
Gly	Ser	Gly	Arg	Arg	Ile	Cys	Pro	Gly	Met	Pro	Met	Gly	Ile	Ala	Ala
				85					90					95	
Val	Glu	Leu	Gly	Leu	Leu	Asn	Leu	Leu	Tyr	Phe	Phe	Asp	Trp	Lys	Leu
			100					105					110		
Pro	Asp	Gly	Met	Thr	His	Lys	Asp	Ile	Asp	Thr	Glu	Glu	Ala	Gly	Thr
			115				120						125		
Leu	Thr	Ile	Val	Lys	Lys	Val	Pro	Leu	Lys	Leu	Val	Pro	Val	Arg	Val
		130				135					140				

Gln

145

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1928 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1928

(D) OTHER INFORMATION: / Ceres Seq. ID 1500614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

tttcctcttc	ttcatctctc	acaaattcca	aacatctctc	tctctttctc	tctcacacac	60
aaaattgcag	aagaagaaga	gtcatgaatg	gtgaagaaag	ctttgtagaa	gattgtctctg	120

tttttgttga	gattgatcct	tctggaagat	atggaagata	cgatgaaata	cttggcaaa	180
gagcttcaaa	gacagtatac	agagcatttg	atgagtatga	aggatataga	gtagcatgga	240
accaagtaaa	gcttcgaaat	ttcacaagga	atcctgagga	attagagaag	tttttcagag	300
agattcatct	ttccaagact	ttgaatcatc	aaaacattat	gaaattctac	acttcttggt	360
ttgatcccaa	caatttatca	atcaattttg	tcactgaact	cttcacctct	ggtagcttca	420
gacagatatag	gttgagacat	agaagagtga	atattagagc	agtgaaagca	tggtgcaagc	480
agattttaaa	agggcttctt	tatttatcata	gtcgttctcc	accaattata	catagagatc	540
tcaaatgtga	taacattttc	atcaatggaa	accaaggtga	agtcgaagtc	ggtagacctg	600
gactcgtctg	gattctctgt	aaatcacatg	ccgttcggtg	cgttggaacc	cctaggttta	660
tggtctcaga	agtgtatgat	gaggaatata	atgagttggt	tgatgtatat	gcttttggca	720
tggtgtgtgt	ggagatgggt	acttttgatt	atccttacag	tgaatgtact	caccggcac	780
aaatctacaa	gaaagtacc	tcggggaaaa	agcctgaagc	tttttactta	gtgaaggatc	840
ctgaggttct	tgagtttgtt	gagaagtgtt	tagctaactg	gacgtgtagg	ctaacggcat	900
tgagagcttt	acaagaccct	tttctacaag	atgataatat	ggatggattt	gcttatgagac	960
ctattgtatta	ctacaatggt	tatgatgaaa	ctggtgtgtt	ccttagacat	cctttgattg	1020
atgatcctct	ttaccatgat	cagtttgagt	cgtcacagat	atgtgagatc	gatctttctg	1080
ctaacgatga	tgaagatcat	gtcgacattt	cgattaaagg	gaagagaaac	ggtagatgat	1140
ggatatattct	gagacttaga	atatctgatg	ctgaaggacg	gataaaggac	atttactctc	1200
cgtttgatcg	ggctattgat	actgcattga	gtgtagcggt	tgagatgggt	tcagagctcg	1260
acataacgaa	tcaagatggt	gcgaaaaatc	cgagatgat	cgatgcagag	attgtgcatt	1320
tggtgcctga	ttggaaaaaa	gatacagaaa	gttcccaaaa	tgtaacgaac	aacaagaaca	1380
acaacactgg	aggtattctgt	ggagagtggt	cttcaaacgg	gtatatcaaa	gagactgtat	1440
catcaggaga	aaatctcat	cataatcatc	atgagttcga	tagttctgaa	gacaagaact	1500
gttcttcgtg	tcacggtagg	tttgcggata	tgtgggggtt	gcgagaatca	tattctgatg	1560
atggagaaaa	acagagctca	aggaaggtta	gaagtggacg	gtgtctcgga	atagagatga	1620
gacgagaact	gagatggctt	aaggcaaggc	acaagattca	acttatgtaa	atgagaggtc	1680
aaacgatctg	cgagacacgc	atagagatct	ctcttacacc	gggaacttca	gtttctgtac	1740
ctcttcttta	cagggctata	tcacttctgt	tggaatcggt	ggatatttga	cattatttga	1800
aagtctgatg	atgattatca	cttatatttg	tatgttttga	catttttaac	tttgtttaag	1860
ttaaaagtta	atgacatagt	gtactttatt	taaagagaag	aagagtaaac	gaaaaacata	1920
aattagtc						

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..595

(D) OTHER INFORMATION: / Ceres Seq. ID 1500615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

Ser	Ser	Ser	Ser	Ile	Ser	Thr	Asn	Ser	Lys	His	Leu	Ser	Leu	Phe	Leu
1				5				10				15			
Ser	His	Thr	Gln	Asn	Cys	Arg	Arg	Arg	Arg	Val	Met	Asn	Gly	Glu	Glu
				20				25				30			
Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu	Ile	Asp	Pro	Ser	Gly
				35				40				45			
Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys	Gly	Ala	Ser	Lys	Thr
				50				55			60				
Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile	Glu	Val	Ala	Trp	Asn
				65				70			75				
Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro	Glu	Glu	Leu	Glu	Lys
				85				90							
Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu	Asn	His	Gln	Asn	Ile
				100				105					110		
Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
				115				120				125			
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
				130				135				140			

Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
145					150					155					160
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
				165					170					175	
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
				180				185					190		
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
				195			200					205			
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
						215					220				
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
225					230					235					240
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
				245					250					255	
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
				260				265					270		
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
				275				280				285			
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
				290			295				300				
Asp	Pro	Phe	Leu	Gln	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro	
305				310				315						320	
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
				325				330						335	
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln
				340				345					350		
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp
				355			360					365			
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg
				370			375				380				
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro
385					390					395					400
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val
				405				410						415	
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met
				420				425					430		
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr
				435			440					445			
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly
				450			455				460				
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu	Thr	Val	Ser
465					470					475					480
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp	Ser	Ser	Glu
				485				490						495	
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp	Met	Trp	Gly
				500				505					510		
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser	Ser	Arg	Lys
				515			520					525			
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg	Glu	Leu	Arg
				530			535				540				
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met	Arg	Gly	Gln
545					550					555					560
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro	Gly	Thr	Ser
				565				570						575	
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro	Val	Asp	Ala
				580				585					590		
Val	Asp	Met													
				595											

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..568  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500616  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

Met	Asn	Gly	Glu	Glu	Ser	Phe	Val	Glu	Asp	Cys	Ser	Val	Phe	Val	Glu
1			5					10					15		
Ile	Asp	Pro	Ser	Gly	Arg	Tyr	Gly	Arg	Tyr	Asp	Glu	Ile	Leu	Gly	Lys
		20					25					30			
Gly	Ala	Ser	Lys	Thr	Val	Tyr	Arg	Ala	Phe	Asp	Glu	Tyr	Glu	Gly	Ile
		35					40				45				
Glu	Val	Ala	Trp	Asn	Gln	Val	Lys	Leu	Arg	Asn	Phe	Thr	Arg	Asn	Pro
	50				55					60					
Glu	Glu	Leu	Glu	Lys	Phe	Phe	Arg	Glu	Ile	His	Leu	Leu	Lys	Thr	Leu
65				70					75					80	
Asn	His	Gln	Asn	Ile	Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn
			85					90					95		
Asn	Leu	Ser	Ile	Asn	Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu
		100					105					110			
Arg	Gln	Tyr	Arg	Leu	Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys
		115					120					125			
Gln	Trp	Cys	Lys	Gln	Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg
	130				135						140				
Ser	Pro	Pro	Ile	Ile	His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile
145				150					155					160	
Asn	Gly	Asn	Gln	Gly	Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala
			165					170					175		
Ile	Leu	Arg	Lys	Ser	His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe
		180						185					190		
Met	Ala	Pro	Glu	Val	Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val
	195						200					205			
Tyr	Ala	Phe	Gly	Met	Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro
	210				215						220				
Tyr	Ser	Glu	Cys	Thr	His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser
225				230						235				240	
Gly	Lys	Lys	Pro	Glu	Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg
			245						250				255		
Glu	Phe	Val	Glu	Lys	Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala
		260					265						270		
Leu	Glu	Leu	Leu	Gln	Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly
		275					280					285			
Phe	Val	Met	Arg	Pro	Ile	Asp	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	
	290				295					300					
Val	Phe	Leu	Arg	His	Pro	Leu	Ile	Asp	Pro	Leu	Tyr	His	Asp	Gln	
305					310					315				320	
Phe	Glu	Ser	Ser	Gln	Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp
			325						330				335		
Glu	Asp	His	Val	Asp	Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp
		340					345						350		
Gly	Ile	Phe	Leu	Arg	Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg
		355					360					365			
Asn	Ile	Tyr	Phe	Pro	Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val
	370					375					380				
Ala	Val	Glu	Met	Val	Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala
385					390					395				400	
Lys	Ile	Ala	Glu	Met	Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp
			405					410					415		

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino ac

(B) TYPE: amino acid

MOLECULE TYPE: pep

FEATURE:

(A) NAME/KEY: peptide

(A) NAME/REF: peptide  
(B) LOCATION: 1...483

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1546:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:1540:  
Lys Phe Tyr Thr Ser Trp Val Asp Thr Asp Asn

Met	Lys	Phe	Tyr	His	Ser	Trp	Val	Asp	10	Asn	Asn	Leu	Ser	15	Asn
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	10	Thr	Leu	Arg	Gln	Tyr	Arg
Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	25	Val	Lys	Gln	Trp	Cys	Lys
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	40	Ser	Arg	Ser	Pro	Pro	Ile
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	55	Phe	Ile	Asn	Gly	Asn	Gln
Glu	Val	Lys	Ile	Gly	Asp	Gly	Gly	Leu	70	Ala	Ala	Ile	Leu	Arg	Gln
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	85	Glu	Phe	Met	Ala	Pro	Glu
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	100	Asp	Val	Tyr	Ala	Phe	Gly
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	115	Tyr	Pro	Tyr	Ser	Glu	Cys
His	Pro	Ala	Gln	Ile	Tyr	Lys	Val	Thr	130	Ser	Gly	Lys	Lys	Pro	Glu
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	145	Val	Arg	Glu	Phe	Val	Glu
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	160	Thr	Ala	Leu	Glu	Leu	Lys
Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	175	Asp	Gly	Phe	Val	Met	Arg
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	190	Thr	Gly	Val	Phe	Leu	Arg
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	205	Asp	Gln	Phe	Glu	Ser	Ser

225				230				235				240
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Val
				245				250				255
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile
			260					265				270
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile
			275					280				285
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val
			290					295				300
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile
			305					310				315
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys
			320					325				330
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn
			335					340				345
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu
			350					355				360
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp
			365					370				375
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp
			380					385				390
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser
			395					400				405
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg
			410					415				420
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met
			425					430				435
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro
			440					445				450
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro
			455					460				465
Val	Asp	Met						470				475

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

attctgaata	agatcaagaa	tttacaggtt	ctctctctc	tctctctcaa	gttctgtttt	60
gtttatataca	attacaactt	tagtttcgta	aatagtgact	cattagttga	tcattgtctct	120
ctatgtcttg	ctatgcaatt	caataggcta	gtgtatcacc	aatcacagat	ccgggatccc	180
ggcttagtaa	acattataaa	gcttgcatat	acactttatt	tggatttggg	tttagtaaaa	240
aaatttcatt	tacagtattt	gaaaaaatac	aaaatggcga	aaatctaccg	gaagttagaca	300
ggctacgggt	gtgaaggagg	gcgtgaatgg	gacgatgatg	tatatgaggg	tgtaagaaaa	360
gtgtatgtag	gacaagatat	caatcgtatc	acttacgtca	aattcgagta	tgtaaggaaa	420
gacggccaag	tagtaacaac	tgaatatggg	aaaatcattc	aacaacccaa	agagtttgtta	480
cttcaatatc	cggaagaaca	tcatatagcg	gtggaaggaa	actatcgccg	agtggtctcta	540
tgtgtccacag	agggtatcac	aaacctcgct	ttcaagacct	caaaagggtag	aaagtcacca	600
ctgttttggtc	caaaacttgct	tggaaattacg	accgggtaca	agttcgttat	tgaggatgga	660
ggaagaagaa	tcgtagggtt	tcattggacgg	tcgggttaag	ctctcgacgc	gcttggaggt	720
tactttgtac	atggctctct	aacaacgtct	ccgcctgttt	acaagctgga	tgcccaaggt	780
ggtagacagc	ggcgtgtttg	ggatgatggt	tcttacgacg	gcgtttaaact	gcgtcgctatt	840
ggccaagata	attctcgtat	tacttattta	gagttcgagt	acgagaaaag	cggtaaagtta	900
gagacatgtc	gccatggggt	gaaacaagaa	agatcactga	agtttagact	taaccggagt	960

```

gaatacatca aatcggtgga agcaacctat gataaaccgg acatttttcg caatgtcgtc 1020
attacatcgc ttmcatttga aacatcgaa gggagmacgt cattctctgg gtataaggga 1080
ggtaagaagt ttaagctaga gcaaaagggt cgtaggcttg tcgggtttcca tggaaaggaa 1140
ggttcagcta ttgatgccct tggagcatat ttgacaccta ttctactcc gactcctata 1200
attccagaag aaactaccag caataggcgg cagcgggagga gtgcatggg atgatggtgt 1260
ctacgatggt gtaagggaaga tacttgtagg acaaggtaac gatggtgtag cctttgtcaa 1320
gtttgaatac aataaaggaa aagatcttgt atctggagat gaccatggga agatgacatt 1380
actcgggaact gaagagtttg tgcttgaaga tggatgaatat ctacgggcca tagatggcta 1440
ttacgataag attttcgagg tcgagacacc aatgattatc tgtcttcagt ttaagacgaa 1500
caaaagggag tc

```

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1500619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

```

Ile Leu Asn Lys Lys Ile Lys Asn Leu Gln Val Leu Ser Ser Leu Ser Leu
1 5 10 15
Lys Phe Cys Phe Val Tyr Thr Asn Tyr Asn Phe Ser Phe Val Asn Arg
20 25 30
Tyr Ser Leu Val Asp His Cys Ser Leu Cys Leu Ala Met Gln Phe Asn
35 40 45
Arg Leu Val Tyr His Gln Ser Gln Ile Arg Asp Pro Gly Leu Val Asn
50 55 60
Ile Ile Lys Leu Ala Tyr Thr Leu Tyr Leu Asp Leu Val Lys
65 70 75 80
Lys Phe Ile Leu Gln Tyr Leu Lys Lys Tyr Lys Met Ala Lys Ile Tyr
85 90 95
Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly Arg Glu Trp Asp Asp
100 105 110
Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val Gly Gln Asp Ile Asn
115 120 125
Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys Glu Asp Gly Gln Val
130 135 140
Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln Pro Lys Glu Phe Val
145 150 155 160
Leu Gln Tyr Pro Asp Glu His Ile Ile Ala Val Glu Gly Asn Tyr Arg
165 170 175
Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr Asn Leu Val Phe Lys
180 185 190
Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly Pro Asn Leu Leu Gly
195 200 205
Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp Gly Gly Lys Lys Ile
210 215 220
Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu Asp Ala Leu Gly Val
225 230 235 240
Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro Pro Val Tyr Lys Leu
245 250 255
Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp Asp Asp Gly Ser Tyr
260 265 270
Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp Asn Ser Arg Ile Thr
275 280 285
Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys Leu Glu Thr Cys Arg
290 295 300
His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe Glu Leu Asn Pro Asp

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(2) INFORMATION FOR SEQ ID NO:1549:

(A) LENGTH: 373 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..373  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500620

Met 1	Gln	Phe	Asn	Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro
Gly	Leu	Val	Asn	Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu
Asp	Leu	Val	Lys	Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met
Ala	Lys	Ile	Tyr	Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg
Glu	Thr	Asp	Asp	Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly
65	Gln	Asp	Ile	Asn	Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys
Asp	Gly	Gln	Val	Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro
Lys	Glu	Phe	Val	Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu
Gly	Asn	Tyr	Arg	Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn
Leu	Val	Phe	Lys	Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro
145	Asn	Leu	Leu	Gly	Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp
Gly	Lys	Lys	Ile	Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp
Ala	Leu	Gly	Val	Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Ser	Pro	Pro	
Val	Tyr	Lys	Leu	Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp
Asp	Gly	Ser	Tyr	Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn
225	Ser	Arg	Ile	Thr	Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys
Glu	Thr	Cys	Arg	His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu

Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp Lys  
275 280 285  
Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu Thr  
290 295 300  
Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys Phe  
305 310 315 320  
Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys Glu  
325 330 335  
Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro Thr  
340 345 350  
Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln Arg  
355 360 365  
Arg Ser Cys Met Gly  
370

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

Met Ala Lys Ile Tyr Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly  
1 5 10 15  
Arg Glu Trp Asp Asp Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val  
20 25 30  
Gly Gln Asp Ile Asn Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys  
35 40 45  
Glu Asp Gly Gln Val Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln  
50 55 60  
Pro Lys Glu Phe Val Leu Gln Tyr Pro Asp Glu His Ile Ala Val  
65 70 75 80  
Glu Gly Asn Tyr Arg Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr  
85 90 95  
Asn Leu Val Phe Lys Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly  
100 105 110  
Pro Asn Leu Leu Gly Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp  
115 120 125  
Gly Gly Lys Lys Ile Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu  
130 135 140  
Asp Ala Leu Gly Val Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro  
145 150 155 160  
Pro Val Tyr Lys Leu Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp  
165 170 175  
Asp Asp Gly Ser Tyr Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp  
180 185 190  
Asn Ser Arg Ile Thr Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys  
195 200 205  
Leu Glu Thr Cys Arg His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe  
210 215 220  
Glu Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp  
225 230 235 240  
Lys Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu  
245 250 255  
Thr Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys  
260 265 270  
Phe Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys

275 280 285  
Glu Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro  
290 295 300  
Thr Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln  
305 310 315 320  
Arg Arg Ser Cys Met Gly  
325

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..721

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

aacttaaaact	cttttagtaa	caatggtttc	ttctttcttta	accaagcttg	tggtcttttg	60
ttgtctcctc	ctgctcacat	tcacggacaa	ccttggtggt	ggaaaatctg	gcaaaagtga	120
gctcaatctt	tactacgaat	caacttgctc	cgggtgtcag	gaattcatcg	tcgatgacct	180
aggtaaaaat	tttgactacg	atctctacac	aatcaactga	ctcaagctgt	ttccatttgg	240
taatgccgaa	ctctccgata	atctgactgt	caactggccag	catggtgaag	aggaatgcga	300
actaaacgcg	cttgaagctt	gcgcattaag	aacttggccc	gatcagaaat	cacaatactc	360
gttcatacgg	tcgcgtcgaaa	gcgatacgaa	aggctgggaa	tcattgtgta	aaaaatactg	420
acgtgagaaa	gacgcaagtg	aagaagactg	ataattctga	agctatttgg	gtaaaaatcca	480
attctcttca	ctcttacttg	agggtttta	ctttttgaat	ttcttttttt	ctttcttattg	540
tcttttggtt	attgttgtta	ttagtgttgt	gtttgttgtt	ttggtgatgt	tgtttgttcta	600
atcatctctt	gtttctttta	ctctggtctt	gattatttga	ataaaggata	ctctagagatt	660
gtgtgtgtgt	tgtttttgta	ataattagag	tttgataaaa	graaatwaaa	tatttaaggt	720

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..142

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

Met	Val	Ser	Ser	Ser	Leu	Thr	Lys	Leu	Val	Phe	Phe	Gly	Cys	Leu	Leu
1				5				10					15		
Leu	Leu	Thr	Phe	Thr	Asp	Asn	Leu	Val	Ala	Gly	Lys	Ser	Gly	Lys	Val
			20					25				30			
Lys	Leu	Asn	Leu	Tyr	Tyr	Glu	Ser	Leu	Cys	Pro	Gly	Cys	Gln	Glu	Phe
		35					40				45				
Ile	Val	Asp	Asp	Leu	Gly	Lys	Ile	Phe	Asp	Tyr	Asp	Leu	Tyr	Thr	Ile
	50					55				60					
Thr	Asp	Leu	Lys	Leu	Phe	Pro	Phe	Gly	Asn	Ala	Glu	Leu	Ser	Asp	Asn
65					70				75					80	
Leu	Thr	Val	Thr	Cys	Gln	His	Gly	Glu	Glu	Glu	Cys	Lys	Leu	Asn	Ala
				85				90					95		
Leu	Glu	Ala	Cys	Ala	Leu	Arg	Thr	Trp	Pro	Asp	Gln	Lys	Ser	Gln	Tyr
			100					105				110			
Ser	Phe	Ile	Arg	Cys	Val	Glu	Ser	Asp	Thr	Lys	Gly	Trp	Glu	Ser	Cys
		115					120					125			
Val	Lys	Asn	Ser	Gly	Arg	Glu	Lys	Asp	Ala	Ser	Glu	Glu	Asp		

130 135 140

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1500633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

gcaccccttt	tattgtacg	acgcaagaag	aagcagctat	agcgtacgat	atcgcgagta	60
tcgagatacc	tggaactcaac	gccgttacta	acttgcacat	cagccggtat	ctgaaacttc	120
cggtgccgga	gaacctatc	gataccgcga	ataatctcct	cgagagtcgc	cattctgatc	180
ttagccatt	tataaaacct	aaccacgagt	ctgaacttatc	acagagtcga	tcttgcacg	240
aggacaaaga	tgatcgga	acaaaagctct	tgaagtcgtc	acctttagt	gcagaggaag	300
taatcgga	atcgacgcca	cctgagattg	ctccgcctcg	tcggagcttc	ccggaagata	360
tcacagacga	tttcgggtgt	caaaactccg	gcaagttaac	ggcggaggaa	gatgatgta	420
tcttcgtgta	tttagattct	ttccttacgc	ctgatttcta	cagcgagtta	aatgattgct	480
aaagtgttgt	ttctctgata	agttttgttt	tttagttgtt	cagaatctcg	gtgtgaaaa	540
tcaacattga	cacatcgatt	attctttctt	gtgacaatct	tatataataa	agtttgaatc	600
ttttt						

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1500634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

Thr	Pro	Phe	Ile	Val	Ala	Thr	Gln	Glu	Glu	Ala	Ala	Ile	Ala	Tyr	Asp	
1				5				10				15				
Ile	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	
			20					25				30				
Ile	Ser	Arg	Tyr	Leu	Lys	Leu	Pro	Val	Pro	Glu	Asn	Pro	Ile	Asp	Thr	
			35					40				45				
Ala	Asn	Asn	Leu	Leu	Glu	Ser	Pro	His	Ser	Asp	Leu	Ser	Pro	Phe	Ile	
			50					55				60				
Lys	Pro	Asn	His	Glu	Ser	Asp	Leu	Ser	Gln	Ser	Gln	Ser	Ser	Ser	Glu	
			65					70				75			80	
Asp	Asn	Asp	Asp	Arg	Lys	Thr	Lys	Leu	Leu	Lys	Ser	Ser	Pro	Leu	Val	
				85				90				95				
Ala	Glu	Glu	Val	Ile	Gly	Pro	Ser	Thr	Pro	Pro	Glu	Ile	Ala	Pro	Pro	
			100					105				110				
Arg	Arg	Ser	Phe	Pro	Glu	Asp	Ile	Gln	Thr	Tyr	Phe	Gly	Cys	Gln	Asn	
			115					120				125				
Ser	Gly	Lys	Leu	Thr	Ala	Glu	Glu	Asp	Asp	Val	Ile	Phe	Gly	Asp	Leu	
			130					135				140				
Asp	Ser	Phe	Leu	Thr	Pro	Asp	Phe	Tyr	Ser	Glu	Leu	Asn	Asp	Cys		
			145					150				155				

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1393

(D) OTHER INFORMATION: / Ceres Seq. ID 1500645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

aagccataga	tattgacaa	atacactttt	tgtctttttt	ttgtcgtgtca	acgtcataga	60
tcttaactccg	gaagaagaag	aagatgagtg	agcaaacgac	gtcatctccg	tcccaagctc	120
cggcgagaag	gaagcagaat	ctgggattgga	tggagtggtg	gaggggatgtg	acgagtgtgt	180
ctggggagat	tctcttccag	aggatcacag	ctctctcaat	ggagaatctc	ctctctcttc	240
cttccgttca	cgactccaat	tgcgtttgtca	ctggctccac	cagcggcat	ggccgtgaaa	300
cccgaggcca	gcttgcaaga	cggtgtgtct	atgtgttttc	ggcgctaaag	aacacaaaag	360
cggctcagga	cggtacatgt	caatgcgcaga	acgaaatggtc	tgtgaaaggt	ctcccactca	420
attattgagc	aatggagatt	gactctactct	catcgattgt	tgttcggaga	tttgtgtgag	480
ctttcaacgc	tcgggttagga	cttttgcatt	tcttgatttaa	caatcgtggg	atgtttgtcta	540
tggtggagag	gcaaaaatct	tacaggagaag	gatatagaca	gcacatcgaa	gtgaatcatt	600
gaatccacgc	gctgctttca	gtactctctt	tggcctctct	gacccgagcg	tctctcagcc	660
tagcatcatta	tgtgaattcc	tttatgcata	tgtctggttt	ttgttgacccg	gactgatgtc	720
atgtttgttt	tggttagactg	aagtatctaa	gccctattcg	atactcaaac	acgaagctgt	780
cccgatttat	tctttagtgc	attcttttca	aaaagcttgc	tctgtaaaag	ggaagtccgc	840
tcgttatgtct	atcccttggt	gtgtgtcttaa	caaatgttgc	cagggatctca	tccaggattc	900
ttcaagctct	ttacgcagtg	ataccttatt	tcatatttct	accocaaaga	tggtgtagaa	960
gttctctctt	ctcgggcaca	gaatccacga	tctcagagta	ctgggaaaca	ctaaaaaacg	1020
atgatattatt	tgtttgccca	tctactcttc	aagattccgc	ccctcgcaat	ccttccgaag	1080
aagcacacaa	ccagaaaact	gcacagagag	tgtggaaaaa	gacgtttagag	ctggttgggtc	1140
ttctctctga	tgcagtttag	aagctcatag	aagtgaaaaa	tatccaatcg	cggtatagag	1200
cacaaacaga	aatgtctttc	aaaaattaca	cagtttaagt	gacccattca	agatcaaaag	1260
gtaggttagt	gagaaaaatc	cttttttttc	tgtttctctg	tattaattca	cacgatcaag	1320
tgaggaaatg	atcccccgac	catgtagtgt	gcttgagaat	gtttgattgt	tggataaaag	1380
ccagagcttta	gct					

(2) INFORMATION FOR SEQ ID NO:1556:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) **FEATURE:**

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1500646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

Met	Ser	Asp	Glu	Thr	Thr	Ser	Ser	Pro	Ser	Pro	Ala	Pro	Ala	Lys	Lys
1			5						10					15	
Lys	Gln	Asn	Leu	Gly	Trp	Met	Glu	Trp	Met	Arg	Gly	Trp	Ser	Ser	Val
		20						25					30		
Phe	Gly	Glu	Ile	Leu	Phe	Gln	Arg	Ile	Thr	Ala	Ser	His	Leu	Glu	Asn
		35					40					45			
Pro	Leu	Pro	Leu	Pro	Ser	Val	Asn	Asp	Leu	Thr	Cys	Val	Val	Thr	Gly
	50					55					60				
Ser	Thr	Ser	Gly	Ile	Gly	Arg	Glu	Thr	Ala	Arg	Gln	Leu	Ala	Glu	Ala
65					70					75				80	
Gly	Ala	His	Val	Val	Met	Ala	Val	Arg	Asn	Thr	Lys	Ala	Ala	Gln	Glu
				85					90					95	
Leu	Ile	Leu	Gln	Trp	Gln	Asn	Glu	Trp	Ser	Gly	Lys	Gly	Leu	Pro	Leu
		100						105					110		
Asn	Ile	Glu	Ala	Met	Glu	Ile	Asp	Leu	Leu	Ser	Leu	Asp	Ser	Val	Ala
		115					120					125			
Arg	Phe	Ala	Glu	Ala	Phe	Asn	Ala	Arg	Leu	Gly	Pro	Leu	His	Val	Leu
130						135					140				

Ile Asn Asn Ala Gly Met Phe Ala Met Gly Glu Ala Gln Lys Phe Ser  
145 150 155 160  
Glu Glu Gly Tyr Glu Gln His Met Gln Val Asn His Leu Ala Pro Ala  
165 170 175  
Leu Leu Ser Val Leu Leu Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser  
180 185 190  
Arg Ile Ile Asn Val Asn Ser Val Met His Ser Val Gly Phe Val Asp  
195 200 205  
Pro Asp Asp Met Asn Val Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu  
210 215 220  
Ile Gly Tyr Ser Ser Ser Lys Leu Ala Gln Ile Met Phe Ser Ser Ile  
225 230 235 240  
Leu Phe Lys Lys Leu Pro Leu Glu Thr Gly Val Ser Val Val Cys Leu  
245 250 255  
Ser Pro Gly Val Val Leu Thr Asn Val Ala Arg Asp Leu Ser Arg Ile  
260 265 270  
Leu Gln Ala Leu Tyr Ala Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln  
275 280 285  
Glu Gly Cys Arg Ser Ser Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro  
290 295 300  
Glu Tyr Trp Glu Thr Leu Lys Asn Asp Asp Trp Pro Val Cys Pro Phe  
305 310 315 320  
Ile Ser Gln Asp Cys Arg Pro Ala Asn Pro Ser Glu Glu Ala His Asn  
325 330 335  
Thr Glu Thr Ala Gln Arg Val Trp Lys Lys Thr Leu Glu Leu Val Gly  
340 345 350  
Leu Pro Leu Asp Ala Val Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln  
355 360 365  
Cys Arg Tyr Gly Ala Gln His Glu  
370 375

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe  
1 5 10 15  
Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser  
20 25 30  
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly  
35 40 45  
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met  
50 55 60  
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln  
65 70 75 80  
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu  
85 90 95  
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe  
100 105 110  
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met  
115 120 125  
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln  
130 135 140  
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu

145 150 155 160  
Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser Arg Ile Ile Asn Val Asn  
165 170  
Ser Val Met His Ser Val Gly Phe Val Asp Pro Asp Asp Met Asn Val  
180 185 190  
Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser  
195 200  
Lys Leu Ala Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro  
210 215 220  
Leu Glu Thr Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu  
225 230 235 240  
Thr Asn Val Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala  
245 250 255  
Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser  
260 265 270  
Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu  
275 280 285  
Lys Asn Asp Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg  
290 295 300  
Pro Ala Asn Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg  
305 310 315 320  
Val Trp Lys Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val  
325 330 335  
Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln  
340 345 350  
His Glu

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..351

(D) OTHER INFORMATION: / Ceres Seq. ID 1500648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe Gln Arg Ile  
1 5 10 15  
Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser Val Asn Asp  
20 25 30  
Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly Arg Glu Thr  
35 40 45  
Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met Ala Val Arg  
50 55 60  
Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln Asn Glu Trp  
65 70 75 80  
Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu Ile Asp Leu  
85 90 95  
Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe Asn Ala Arg  
100 105 110  
Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met Phe Ala Met  
115 120 125  
Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln His Met Gln  
130 135 140  
Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu Leu Pro Ser  
145 150 155 160  
Leu Ile Arg Gly Ser Pro Ser Arg Ile Ile Asn Val Asn Ser Val Met  
165 170 175

His	Ser	Val	Gly	Phe	Val	Asp	Pro	Asp	Asp	Met	Asn	Val	Val	Ser	Gly
			180					185					190		
Arg	Arg	Lys	Tyr	Ser	Ser	Leu	Ile	Gly	Tyr	Ser	Ser	Ser	Lys	Leu	Ala
		195					200					205			
Gln	Ile	Met	Phe	Ser	Ser	Ile	Leu	Phe	Lys	Lys	Leu	Pro	Leu	Gly	Thr
		210				215					220				
Gly	Val	Ser	Val	Val	Cys	Leu	Ser	Pro	Gly	Val	Val	Leu	Thr	Asn	Val
		225			230				235					240	
Ala	Arg	Asp	Leu	Ser	Arg	Ile	Leu	Gln	Ala	Leu	Tyr	Ala	Val	Ile	Pro
			245					250						255	
Tyr	Phe	Ile	Phe	Ser	Pro	Gln	Glu	Gly	Cys	Arg	Ser	Ser	Leu	Phe	Ser
		260						265					270		
Ala	Thr	Asp	Pro	Gln	Ile	Pro	Glu	Tyr	Trp	Glu	Thr	Leu	Lys	Asn	Asp
		275					280					285			
Asp	Trp	Pro	Val	Cys	Pro	Phe	Ile	Ser	Gln	Asp	Cys	Arg	Pro	Ala	Asn
		290				295					300				
Pro	Ser	Glu	Glu	Ala	His	Asn	Thr	Glu	Thr	Ala	Gln	Arg	Val	Trp	Lys
		305			310					315				320	
Lys	Thr	Leu	Glu	Leu	Val	Gly	Leu	Pro	Leu	Asp	Ala	Val	Glu	Lys	Leu
			325					330						335	
Ile	Glu	Gly	Glu	Asn	Ile	Gln	Cys	Arg	Tyr	Gly	Ala	Gln	His	Glu	
			340					345					350		

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

atagtaaac	tattagccct	gtctttgctc	ttgaagcaac	ttctccagg	agggttggtt	60
jcaaaagctgc	tgctgggtg	tcaggtgact	tacctgagag	tactcctaag	gaacttagtc	120
agtatgagaa	gattattgag	cttttgacaa	ccctttttcc	actttgggtt	attttgggaa	180
cacttggttg	catcttcaag	ccatccttgg	ttacatgggt	ggaaacagat	ctctttactc	240
taggtcttgg	atttcttatg	ctttccatgg	gtttgactct	tacgtttgaa	gatctcagaa	300
gatgtttacg	taatccatgg	acggtgggtg	ttggttttct	tgctcaatat	atgatcaagc	360
caattctagg	ttttctcatt	gcaatgactc	ttaaagcttc	ggcacctctt	gcgactggcc	420
ttatcctagt	ctcatgtctc	cctggaggac	aggcgctcaa	cgttgctact	tacatttcca	480
aggggaaagt	agcgctctct	gtactcatga	caacgtgttc	aaccattggg	gctattataa	540
tgactcctct	cttactaaag	cttcttgctg	gtcagctgtg	tcccggtgac	gctgctggac	600
ttgctcttag	tacgttccaa	gtagtgttgg	ttctccacct	aattggagtt	ctggcacaatg	660
agttctttcc	taaattttacg	tctaagatca	taacagtgac	gcctcctaact	ggagtcatct	720
tgactactct	gctctgtgcc	agccctattg	gacaagtgtc	agatgttttg	aaaacccaag	780
gagctcaact	tatactcccg	gtggcactcc	ttcatgtctc	agcctttgct	attggctatt	840
ggatttcaaa	gttttcttcc	ggcgagtgca	cttcgcgtac	catcttctata	gaatgtggaa	900
tgcaaaagtg	agcgctcggg	ttcttgcttg	cacaaaaagca	tttcacaaac	ccctctagttg	960
ctgttctctc	tgacgtcagt	gtttctctgta	tggcgcttgg	cggggagcggc	ctggcctgtg	1020
ctctggagaaa	cctaccgatt	ccggcagatg	acaaggatga	cttcaaaagag	taaatgaagt	1080
aggaaagcgt	gtttgcatct	ttctccaaagc	atgtgattgt	tttgttgtaa	tgtagtaaaa	1140
cattacaaca	tttgtgttga	aaaaacatgaa	acaaaatgtg	tttaagagac	atagaacaaa	1200
gggcgtgcac	gatgacaact	ttgtgggtcaa	cctttttttt	atttctcaat	taatggacaa	1260
atcttttttg	gc					

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..356  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Ser Lys Pro Ile Ser Pro Val Phe Ala Leu Glu Ala Thr Ser Ser Arg  
1 5 10 15  
Arg Val Val Cys Lys Ala Ala Ala Gly Val Ser Gly Asp Leu Pro Glu  
20 25 30  
Ser Thr Pro Lys Glu Leu Ser Gln Tyr Glu Lys Ile Ile Glu Leu Leu  
35 40 45  
Thr Thr Leu Phe Pro Leu Trp Val Ile Leu Gly Thr Leu Val Gly Ile  
50 55 60  
Phe Lys Pro Ser Leu Val Thr Trp Leu Glu Thr Asp Leu Phe Thr Leu  
65 70 75 80  
Gly Leu Gly Phe Leu Met Leu Ser Met Gly Leu Thr Leu Thr Phe Glu  
85 90 95  
Asp Phe Arg Arg Cys Leu Arg Asn Pro Trp Thr Val Gly Val Gly Phe  
100 105 110  
Leu Ala Gln Tyr Met Ile Lys Pro Ile Leu Gly Phe Leu Ile Ala Met  
115 120 125  
Thr Leu Lys Leu Ser Ala Pro Leu Ala Thr Gly Leu Ile Leu Val Ser  
130 135 140  
Cys Cys Pro Gly Gly Gln Ala Ser Asn Val Ala Thr Tyr Ile Ser Lys  
145 150 155 160  
Gly Asn Val Ala Leu Ser Val Leu Met Thr Thr Cys Ser Thr Ile Gly  
165 170 175  
Ala Ile Ile Met Thr Pro Leu Leu Thr Lys Leu Leu Ala Gly Gln Leu  
180 185 190  
Val Pro Val Asp Ala Ala Gly Leu Ala Leu Ser Thr Phe Gln Val Val  
195 200 205  
Leu Val Pro Thr Ile Ile Gly Val Leu Ala Asn Glu Phe Phe Pro Lys  
210 215 220  
Phe Thr Ser Lys Ile Ile Thr Val Thr Pro Leu Ile Gly Val Ile Leu  
225 230 235 240  
Thr Thr Leu Leu Cys Ala Ser Pro Ile Gly Gln Val Ala Asp Val Leu  
245 250 255  
Lys Thr Gln Gly Ala Gln Leu Ile Leu Pro Val Ala Leu Leu His Ala  
260 265 270  
Ala Ala Phe Ala Ile Gly Tyr Trp Ile Ser Lys Phe Ser Phe Gly Glu  
275 280 285  
Ser Thr Ser Arg Thr Ile Ser Ile Glu Cys Gly Met Gln Ser Ser Ala  
290 295 300  
Leu Gly Phe Leu Leu Ala Gln Lys His Phe Thr Asn Pro Leu Val Ala  
305 310 315 320  
Val Pro Ser Ala Val Ser Val Val Cys Met Ala Leu Gly Gly Ser Gly  
325 330 335  
Leu Ala Val Phe Trp Arg Asn Leu Pro Ile Pro Ala Asp Asp Lys Asp  
340 345 350 355  
Asp Phe Lys Glu

(2) INFORMATION FOR SEQ ID NO:1561:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1500651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys	
1				5					10						15	
Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met	
			20						25					30		
Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser	
			35						40					45		
Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly	
			50						55					60		
Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu	
			65						70					80		
Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr	
				85					90					95		
Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu	Val	Pro	Val	Asp	Ala	
				100					105					110		
Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val	Leu	Val	Pro	Thr	Ile	
				115					120					125		
Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys	Phe	Thr	Ser	Lys	Ile	
				130					135					140		
Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu	Thr	Thr	Leu	Leu	Cys	
				145					150					155		
Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu	Lys	Thr	Gln	Gly	Ala	
				165					170					175		
Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala	Ala	Ala	Phe	Ala	Ile	
				180					185					190		
Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu	Ser	Thr	Ser	Arg	Thr	
				195					200					205		
Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala	Leu	Gly	Phe	Leu	Leu	
				210					215					220		
Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala	Val	Pro	Ser	Ala	Val	
				225					230					235		
Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly	Leu	Ala	Val	Phe	Trp	
				245					250					255		
Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp	Asp	Phe	Lys	Glu		
				260					265					270		

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1500652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn	
1				5					10					15		
Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro	
				20					25					30		
Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu	
				35					40					45		
Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser	
				50					55					60		
Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu	Ser	Val	Leu	
				65					70					80		
Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu	

Met	Glu	Asp	Lys	Ser	Pro	Thr	Leu	Pro	Ile	Ser	Glu	Asp	Leu	Ser	Arg
1				5					10					15	
Lys	Ile	Ile	Ser	Leu	Ala	Ala	Gly	Glu	Ala	His	Thr	Ile	Ala	Leu	Thr
			20					25					30		
Gly	Asp	Gly	Cys	Val	Tyr	Ser	Trp	Gly	Arg	Gly	Met	Phe	Gly	Arg	Leu

[illegible]

(2) INFORMATION FOR SEO ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..99  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

```
(D) TOPOLOGY: linear
```

## (ii) MOLECULE

- ```
FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
```

(D) OTHER INFORMATION: / Ceres Seq.  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Gly | Arg | Leu | Gly | Thr | Gly | Lys | Glu | Ser | Asp | Glu | Leu | Val | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Arg | Val | Glu | Phe | Glu | Phe | Pro | Asn | Gln | Ala | Glu | Gly | Glu | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ile | Ile | Gly | Val | Ala | Ala | Gly | Ala | Tyr | His | Ser | Leu | Ala | Val | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Asp | Gly | Ser | Val | Trp | Cys | Trp | Gly | Tyr | Asn | Ile | Tyr | Gly | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gly | Phe | Asp | Gly | Glu | Asn | Ser | Leu | Ala | Pro | Cys | Leu | Val | Lys | Asn | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |

Phe Glu Gln Glu Ala Ser Ser Ser Ser

85

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

```
aaaaacccta gaaaacctct ggagctatgg agatgatgca ggatctgctt caagtccata      60
ggattccaca atcgaaagtat gtcgatggag ttatgatggct tccacaagct ctctgcttga      120
atcgctttctt cgcacaacgcg tccatgatgac cggattgtga ttcttcaatca atcgagatcc      180
aatcgtctga cccaaaacctt agaggggaatc acaacacgaa cccgttaatc gagtcgttat      240
cttcattggac ttcaactctct cgcgtttcgt ctctagaagt cgcgggaaac ggcggtgttg      300
ggcggttcatt caaacaatg gttcagcgt ctacgtctct tggttctctt caagttctga      360
tgattgtattt gtgggaaggga gctgcgattg aagaggttta cgcggcgga gggggaagag      420
tttcatrctg ggacgcgtg agaggtgtgga ttggagagag ggagagaaat gtgttactgt      480
tggtgaagat gggagagtgga atgtagtga gattgtgaat ggtgaaggtt taaggtatag      540
aaaggtctttt gtatgggaatg gattgtgtgc ttatagagct gtgaaatggg cttctccgac      600
tgagtttgtt actggaggat atggttttgg ttgcaattg tggggtcaga ggaagtcttg      660
tgaagctgtt tcacaactca aagggaaactg gtttcaaggc aaaacttctg caattgtcca      720
ctccattgac attcatccat ctcggaagca cacttgcatc gcgggaggtt cttcaggtac      780
tgtatttgct tgggattcttc ggtggccaca gcaaccattt gttcttctg gggtgtggagc      840
aagtgtgaag ataacaacat ctctgtctga aagtgaggta tgggaagttc aggtatgactc      900
atcacaaaaa tccaactctc catcctcaag gattctccct gttatgacct gctctgaaga      960
tggaatccctt ggtatcatag aacaagggga agaaccaatc gagcttctg ctgaaccttg      1020
tgccattaac agttttgaca tcgacaggca aaatccacag gatgtgatat gtacgtctga      1080
gtgggaatca atagcagttt tctcaaggcc ttagtataat atggaactgt gcacggtatg      1140
ctatgttttc ttctgcgagc tacacaagaa aaattgagga aggtagtgat agatgatgag      1200
agacaagttt atggaagagg gttgtggaat gtgtttataa ttccattata caaatgattc      1260
aaaatacatt ctgcacaaac agagttttgt attcatctta aagttagtgt gatcttgaag      1320
atttgc
```

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

```
Met Glu Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser      1
1 5 10 15
Lys Tyr Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn      20
25 30
Arg Phe Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ser      35
40 45
Ile Glu Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr      50
55 60
Asn Pro Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val      65
70 75 80
Ser Ser Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Ser Phe Lys      85
90 95
```

Pro Met Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met  
100 105 110  
Ile Asp Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu  
115 120 125  
Gly Gly Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu  
130 135 140  
Arg Glu Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr  
1 5 10 15  
Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe  
20 25 30  
Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ile Glu  
35 40 45  
Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro  
50 55 60  
Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser  
65 70 75 80  
Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Ser Phe Lys Pro Met  
85 90 95  
Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met Ile Asp  
100 105 110  
Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu Gly Gly  
115 120 125  
Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu Arg Glu  
130 135 140  
Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr Val  
1 5 10 15  
Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe  
20 25 30  
Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ile Glu Ile  
35 40 45  
Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro Leu  
50 55 60  
Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|--|--|----|
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     | 75  |  |  |  |  |  |  |  |  |  |  |  |  |  | 80 |
| Glu | Val | Ala | Gly | Asn | Gly | Gly | Gly | Gly | Gly | Ser | Phe | Lys | Pro | Met | Val |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Ser | Ala | Ala | Thr | Ser | Ser | Gly | Ser | Leu | His | Val | Leu | Met | Ile | Asp | Leu |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Val | Glu | Gly | Ala | Ala | Ile | Glu | Glu | Val | Tyr | Ala | Ala | Glu | Gly | Gly | Glu |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Val | Ser | Xaa | Trp | Asp | Ala | Trp | Lys | Val | Trp | Ile | Gly | Glu | Arg | Glu | Glu |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
| Asn | Val | Leu | Leu | Leu | Val | Lys | Met | Gly | Glu |     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |
|     |     |     |     | 145 |     |     |     |     |     | 150 |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |  |  |    |

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| acataagtct | ctctcttaca | ttttgaacc  | ctaattctct  | aaaaataatg  | tctgaagtgt  | 60  |
| agtaccggtg | ctttgtcggc | ggccttgcc  | gggccaccaa  | tgatgaagat  | cttcaaaagga | 120 |
| cgttctcaca | gttcggcgac | gttatcgatt | ctaagatcat  | taacgaccgc  | gagagtggaa  | 180 |
| gatcaagggg | attcggattc | gtcaccttca | aggacgagaa  | agccatgagg  | gatcgcatgt  | 240 |
| agagatgaa  | cggtaaagag | ctcgatggac | gtgtcatcac  | cggtgaacgag | gctcagtcga  | 300 |
| gaggtacggg | cggtgatggt | gaaagttaac | gaggcggtgg  | tggtcggtgg  | taatcaaaaga | 360 |
| tagagtgtgt | tgcgtgctgc | tgcctctgtt | ttgtgtttaga | tttggatttg  | tgtcaccact  | 420 |
| tctggtttgg | ttatcgtttc | tttggtttac | tttttggatg  | aaacagtttc  | gtttaagtct  | 480 |
| tccttgtctg | gatcgaaatg | ttaattcgcg | tggtgtttac  | taaattttata | acgtttctct  | 540 |
| tt         |            |            |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Val | Glu | Tyr | Arg | Cys | Phe | Val | Gly | Gly | Leu | Ala | Trp | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Thr | Asn | Asp | Glu | Asp | Leu | Gln | Arg | Thr | Phe | Ser | Gln | Phe | Gly | Asp | Val |
|     |     |     |     | 20  |     |     |     |     |     |     |     |     |     | 30  |     |
| Ile | Asp | Ser | Lys | Ile | Ile | Asn | Asp | Arg | Glu | Ser | Gly | Arg | Ser | Arg | Gly |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Phe | Gly | Phe | Val | Thr | Phe | Lys | Asp | Glu | Lys | Ala | Met | Arg | Asp | Ala | Ile |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Glu | Glu | Met | Asn | Gly | Lys | Glu | Leu | Asp | Gly | Arg | Val | Ile | Thr | Val | Asn |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Glu | Ala | Gln | Ser | Arg | Gly | Ser | Gly | Gly | Asp | Gly | Glu | Ser | Tyr | Gly | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gly | Gly | Gly | Gly | Trp |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..931

(D) OTHER INFORMATION: / Ceres Seq. ID 1500667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

|             |            |             |            |             |             |     |
|-------------|------------|-------------|------------|-------------|-------------|-----|
| aagatgggga  | cgaattgag  | ctggatata   | aagctgtcga | caatgagact  | ctatggggagc | 60  |
| ttgatcggtt  | tgtgacgaac | tacaagaaga  | tggctagcaa | aatcaagcgc  | caagggtttta | 120 |
| tcaggaaact  | gtcaactcca | cttaggaaca  | tggcttcggt | agcagaaatg  | ggtagtgcgg  | 180 |
| aaagagagaac | aaggagagga | gatgcagggg  | aaagagatgt | tgacattgga  | ggagacatac  | 240 |
| caatcgaaga  | ttatccatct | stagaagatc  | aaagagatgg | gtactgcagt  | tgcagtgctc  | 300 |
| gtctagtgtg  | gttctatgtc | ttcagcgagt  | tccagttcta | gtgtgtgtag  | ttcctctgct  | 360 |
| agtgtttcag  | ggtcagggtg | gagttcatca  | ggtagtgtat | ctgatgcaga  | tagtgttcaa  | 420 |
| tcgccattct  | tgggaagcaa | agaagcccaa  | tgttaaaatc | atttggggaat | ttaaccgttg  | 480 |
| attcttctct  | gaagtactag | gaacgttttag | ctgaggggtg | aaaggggaga  | atgaaggggga | 540 |
| aaactgaagg  | aaaggtattg | ttttttcttt  | cgatgataaa | cttaggaagc  | agatgtagtt  | 600 |
| agaaagamaa  | aattgtaaat | gtagatagaa  | agagaatgct | agtttaagca  | agaagaagag  | 660 |
| ttcgttattt  | ataacttttt | acatttagga  | gttggtttag | gtatttgga   | gatgctgaac  | 720 |
| agagggtagg  | agtgtagggg | taggtactgt  | aggagaagaa | gaagaagaaa  | agagttctttt | 780 |
| taggttctat  | gacttttatt | atttttcttt  | gttagtagtg | ttaaagagtc  | tggttggtgtg | 840 |
| aggaaaaaat  | gtgtataga  | agaagaagaa  | aatcaatgca | atgtatcaga  | tgtaaatggt  | 900 |
| tgccatatta  | aaaaagaaa  | gttgattttc  | c          |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Gly | Asp | Glu | Ile | Glu | Leu | Asp | Ile | Glu | Ala | Val | Asp | Asn | Glu | Thr |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |  |
| Leu | Trp | Glu | Leu | Asp | Arg | Phe | Val | Thr | Asn | Tyr | Lys | Lys | Met | Ala | Ser |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |  |
| Lys | Ile | Lys | Arg | Gln | Gly | Phe | Ile | Arg | Asn | Val | Ser | Thr | Pro | Leu | Arg |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Asn | Met | Ala | Ser | Val | Ala | Glu | Met | Gly | Ser | Ala | Glu | Lys | Arg | Thr | Arg |  |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | Gly | Asp | Ala | Gly | Glu | Glu | Asp | Val | Asp | Ile | Gly | Glu | Asp | Ile | Pro |  |
|     |     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |  |
| Ile | Glu | Asp | Tyr | Pro | Ser | Xaa | Glu | Ile | Glu | Arg | Asp | Gly | Tyr | Cys | Ser |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Cys | Ser | Cys | Cys |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1500669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Lys | Ile | Lys | Arg | Gln | Gly | Phe | Ile | Arg | Asn | Val | Ser | Thr |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Pro | Leu | Arg | Asn | Met | Ala | Ser | Val | Ala | Glu | Met | Gly | Ser | Ala | Glu | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Thr | Arg | Arg | Gly | Asp | Ala | Gly | Glu | Glu | Asp | Val | Asp | Ile | Gly | Glu |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Asp | Ile | Pro | Ile | Glu | Asp | Tyr | Pro | Ser | Xaa | Glu | Ile | Glu | Arg | Asp | Gly |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Tyr | Cys | Ser | Cys | Ser | Cys |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Ala | Val | Ala | Ala | Ala | Ser | Ser | Gly | Ser | Ser | Ser | Ser |     |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Ser | Ser | Ser | Ser | Ser | Ser | Gly | Gly | Ser | Ser | Ser | Ser | Asp | Ser | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Gly | Gly | Ser | Ser | Ser | Gly | Ser | Asp | Ser | Asp | Ala | Asp | Ser | Val | Gln |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Pro | Phe | Val | Glu | Ala | Lys | Glu | Ala | Gln | Cys |     |     |     |     |     |
| 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1506

(D) OTHER INFORMATION: / Ceres Seq. ID 1500675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| accgagaaat  | gggatcgta   | gcgaatacac  | aaaccaacgg  | caacgcaccg  | ccaccgtcgt  | 60  |
| cgaatcaaaa  | gcctccggct  | acgaacggcg  | ttgatgggtc  | tcactctcct  | cctcctcctt  | 120 |
| taactcctga  | tcaagctatt  | atagagtcgg  | atccgtcgaa  | gaagaggaaa  | atggggatgc  | 180 |
| ttcctctaga  | agtggtgtact | cgtgtgatgt  | gtcgggtggag | agacgggaaa  | caccatccgg  | 240 |
| tgaagagta   | tgagcgcgg   | cggataycat  | aacggcggtc  | aaaatgatta  | cgagtattac  | 300 |
| gttcattaca  | ctgagtttaa  | taggaggtcg  | gatgaatgga  | ctcagctgga  | ccaaactggac | 360 |
| ctgtattcag  | tagagtgccg  | tgtagatgaa  | aaattggaag  | acaaggtaac  | aagccttgaag | 420 |
| gatgacacgt  | caccagaaga  | ggaagatcga  | tgaggacaca  | tatagaggtg  | catgaagagc  | 480 |
| tggatgcagc  | aagtttgcgt  | gaacatgaa   | agttcacgaa  | agtgaagaac  | atatcaacaa  | 540 |
| ttgagcctgg  | aaaatatgag  | atgagagact  | ggtaactctc  | cccttttcgc  | ccagaataca  | 600 |
| atgactgtgt  | gaagctcttt  | ttttgtgagt  | tttgctgtaa  | cttcattgaa  | cgcaaaagagc | 660 |
| gaagctcaaa  | gcatatgag   | aagttgtgacc | tgaagcacc   | acctgtgtat  | gaaatttacc  | 720 |
| gaagtgtgtac | cttgtcaatg  | cttgtggtag  | atggcaaaaa  | gaacaagggtt | tatgcacaga  | 780 |
| atctctgtcta | cctggcaaa   | ttatttcttg  | accacaaaac  | tcctttactac | gatgttgatt  | 840 |
| tgtttctatt  | ctacgctctt  | tgcgaatgtg  | atgaccgagg  | atgccacatg  | gttgggtact  | 900 |
| tttcaaaagga | gaagcattcg  | gaagaagcat  | acaacttagc  | ttgcattcta  | accctgcctt  | 960 |

catatcaaaag aaaaggctat ggaaagttct taatagcctt ttccatgtaa ctgtcaaaaga 1020  
aagaggggaaa agttggggaca ccgggraaaga cccttgctcg atctaggcctt actaagctac 1080  
agaggttatt ggactcgtgt tctattagaa atcttgaaaa aacataaggg aaacatttct 1140  
atcaaggagc tgagcgagctg gagacgaatc aaagcggaag atatatataa cacacttcag 1200  
agcctagaac tgatacagta caggaaaagga cagcatgtga tctgtgcgga tccaaaaggtt 1260  
ctggaccgac atctgaaagc tgcaggccga ggtgtctctg atgtagatgc tagcaaaactg 1320  
atttgagacac cttacaagga ccagagttaa gagtaagtac actcctcttg tgccatttga 1380  
tttgatttga gtgtgtaagt aaggggctgt cttattctcc tgaatgttaa gtgtacttta 1440  
cttgtaaatg ttgaaatcgt acttggaatg gtgtttgttt acaactnctt ataagtaggga 1500  
aatttg

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met Arg Thr His Ile Glu Gly His Glu Leu Asp Ala Ala Ser Leu  
1 5 10 15  
Arg Glu His Glu Glu Phe Thr Lys Val Lys Asn Ile Ser Thr Ile Glu  
20 25 30  
Leu Gly Lys Tyr Glu Ile Glu Thr Trp Tyr Phe Ser Pro Phe Pro Pro  
35 40 45  
Glu Tyr Asn Asp Cys Val Lys Leu Phe Phe Cys Glu Phe Cys Leu Asn  
50 55 60  
Phe Met Lys Arg Lys Glu Gln Leu Gln Arg His Met Xaa Lys Cys Asp  
65 70 75  
Leu Lys His Pro Pro Gly Asp Glu Ile Tyr Arg Ser Gly Thr Leu Ser  
85 90 95  
Met Phe Glu Val Asp Gly Lys Lys Asn Lys Val Tyr Ala Gln Asn Leu  
100 105 110  
Cys Tyr Leu Ala Lys Leu Phe Leu Asp His Lys Thr Leu Tyr Tyr Asp  
115 120 125  
Val Asp Leu Phe Leu Phe Tyr Val Leu Cys Glu Cys Asp Asp Arg Gly  
130 135 140  
Cys His Met Val Gly Tyr Phe Ser Lys Glu Lys His Ser Glu Glu Ala  
145 150 155  
Tyr Asn Leu Ala Cys Ile Leu Thr Leu Pro Ser Tyr Gln Arg Lys Gly  
160 165 170  
Tyr Gly Lys Phe Leu Ile Ala Phe Ser Tyr Glu Leu Ser Lys Lys Glu  
180 185 190  
Gly Lys Val Gly Thr Pro Xaa Lys Thr Leu Val Gly Ser Arg Leu Thr  
195 200 205  
Lys Leu Gln Arg Leu Leu Asp Ser Cys Ser Ile Arg Asn Leu Glu Lys  
210 215 220

Thr  
225

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Arg | Lys | Glu | Gln | Leu | Gln | Arg | His | Met | Xaa | Lys | Cys | Asp | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg | Ser | Gly | Thr | Leu | Ser | Met |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val | Tyr | Ala | Gln | Asn | Leu | Cys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys | Thr | Leu | Tyr | Tyr | Asp | Val |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu | Cys | Asp | Asp | Arg | Gly | Cys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys | His | Ser | Glu | Glu | Ala | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser | Tyr | Gln | Arg | Lys | Gly | Tyr |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu | Leu | Ser | Lys | Lys | Glu | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val | Gly | Ser | Arg | Leu | Thr | Lys |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile | Arg | Asn | Leu | Glu | Lys | Thr |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Xaa | Lys | Cys | Asp | Leu | Lys | His | Pro | Pro | Gly | Asp | Glu | Ile | Tyr | Arg |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser | Gly | Thr | Leu | Ser | Met | Phe | Glu | Val | Asp | Gly | Lys | Lys | Asn | Lys | Val |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Tyr | Ala | Gln | Asn | Leu | Cys | Tyr | Leu | Ala | Lys | Leu | Phe | Leu | Asp | His | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Leu | Tyr | Tyr | Asp | Val | Asp | Leu | Phe | Leu | Phe | Tyr | Val | Leu | Cys | Glu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Cys | Asp | Asp | Arg | Gly | Cys | His | Met | Val | Gly | Tyr | Phe | Ser | Lys | Glu | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| His | Ser | Glu | Glu | Ala | Tyr | Asn | Leu | Ala | Cys | Ile | Leu | Thr | Leu | Pro | Ser |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Tyr | Gln | Arg | Lys | Gly | Tyr | Gly | Lys | Phe | Leu | Ile | Ala | Phe | Ser | Tyr | Glu |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Leu | Ser | Lys | Lys | Glu | Gly | Lys | Val | Gly | Thr | Pro | Xaa | Lys | Thr | Leu | Val |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Ser | Arg | Leu | Thr | Lys | Leu | Gln | Arg | Leu | Leu | Asp | Ser | Cys | Ser | Ile |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Asn | Leu | Glu | Lys | Thr |     |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..889  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

|            |             |             |            |            |             |     |
|------------|-------------|-------------|------------|------------|-------------|-----|
| aaaacgaact | agagacagtt  | tgattcgaaa  | atcttgcg   | aaaatggagg | atatcgtcga  | 60  |
| ccaagaatta | agcaattact  | gggaacctag  | ctctctgctc | caaaacgaat | acttcgaata  | 120 |
| cgacagctgg | ccctttggaag | aagccatttc  | tggttcgtat | gattcgagtt | cgccggatgg  | 180 |
| agctgccttg | tcgcccgtct  | ctaagaatat  | tggtcggagg | agaaacagaa | gacagaaact  | 240 |
| taaccagaga | ctcttcgctc  | ttcgatcagt  | tggtcccaat | atcactaaga | tggataaagc  | 300 |
| ctcaataatc | aaagatgcta  | ttagttacat  | agaaggatta | caatatgaag | aaaagaagct  | 360 |
| cgaagctgag | atcagagaaac | ttgaattctac | accaaagagt | agccttagtt | tcagcaaaagg | 420 |
| atttttgatc | tgatttactt  | gttcctgtca  | catccaagaa | gatgaagcag | cttgattctc  | 480 |
| gttcttcgac | tctctccatc  | gaagttctcg  | aattgaaggt | aacattcatg | ggagagagga  | 540 |
| caatggtggt | gagtgtaaca  | tgtaataaga  | ggacagatac | aatggtgaaa | ctgtgtgaag  | 600 |
| tctttgagtc | attgaatctc  | aaaatcctca  | cttccaatct | cacctctttc | tctggcaatg  | 660 |
| tcttccacac | tgtctttatt  | gagggcgatg  | aagaagaaca | agaggtgttg | cggttaaaaa  | 720 |
| tagaaacagg | aataaggagct | tataatgaaa  | ctcaaaagcc | tactttgagc | atcgactctc  | 780 |
| tttactaata | atactttttt  | tcttcttttt  | ttggttcatt | ttggtctctc | tctttacaat  | 840 |
| aatgtatgtc | tctcttttca  | tttttatgat  | ctctacggt  | tgtttgtcc  |             |     |

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..141  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Arg | Thr | Arg | Asp | Ser | Leu | Ile | Arg | Lys | Ser | Cys | Arg | Lys | Met | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Ile | Val | Asp | Gln | Glu | Leu | Ser | Asn | Tyr | Trp | Glu | Pro | Ser | Ser | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Gln | Asn | Glu | Tyr | Phe | Glu | Tyr | Asp | Ser | Trp | Pro | Leu | Glu | Glu | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ile | Ser | Gly | Ser | Tyr | Asp | Ser | Ser | Ser | Pro | Asp | Gly | Ala | Ala | Ser | Ser |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Ala | Ser | Lys | Asn | Ile | Val | Ser | Glu | Arg | Asn | Arg | Arg | Gln | Lys | Leu |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asn | Gln | Arg | Leu | Phe | Ala | Leu | Arg | Ser | Val | Val | Pro | Asn | Ile | Thr | Lys |  |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Met | Asp | Lys | Ala | Ser | Ile | Ile | Lys | Asp | Ala | Ile | Ser | Tyr | Ile | Glu | Gly |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Leu | Gln | Tyr | Glu | Glu | Lys | Lys | Leu | Glu | Ala | Glu | Ile | Arg | Glu | Leu | Glu |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Thr | Pro | Lys | Ser | Ser | Leu | Ser | Phe | Ser | Lys | Gly | Phe |     |     |     |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..127  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500681  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:  
Met Glu Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser  
1 5 10 15  
Ser Leu Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu  
20 25 30  
Glu Ala Ile Ser Gly Ser Tyr Asp Ser Ser Pro Asp Gly Ala Ala  
35 40 45  
Ser Ser Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln  
50 55 60  
Lys Leu Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile  
65 70 75 80  
Thr Lys Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile  
85 90 95  
Glu Gly Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu  
100 105 110  
Leu Glu Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

Met Lys Lys Arg Ser Ser Lys Leu Arg Ser Glu Asn Leu Asn Leu His  
1 5 10 15  
Gln Arg Val Ala Leu Val Ser Ala Lys Asp Phe Asp Arg Asp Leu Leu  
20 25 30  
Val Pro Val Thr Ser Lys Lys Met Lys Gln Leu Asp Ser Gly Ser Ser  
35 40 45  
Thr Ser Leu Ile Glu Val Leu Glu Leu Lys Val Thr Phe Met Gly Glu  
50 55 60  
Arg Thr Met Val Val Ser Val Thr Cys Asn Lys Arg Thr Asp Thr Met  
65 70 75 80  
Val Lys Leu Cys Glu Val Phe Glu Ser Leu Asn Leu Lys Ile Leu Thr  
85 90 95  
Ser Asn Leu Thr Ser Phe Ser Gly Met Ile Phe His Thr Val Phe Ile  
100 105 110  
Glu Ala Asp Glu Glu Glu Gln Glu Val Leu Arg Leu Lys Ile Glu Thr  
115 120 125  
Gly Ile Gly Ala Tyr Asn Glu Thr Gln Ser Pro Thr Leu Ser Ile Asp  
130 135 140  
Ser Leu Tyr  
145

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro  
1 5 10 15  
Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr  
20 25 30  
Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala  
35 40 45  
Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys  
50 55 60  
Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys  
65 70 75 80  
Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys  
85 90 95  
Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala  
100 105 110  
Gly Gly Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro  
115 120 125  
Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly  
130 135 140  
Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1500686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg  
1 5 10 15  
Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala  
20 25 30  
Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser  
35 40 45  
Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr  
50 55 60  
Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Pro Thr Ser  
65 70 75 80  
Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp  
85 90 95  
Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly  
100 105 110  
Phe Leu Lys  
115

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1057

(D) OTHER INFORMATION: / Ceres Seq. ID 1500687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

aagcttttctt ctgtgttccta catacccatc ttccctcacc tacatcaaac ctagggtttc

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| tataactata  | caacaacata  | tataaaattta | tatataggtt  | gtgatctatt  | gaagatcata  | 120  |
| aagatcaaaa  | ggagagaggt  | atataaaaaa  | gatgtgtagt  | cgaggccatt  | ggagacagct  | 180  |
| agaagacagag | aactcgtcga  | acattcttgg  | cctcataaatt | ggaagccgat  |             | 240  |
| agctcagaag  | ctctctgtgc  | gagcttggtta | ttgagatggt  | tttaactcaat |             | 300  |
| ggatctcagg  | attaaccgaa  | accctttcac  | ggaggagaaga | taagaagaagc | ttttagcgct  | 360  |
| tcatcggtatc | cattgggaaca | ggtcgtctgt  | gatcgtcgata | ttttttcccg  | gcgcgaactga | 420  |
| ttaacgtgtt  | aaaaaacatt  | ggcagctcat  | catggtctgt  | cgtggccgag  | aacggtccaa  | 480  |
| ctgcctgcct  | ggagcctgtg  | agcataatgt  | cacggtgtgc  | gcgactggga  | tgttgtgtaa  | 540  |
| ttataaaagc  | tgcgataaag  | ggcaagaagt  | ggagacacca  | accgctatca  | attttctcta  | 600  |
| ccaattctct  | catattaatc  | attttcaagt  | cctcaaaagag | tcttcgaccg  | taaaagatgat | 660  |
| ttcgcagaat  | agtactactc  | caatacaca   | aggagcaata  | gaccaaacta  | aacagccgat  | 720  |
| ggagttctac  | aaattttctc  | aagtaaacac  | tgattcgaag  | atacacagat  | tgtagatata  | 780  |
| ttcaagaaaa  | gacgaaagaa  | aagatgtcga  | cgaaaactac  | cgaattccta  | acgagaattg  | 840  |
| tgttctcatt  | ttcgactttt  | tgtctttgtg  | aaactctgcc  | tctcaggggt  | tatgttaatt  | 900  |
| tgttcgtact  | acatgtacta  | taaggtggac  | catatgttta  | taagaagata  | tgttagaaagt | 960  |
| actaatcaat  | tagagctctt  | gtttgagcca  | aattgtaaaa  | ctgtttaagc  | catcccaaac  | 1020 |
| attttctctt  | ataagaataa  | taaggttcta  | cttttgc     |             |             |      |

(2) INFORMATION FOR SEO ID NO:1590:

### (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 249 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..249  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

|            |            |            |            |          |            |            |            |            |            |            |            |            |            |            |     |
|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|
| Met<br>1   | Met        | Cys        | Ser        | Arg<br>5 | Gly        | His        | Trp        | Arg        | Pro<br>10  | Ala        | Glu        | Asp        | Glu        | Lys<br>15  | Leu |
| Arg        | Glu        | Leu        | Val<br>20  | Glu      | Gln        | Phe        | Gly        | Pro<br>25  | His        | Asn        | Trp        | Asn        | Ala<br>30  | Ile        | Ala |
| Gln        | Lys        | Leu        | Ser<br>35  | Gly      | Arg        | Ser        | Gly<br>40  | Lys        | Ser        | Cys        | Arg        | Leu<br>45  | Arg        | Trp        | Phe |
| Asn        | Gln<br>50  | Leu        | Asp        | Pro      | Arg        | Ile<br>55  | Asn        | Arg        | Asn        | Pro        | Phe<br>60  | Thr        | Glu        | Glu        | Glu |
| Glu<br>65  | Glu        | Arg        | Leu        | Leu      | Ala<br>70  | Ser        | His        | Arg        | Ile        | His<br>75  | Gly        | Asn        | Arg        | Trp        | Ser |
| Val        | Ile        | Ala        | Arg<br>85  | Phe      | Phe        | Pro        | Gly        | Arg        | Thr<br>90  | Asp        | Asn        | Ala        | Val        | Lys<br>95  | Asn |
| His        | Trp        | His<br>100 | Val        | Ile      | Met        | Ala        | Arg        | Arg<br>105 | Gly        | Arg        | Glu        | Arg        | Ser<br>110 | Lys        | Leu |
| Arg        | Pro        | Arg<br>115 | Gly        | Leu      | Gly        | His        | Asp<br>120 | Gly        | Thr        | Val        | Ala        | Ala<br>125 | Thr        | Gly        | Met |
| Ile        | Gly<br>130 | Asn        | Tyr        | Lys      | Asp        | Cys<br>135 | Asp        | Lys        | Glu        | Arg        | Arg<br>140 | Leu        | Ala        | Thr        | Thr |
| Thr<br>145 | Ala        | Ile        | Asn        | Phe      | Pro<br>150 | Tyr        | Gln        | Phe        | Ser        | His<br>155 | Ile        | Asn        | His        | Phe        | Gln |
| Val        | Leu        | Lys        | Glu<br>165 | Phe      | Leu        | Thr        | Val        | Lys        | Ile<br>170 | Gly        | Phe        | Arg        | Asn        | Ser<br>175 | Thr |
| Thr        | Pro        | Ile<br>180 | Gln        | Glu      | Gly        | Ala        | Ile        | Asp<br>185 | Gln        | Thr        | Lys        | Arg        | Pro<br>190 | Met        | Glu |
| Phe        | Tyr        | Asn<br>195 | Phe        | Leu      | Gln        | Val        | Asn<br>200 | Thr        | Asp        | Ser        | Lys        | Ile<br>205 | His        | Glu        | Leu |
| Ile        | Asp<br>210 | Asn        | Ser        | Arg      | Lys        | Asp<br>215 | Glu        | Glu        | Glu        | Asp        | Val<br>220 | Asp        | Gln        | Asn        | Asn |
| Arg<br>225 | Ile        | Pro        | Asn        | Glu      | Asn<br>230 | Cys        | Val        | Pro        | Phe        | Phe<br>235 | Asp        | Phe        | Leu        | Ser        | Val |
| Gly        | Asn        | Ser        | Ala<br>245 | Ser      | Gln        | Gly        | Leu        | Cys        |            |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1500689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg  
1 5 10 15  
Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln  
20 25 30  
Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn  
35 40 45  
Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu Glu  
50 55 60  
Glu Arg Leu Leu Ala Ser His Arg Ile His Gly Asn Arg Trp Ser Val  
65 70 75 80  
Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His  
85 90 95  
Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg  
100 105 110  
Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile  
115 120 125  
Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr  
130 135 140  
Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val  
145 150 155 160  
Leu Lys Glu Phe Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr  
165 170 175  
Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe  
180 185 190  
Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile  
195 200 205  
Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg  
210 215 220  
Ile Pro Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly  
225 230 235 240  
Asn Ser Ala Ser Gln Gly Leu Cys  
245

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1500690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu  
1 5 10 15  
Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys  
20 25 30  
Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Tyr | Gln | Phe | Ser | His | Ile | Asn | His | Phe | Gln | Val | Leu | Lys | Glu | Phe |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Leu | Thr | Val | Lys | Ile | Gly | Phe | Arg | Asn | Ser | Thr | Thr | Pro | Ile | Gln | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ala | Ile | Asp | Gln | Thr | Lys | Arg | Pro | Met | Glu | Phe | Tyr | Asn | Phe | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gln | Val | Asn | Thr | Asp | Ser | Lys | Ile | His | Glu | Leu | Ile | Asp | Asn | Ser | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Lys | Asp | Glu | Glu | Glu | Asp | Val | Asp | Gln | Asn | Asn | Arg | Ile | Pro | Asn | Glu |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Cys | Val | Pro | Phe | Phe | Asp | Phe | Leu | Ser | Val | Gly | Asn | Ser | Ala | Ser |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Gly | Leu | Cys |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..546
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| agtaattttc | agtcggcgtc | cttcttttgt  | ctgaaccacc | ggaggagctc | gatccattga | 60  |
| ttagaagatg | acaactccac | aagtgaaagac | cggtttgttc | gttgggttga | acaagggaca | 120 |
| tgttgttacc | agacgtgaat | tagctcctcg  | tcctcgttct | cgcaagga   | aaacgagcaa | 180 |
| gaggacaatc | ttatcagaaa | acttgataaa  | ggaagtgtct | gttcaagctc | cctatgagaa | 240 |
| gagaatcact | gagcttttga | aggttgctaa  | gaggaagtgt | ggaaccaca  | agagagccaa | 300 |
| gcgaagagag | gaggagatgt | ccagtgttct  | ccgcaagatg | aggtctggcg | gtgttggtgc | 360 |
| aactgagaag | aagaagtga  | cgtcatctta  | agtttgtgaa | tcgctctgaa | agagttatgg | 420 |
| ttcttgtttg | caaaatcggt | attatgattc  | ctaagctctt | cgtattatgt | ttgttagaaa | 480 |
| tatcggaatt | aaagagagtt | ttgtctgaga  | ccagtgactc | tgscetttaa | ctatttgctt | 540 |
| ctttttg    |            |             |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Pro | Gln | Val | Lys | Thr | Gly | Leu | Val | Gly | Leu | Asn | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | His | Val | Val | Thr | Arg | Arg | Glu | Leu | Ala | Pro | Arg | Pro | Arg | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |
| Lys | Gly | Lys | Thr | Ser | Lys | Arg | Thr | Ile | Phe | Ile | Arg | Asn | Leu | Ile |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |
| Glu | Val | Ala | Gly | Gln | Ala | Pro | Tyr | Glu | Lys | Arg | Ile | Thr | Glu | Leu |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |
| Lys | Val | Ala | Lys | Arg | Lys | Leu | Gly | Thr | His | Lys | Arg | Ala | Lys | Arg |
|     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Glu | Glu | Met | Ser | Ser | Val | Leu | Arg | Lys | Met | Arg | Ser | Gly | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |

Gly Ala Thr Glu Lys Lys Lys  
100

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

|            |             |            |            |            |            |     |
|------------|-------------|------------|------------|------------|------------|-----|
| tcttttgcgt | gactgtcaaa  | tctcattctt | ctctttotto | tctctctcca | agagaaagaa | 60  |
| aatcttgagt | tccgagaaaa  | taaaatctca | agagttaaaa | agaaagaaac | ttttgtcgaa | 120 |
| gagattccaa | tcggtgatct  | ttgtctttct | tttctctaga | aaatctctgt | tgctctatat | 180 |
| atatccatat | agatgtctcta | agactatagt | tggtgttgca | gataataatg | gagggagaca | 240 |
| caatacttag | gatgatggga  | agtggagttc | aaatggatgg | gaagattctt | caaacgtttg | 300 |
| agaaaagt   | ttgttcaagt  | caaaacatat | tggaaccaca | cagattgctt | ataaacgaga | 360 |
| taaaacaaaa | ccatgagttc  | aaaatcccg  | acaacctcgg | acgaaacgtg | ggtttgatcc | 420 |
| gagaattgaa | caataacgtg  | agaaggggtg | ctcatcttta | tgctgatctt | tccacaacct | 480 |
| tctccaaatc | catggaaagt  | cttctgaaag | gagactcaac | agaaggacga | ggtaacagaa | 540 |
| gaatcaggcc | tgcttaatta  | agaatcaggg | ttgtttotto | aaaattagct | tcgaatttag | 600 |
| cttttaattg | gggctaattc  | cttttctcaa | gtgattggcg | ataaatgttt | taaagcagaa | 660 |
| atggtgattg | taattgaaaa  | atatgttcaa | tactattatt | tg         |            |     |

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Gly | Asp | Thr | Ile | Ser | Arg | Met | Met | Gly | Ser | Gly | Val | Gln | Met |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Asp | Gly | Lys | Ile | Leu | Gln | Thr | Phe | Glu | Lys | Ser | Phe | Val | Gln | Val | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Asn | Ile | Leu | Asp | His | Asn | Arg | Leu | Leu | Ile | Asn | Glu | Ile | Asn | Gln | Asn |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| His | Glu | Ser | Lys | Ile | Pro | Asp | Asn | Leu | Gly | Arg | Asn | Val | Gly | Leu | Ile |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | Glu | Leu | Asn | Asn | Asn | Val | Arg | Arg | Val | Ala | His | Leu | Tyr | Val | Asp |  |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Ser | Asn | Asn | Phe | Ser | Lys | Ser | Met | Glu | Ala | Ser | Ser | Glu | Gly | Asp |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Ser | Glu | Gly | Arg | Gly | Asn | Arg | Arg | Ile | Arg | Pro | Ala |     |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

```
Met Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe
1      5      10      15
Glu Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu
20      25      30
Leu Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn
35      40      45
Leu Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Asn Val Arg
50      55      60
Arg Val Ala His Leu Tyr Val Asp Leu Ser Asn Phe Ser Lys Ser
65      70      75      80
Met Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg
85      90      95
Arg Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

```
Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe Glu
1      5      10      15
Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu Leu
20      25      30
Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn Leu
35      40      45
Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Asn Val Arg Arg
50      55      60
Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser Met
65      70      75      80
Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg Arg
85      90      95
Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1422

(D) OTHER INFORMATION: / Ceres Seq. ID 1500703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

```
amnnacaaaag tctctctccc tctctctatc aactttttca gttactttac tccgttcac 60
ttttattttt cttttctgcg attctcatca atactacaaa aatatatact tctatatatc 120
gtgcagaggt tacatgcatt gtrcaatttt gttgtscbga gaaacaagcg gatcagagac 180
aaaatcagag tcggtttctc gctttttgat tctcttttat taatcagcaa agatcgattc 240
cactctctct ctctctctct ctctctctct gttctttaat ttagagagaa aaaataagca 300
tctctccttc tctggtttcg agcgggaaat tctggagatg gctatacaag cgcagttgaa 360
```

[illegible]

(2) INFORMATION FOR SEO ID NO:1600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..265  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Gln | Ala | Gln | Leu | Asn | Tyr | Asn | Ala | Pro | Asn | Ala | Asn | Gln |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Gly | Phe | Gly | Gly | Ser | Glu | Phe | Ser | Leu | Ile | Asn | Asn | Asn | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Ile | Gly | Asn | Asp | Gln | Ser | Tyr | Leu | Val | Asn | Asn | Leu | Gln | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Lys | Asp | Phe | Asn | Gln | His | Ala | Leu | Phe | His | His | Gln | His | His | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Gln | Ser | Pro | Ser | Gln | Ser | Phe | Leu | Ala | Ala | Gln | Met | Glu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Lys | Gln | Glu | Ile | Asp | Gln | Phe | Ile | Lys | Ile | Gln | Asn | Glu | Arg | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Tyr | Val | Leu | Gln | Glu | Gln | Arg | Lys | Arg | Glu | Met | Glu | Met | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Lys | Met | Glu | Ser | Lys | Ala | Leu | Leu | Met | Ser | Gln | Lys | Glu | Glu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Glu | Met | Ser | Lys | Ala | Leu | Asn | Lys | Asn | Met | Glu | Leu | Glu | Asp | Leu | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Lys | Met | Glu | Met | Glu | Asn | Gln | Thr | Trp | Gln | Arg | Met | Ala | Arg | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Glu | Ala | Ile | Val | Gln | Thr | Leu | Asn | Thr | Thr | Leu | Glu | Gln | Val | Arg |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Arg | Ala | Ala | Thr | Cys | Tyr | Asp | Ala | Gly | Glu | Ala | Glu | Val | Glu | Asp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Gly | Ser | Phe | Cys | Gly | Xaa | Glu | Gly | Asp | Gly | Asn | Ser | Leu | Pro | Ala |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Lys | Met | Lys | Met | Ser | Ser | Cys | Cys | Cys | Asn | Cys | Gly | Ser | Asn | Gly |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Thr | Xaa | Val | Leu | Phe | Xaa | Pro | Phe | Arg | His | Leu | Cys | Cys | Cys | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Xaa | Glu | Xaa | Gly | Leu | Xaa | Leu | Cys | Pro | Ile | Cys | Asn | Thr | Pro | Lys |

245 250 255  
Lys Ser Arg Ile Glu Ala Leu Ile Xaa  
260 265  
(2) INFORMATION FOR SEQ ID NO:1601:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..188  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500705  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:  
Met Glu Lys Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn  
1 5 10 15  
Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu  
20 25 30  
Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met Ser Gln  
35 40 45  
Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu  
50 55 60  
Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met  
65 70 75  
Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu  
85 90 95  
Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu  
100 105 110  
Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser  
115 120 125  
Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Asn Cys Gly  
130 135 140  
Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys  
145 150 155 160  
Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn  
165 170 175  
Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa  
180 185  
(2) INFORMATION FOR SEQ ID NO:1602:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..158  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500706  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:  
Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met  
1 5 10 15  
Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu  
20 25 30  
Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln  
35 40 45  
Arg Met Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr  
50 55 60  
Leu Glu Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu  
65 70 75 80

Ala Glu Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly  
85 90 95  
Asn Ser Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn  
100 105 110  
Cys Gly Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His  
115 120 125  
Leu Cys Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile  
130 135 140  
Cys Asn Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1188

(D) OTHER INFORMATION: / Ceres Seq. ID 1500707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

atcattctcg gtttaactga aacacataat aaaacaaaaga gaaagagata taatatgggt 60  
gggtggggcaa tcgcagtaga cgggtggtgcc ggtatcgacc ctaattcttcc ggcagagaga 120  
caagaagagg cgaacacagt tttaactcgt tgtctcaacc tcggcataat agctttgcgt 180  
tccaatgttt ccggcattga cgtcgttgag ctgcgtatta gagaattgga gacggatcct 240  
ctgtttaatt cagcccgctgg atctctctttg acggagaaaag gaacgggttga gatggaaagt 300  
acgattatgg acggtacgaa gagacgatgc ggtgcggttt cggggataac cacgtgtaaa 360  
aatcctatat ctcttgcctc tctcgtcatg gacaaatctc ccactcttta ccttgccttc 420  
tcaggtgcag aggatttcgc ccgcaaacag ggagttgaaa ttgtggacaa cgagtaacttt 480  
gtcacggagg acaacgtagg aatgctcaag ttggccaagg aagctaacct catcttgttt 540  
gattaccgga ttccgcgatg gggatgtgcc ggccgacgtc cgaccogacag tccaatccaa 600  
atgaacggtc ttccgcatcag catttacgca ccgggagaca gtcgggtgcg ttgtggttga 660  
cgggaaggga cattgtccgc ccgggaacatc caccgggtggt ttaatgaaca agatgatggg 720  
aaggatttgt gactcgccgc tgataggagc cgggacgtat gcgtcggagt ttgtgttgtt 780  
gtcgtgtacc ggagaaggag aagccattat aagagcaacc ctagctcgtg atgtgtcagc 840  
tgttatggag tataaaggag ttaacctcca agaagcgggt gattacgtca tcaagcatcg 900  
acttgacgaa gggttcgtc gactcattgc tgtctcgaat aaaggagagtg tggtttgttg 960  
ttttaacctt aatgggatgt tcagggggatg tgcaactgtg gatggattca tggacgttgc 1020  
tatttgggag tgagaaatat tttagattaa gaaaatgtct tactagtatt taatcagtca 1080  
tcgctctatt aatttgggta ttcattatca taaagctgga gtagtataat tagttctgtc 1140  
gttatccaca gtccatatatt gatttgtggt taatgcgggt tcataatgg

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1500708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Ile Ile Leu Gly Leu Thr Glu Thr His Asn Lys Thr Lys Arg Lys Arg  
1 5 10 15  
Tyr Asn Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile  
20 25 30  
Asp Pro Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu  
35 40 45  
Thr Arg Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Ala Ile Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro |     |     |
| 65                                                              | 70  | 75  |
| Leu Phe Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val |     | 80  |
|                                                                 | 85  | 90  |
| Glu Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala |     | 95  |
|                                                                 | 100 | 105 |
| Val Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu |     | 110 |
|                                                                 | 115 | 120 |
| Val Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu |     | 125 |
|                                                                 | 130 | 135 |
| Asp Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe |     | 140 |
|                                                                 | 145 | 150 |
| Val Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn |     | 155 |
|                                                                 | 165 | 170 |
| Ser Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala |     | 175 |
|                                                                 | 180 | 185 |
| Ala Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile |     | 190 |
|                                                                 | 195 | 200 |
| Tyr Ala Pro Gly Asp Ser Arg Val Arg Cys Gly                     |     | 205 |
| 210                                                             | 215 |     |

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1500709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile Asp Pro |     |     |
| 1                                                               | 5   | 10  |
| Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu Thr Arg |     | 15  |
|                                                                 | 20  | 25  |
| Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser Ala Ile |     | 30  |
|                                                                 | 35  | 40  |
| Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro Leu Phe |     | 45  |
|                                                                 | 50  | 55  |
| Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val Glu Met |     | 60  |
|                                                                 | 65  | 70  |
| Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val Ser |     | 75  |
|                                                                 | 85  | 90  |
| Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val Met |     | 95  |
|                                                                 | 100 | 105 |
| Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp Phe |     | 110 |
|                                                                 | 115 | 120 |
| Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val Thr |     | 125 |
|                                                                 | 130 | 135 |
| Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser Ile |     | 140 |
|                                                                 | 145 | 150 |
| Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala Ala |     | 155 |
|                                                                 | 165 | 170 |
| Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala |     | 175 |
|                                                                 | 180 | 185 |
| Pro Gly Asp Ser Arg Val Arg Cys Gly                             |     | 190 |
|                                                                 | 195 | 200 |

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..122  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500710  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:  
Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val  
1 5 10 15  
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val  
20 25 30  
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp  
35 40 45  
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val  
50 55 60  
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Asn Ser  
65 70 75 80  
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala  
85 90 95  
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr  
100 105 110  
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 868 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..868  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500719  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

aatcacttgt taattctaag ctctctctct ttccaaaaat ggcgtcatca tcggcttttg 60  
ctctcaggag acttctctct tcttccacgc tcgccgtccc tcgcgcctta agagccgttc 120  
gtccgggtgc tgctctctct cgctctcttca ataccacacg ccgccagaaac tatgaagacg 180  
gtgtcgatag gaaccatcac tcaaacccgac atgtttctcg ccacggcgcg gatttctctc 240  
cagatatact cgatccgttt actccaacga gaagcttgag ccagatgctg aatttcatgg 300  
accaggtaag cgaatacctc ttggtatcag ctactcgtgg aatgggagct tctggagtta 360  
gacgtgggtg gaacgtgaaa gagaagacgc acgcgttgca tctaaggata gatatgccgg 420  
gactaagcag agaggatgtg aaattggctt tggaacagaa cacattgggtg attagaggag 480  
aaggggaaac agaggaggga gaagatgttt ctggagatgg accgaggttt acgagtagga 540  
ttgagttacc ggagaaaagta tacaagactg atgagattaa ggcggaatag aagaattgggtg 600  
ttgttgaaagt ggtgattcca aagattaaag aggatgagcg taacaatatt cgctcacataa 660  
acgttgacta gagtggtttt tttggattg ttgagatgg aatggaaagta agtgagtgaa 720  
tttgtgaact ttaagggtgc ctttggtgaa tcaaggagaa tgacatttcc cacggtctcta 780  
tgtgttcggg attttgactt ttttcttacc atcaatgatc tatgtacggt tgactacttt 840  
catatcatag gttcggattt ttgttccc

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1500720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Val | Asn | Ser | Lys | Leu | Leu | Leu | Phe | Pro | Lys | Met | Ala | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ala | Leu | Ala | Leu | Arg | Arg | Leu | Leu | Ser | Ser | Thr | Val | Ala | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Arg | Ala | Leu | Arg | Ala | Val | Arg | Pro | Val | Ser | Ala | Ser | Ser | Arg | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Asn | Thr | Asn | Ala | Ala | Arg | Asn | Tyr | Glu | Asp | Gly | Val | Asp | Arg | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | His | Ser | Asn | Arg | His | Val | Ser | Arg | His | Gly | Gly | Asp | Phe | Phe | Ser |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Ile | Leu | Asp | Pro | Phe | Thr | Pro | Thr | Arg | Ser | Leu | Ser | Gln | Met | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Phe | Met | Asp | Gln | Val | Ser | Glu | Ile | Pro | Leu | Val | Ser | Ala | Thr | Arg |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Met | Gly | Ala | Ser | Gly | Val | Arg | Arg | Gly | Trp | Asn | Val | Lys | Glu | Lys |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Asp | Asp | Ala | Leu | His | Leu | Arg | Ile | Asp | Met | Pro | Gly | Leu | Ser | Arg | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Asp | Val | Lys | Leu | Ala | Leu | Glu | Gln | Asn | Thr | Leu | Val | Ile | Arg | Gly | Glu |
|     |     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Gly | Glu | Thr | Glu | Glu | Gly | Glu | Asp | Val | Ser | Gly | Asp | Gly | Arg | Arg | Phe |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Ser | Arg | Ile | Glu | Leu | Pro | Glu | Lys | Val | Tyr | Lys | Thr | Asp | Glu | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Ala | Glu | Met | Lys | Asn | Gly | Val | Leu | Lys | Val | Val | Ile | Pro | Lys | Ile |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Lys | Glu | Asp | Glu | Arg | Asn | Asn | Ile | Arg | His | Ile | Asn | Val | Asp |     |     |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1500721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Ser | Ala | Leu | Ala | Leu | Arg | Arg | Leu | Leu | Ser | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Ala | Val | Pro | Arg | Ala | Leu | Arg | Ala | Val | Arg | Pro | Val | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ser | Ser | Arg | Leu | Phe | Asn | Thr | Asn | Ala | Ala | Arg | Asn | Tyr | Glu | Asp | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Asp | Arg | Asn | His | His | Ser | Asn | Arg | His | Val | Ser | Arg | His | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Phe | Phe | Ser | Asp | Ile | Leu | Asp | Pro | Phe | Thr | Pro | Thr | Arg | Ser | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Gln | Met | Leu | Asn | Phe | Met | Asp | Gln | Val | Ser | Glu | Ile | Pro | Leu | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ser | Ala | Thr | Arg | Gly | Met | Gly | Ala | Ser | Gly | Val | Arg | Arg | Gly | Trp | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Glu | Lys | Asp | Asp | Ala | Leu | His | Leu | Arg | Ile | Asp | Met | Pro | Gly |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Leu | Ser | Arg | Glu | Asp | Val | Lys | Leu | Ala | Leu | Glu | Gln | Asn | Thr | Leu | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |  |  |  |  |
| Ile | Arg | Gly | Glu | Gly | Glu | Thr | Glu | Glu | Gly | Glu | Asp | Val | Ser | Gly | Asp |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Gly | Arg | Arg | Phe | Thr | Ser | Arg | Ile | Glu | Leu | Pro | Glu | Lys | Val | Tyr | Lys |  |  |  |  |
|     |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |  |  |  |  |
| Thr | Asp | Glu | Ile | Lys | Ala | Glu | Met | Lys | Asn | Gly | Val | Leu | Lys | Val | Val |  |  |  |  |
|     |     |     | 180 |     |     |     |     |     | 185 |     |     |     | 190 |     |     |  |  |  |  |
| Ile | Pro | Lys | Ile | Lys | Glu | Asp | Glu | Arg | Asn | Asn | Ile | Arg | His | Ile | Asn |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |
| Val | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
| 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:1610:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Phe | Met | Asp | Gln | Val | Ser | Glu | Ile | Pro | Leu | Val | Ser | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Thr | Arg | Gly | Met | Gly | Ala | Ser | Gly | Val | Arg | Arg | Gly | Trp | Asn | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Glu | Lys | Asp | Asp | Ala | Leu | His | Leu | Arg | Ile | Asp | Met | Pro | Gly | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Asp | Val | Lys | Leu | Ala | Leu | Glu | Gln | Asn | Thr | Leu | Val | Ile | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Glu | Gly | Glu | Thr | Glu | Glu | Gly | Glu | Asp | Val | Ser | Gly | Asp | Gly | Arg |
|     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Phe | Thr | Ser | Arg | Ile | Glu | Leu | Pro | Glu | Lys | Val | Tyr | Lys | Thr | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Ile | Lys | Ala | Glu | Met | Lys | Asn | Gly | Val | Leu | Lys | Val | Val | Ile | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Ile | Lys | Glu | Asp | Glu | Arg | Asn | Asn | Ile | Arg | His | Ile | Asn | Val | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:1611:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 763 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..763
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

|            |            |             |             |             |            |     |
|------------|------------|-------------|-------------|-------------|------------|-----|
| ctgttttttg | tctctcgac  | tcacaagtct  | cacataatgc  | aaagctcgca  | gaagtcaaga | 60  |
| ggaagaagat | gagtggtaca | gtgacaatgc  | acagtgtctt  | cgtctacggc  | agtctcatgg | 120 |
| cggacgacgt | cgttcgtctc | ctctcacaac  | gtatccctca  | aaccgcttcc  | gcaacctctc | 180 |
| ctgaktkatt | cagcatcaaa | ggctcgtgtt  | atccggcgat  | tataccagct  | aagtcttgat | 240 |
| aaagtctctg | gaaaggtgtt | atttggaaac  | acagatgatg  | aacttaagt   | tttagatgag | 300 |
| tttgaggatg | ttgagtatga | aaagagagaat | gttcaagttt  | tgtttaacaga | tagttcagac | 360 |
| gagaaactgc | aaacaaaac  | ctacgttttg  | gccaaagaaag | atgatcctga  | cctatacggg | 420 |
| acatgggatt | tcgaggaatg | gaagcaactt  | cacatggaaag | gtttcttgaa  | gatgactaaa | 480 |

gaatttgctg aagagttgaa tttaccgaaa tccgagatat gactcgccgc tacattcggg 540  
tcagtaaagt aaatcttggt tagtttccctc aatgaattgg tcaatatatt cttgggtgttc 600  
tctctaggaa gggtagatt cttcttcattg aatacacata catgagggggg atttgggggtt 660  
tttggtgtatt acttaattca actgataaagg aataagaaaa cagctacata ttctgtgctg 720  
gtatgttatt atacaatata catatagaca tgtgttttagc ttc

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

Val Phe Gly Leu Ser His Ser Gln Val Ser His Asn Arg Lys Leu Ala  
1 5 10  
Glu Val Lys Arg Lys Lys Met Ser Gly Thr Val Thr Met His Ser Val  
20 25 30  
Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val Arg Leu Leu Leu  
35 40 45  
Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser  
50 55 60  
Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala Lys Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

Met Ser Gly Thr Val Thr Met His Ser Val Phe Val Tyr Gly Ser Leu  
1 5 10 15  
Met Ala Asp Asp Val Val Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr  
20 25 30  
Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr  
35 40 45  
Pro Ala Ile Ile Pro Ala Lys Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met His Ser Val Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val  
1 5 10 15

Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro  
20 25 30  
Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala  
35 40 45  
Lys Ser  
50

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 846 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..846

(D) OTHER INFORMATION: / Ceres Seq. ID 1500742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| atcctgatgc | ggaaccacaa  | aacgagtggt  | cgaaatagttt | ccgactgatt  | cttccgagggc | 60  |
| ttgaagctca | atagctatgg  | cttctctttc  | agtctcttcc  | tcttcaacca  | tcaatcgattc | 120 |
| aagagctcc  | cttctcgcac  | tagcctccgc  | ctccgcctct  | tctccgctcg  | gcatttcaact | 180 |
| tcccacactt | ccgattcagt  | ctcataccgc  | tgcgcctaaa  | gccactgctt  | actgtcgga   | 240 |
| gattgtgagg | aacgttgtga  | cgagagctac  | tactgaagtt  | gggtgaagctc | ctgccactac  | 300 |
| taccgaagct | gagactactg  | agttaccctga | aatcgctcaag | actgctcaag  | aagcttggga  | 360 |
| gaaagtgat  | gacaagtagc  | ctattgggtt  | tcttgccttt  | gctagtgtag  | tggtcttttg  | 420 |
| gggtcttctg | ggaatgawtt  | csgcaatcga  | taggcttcca  | ttggttccctg | gtgttcttga  | 480 |
| actgttaggc | ttgggtttaca | caggatgggtt | cacttacaag  | aaactgggtct | tcaaacaccga | 540 |
| cagggaagct | atgtttgaga  | aggtcaagag  | cacatacaaa  | gacattattag | ggagcagctg  | 600 |
| aatcaaaagg | ggaagaagaa  | gaagaagagc  | ctttttgagg  | ccattcatga  | attggaatga  | 660 |
| aggataatca | aagaatctaa  | caaaaaggcc  | acgtccttcc  | ttcaatcttt  | cctcttttga  | 720 |
| actaaataat | gttcatcctt  | tctctctctc  | tgctctctgt  | cttttttagc  | tcaaatgata  | 780 |
| atccatttat | gtcaaatgtg  | tgtaaattcc  | tcaagactat  | atatgagatg  | ttttgtttca  | 840 |
| ttttcc     |             |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1500743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Ser Leu Ser Val Ser Ser Ser Ser Thr Ile Ile Asp Ser Arg |  |
| 1 5 10 15                                                       |  |
| Ala Pro Pro Ser Arg Leu Ala Ser Ala Ser Ala Ser Ser Pro Ser Cys |  |
| 20 25 30                                                        |  |
| Ile Ser Leu Pro Thr Leu Pro Ile Gln Ser His Thr Arg Ala Ala Lys |  |
| 35 40 45                                                        |  |
| Ala Thr Ala Tyr Cys Arg Lys Ile Val Arg Asn Val Val Thr Arg Ala |  |
| 50 55 60                                                        |  |
| Thr Thr Glu Val Gly Glu Ala Pro Ala Thr Thr Thr Glu Ala Glu Thr |  |
| 65 70 75 80                                                     |  |
| Thr Glu Leu Pro Glu Ile Val Lys Thr Ala Gln Glu Ala Trp Glu Lys |  |
| 85 90 95                                                        |  |
| Val Asp Asp Lys Tyr Ala Ile Gly Ser Leu Ala Phe Ala Ser Val Val |  |
| 100 105 110                                                     |  |
| Ala Leu Trp Gly Ser Ala Gly Met Xaa Xaa Ala Ile Asp Arg Leu Pro |  |
| 115 120 125                                                     |  |

Leu Val Pro Gly Val Leu Glu Leu Val Gly Ile Gly Tyr Thr Gly Trp  
130 135 140  
Phe Thr Tyr Lys Asn Leu Val Phe Lys Pro Asp Arg Glu Ala Leu Phe  
145 150 155 160  
Glu Lys Val Lys Ser Thr Tyr Lys Asp Ile Leu Gly Ser Ser  
165 170

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| aaatcaaaac  | acaacattaa  | aagctttggc | gatttttttc  | tctgattcaa  | tcttttcata  | 60  |
| gtttctaaagc | tctcagattc  | ttaagaagc  | catggctcgt  | acgaagcaaa  | ccgcgagaaa  | 120 |
| atcacacgga  | ggaagaagctc | cgacgaagca | gctcgctacc  | aaggcggcaa  | ggaaaatctgc | 180 |
| accgaactacc | ggaggagtca  | agaaacctca | cgttttccgt  | cctggaaaccg | tcgtctctcg  | 240 |
| tgagattcgt  | aaataccaaa  | agagcacaga | gtgtttgaac  | cgtaaacttc  | cattccaacg  | 300 |
| tcttgttgt   | gaaatcgctc  | aagatttcaa | gacggatctg  | agattccaaa  | gccatgcagt  | 360 |
| gttagctctt  | caagaagctg  | cggaggcata | tttggttggt  | ttgtttgaag  | acacaaatct  | 420 |
| ctgtgcatt   | catgcaaaaga | gggttaccat | tatgctctaa  | gatgttcaat  | tgccaagaag  | 480 |
| gatctgtgca  | gagcgtgctt  | agaaattaga | atttaatacca | tcatatgaa   | ctagattattt | 540 |
| tttttttcta  | ttagggttt   | cgattgtttt | tgctttgttg  | ctttttaaca  | aaaatacatt  | 600 |
| atgtcacatt  | ctcttgaga   |            |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Thr | Lys | Gln | Thr | Ala | Arg | Lys | Ser | Gly | Gly | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Thr | Lys | Gln | Leu | Ala | Thr | Lys | Ala | Ala | Arg | Lys | Ser | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Thr | Gly | Gly | Val | Lys | Lys | Pro | His | Arg | Phe | Arg | Pro | Gly | Thr | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Leu | Arg | Glu | Ile | Arg | Lys | Tyr | Gln | Lys | Ser | Thr | Glu | Leu | Leu | Asn |
|     |     |     | 50  |     |     |     |     | 55  |     |     | 60  |     |     |     |
| Lys | Leu | Pro | Phe | Gln | Arg | Leu | Val | Arg | Glu | Ile | Ala | Gln | Asp | Phe |
|     |     |     | 65  |     |     |     |     | 70  |     |     | 75  |     |     | 80  |
| Thr | Asp | Leu | Arg | Phe | Gln | Ser | His | Ala | Val | Leu | Ala | Leu | Gln | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Glu | Ala | Tyr | Leu | Val | Gly | Leu | Phe | Glu | Asp | Thr | Asn | Leu | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ile | His | Ala | Lys | Arg | Val | Thr | Ile | Met | Pro | Lys | Asp | Val | Gln | Leu |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Arg | Arg | Ile | Arg | Ala | Glu | Arg | Ala |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1795  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| agagatcaag | agagagatat | ggagagaact | ttgcttcaat  | ggagactatt  | gcctcttctc  | 60   |
| gcactcatcg | ttgctctttt | ctccttcttc | ttcgcttctc  | ctcgctcttt  | acaggggaaat | 120  |
| aataaagtgt | gtcttcttcc | tcatgatcat | tactggatct  | caagtaaacc  | catcgtcaca  | 180  |
| cctaattgtc | tcatctctgg | ttctgtggag | gtgaagggag  | gaattattgt  | gtcgggtggg  | 240  |
| aaggaaagtt | attggcataa | gaagtcaagg | agtcgagtga  | aagtgattga  | ttagtgagaa  | 300  |
| ctgtctctca | tgcttggctc | catgtatgtg | catgttcttc  | ttgatgatcc  | tggaagaagt  | 360  |
| gaatgggaag | gttttccctc | tggaactaag | gctgctgtcg  | ctgggggaaat | aactacattg  | 420  |
| gttgacatgc | ctcttaaacg | tttcccttca | actgatatct  | ctgaaacttt  | gaaactcaag  | 480  |
| attgaagctg | cgaaaaaacg | aatacatgtt | agtgttgggt  | tctggggagg  | tctgtacctt  | 540  |
| gacaaatgc  | tcaactcaag | tgctctttag | tctctcttag  | atgctggagt  | tcttggcttc  | 600  |
| aagtccttta | tggtcccttc | aggaatcaac | gattttccaa  | tgacaaacat  | catcatata   | 660  |
| aagggaagac | tatctgtatt | agctaataac | aaacgaccat  | tgcttgtaca  | cgagagatc   | 720  |
| gagagagact | tagagattga | agatggtagt | gaaaatgac   | ctgcttctta  | tctgacctat  | 780  |
| ttaaaaacca | ggcttacttc | atgggaggag | gagagcaatc  | gaaacctatt  | atcggttact  | 840  |
| gaaaacacaa | gaattggggg | ttctgcagaa | ggagctctac  | ttcatattgt  | acatttatct  | 900  |
| gatgccagtt | gttctcttga | tttgataaaa | gaagcctaat  | gcaaaggaga  | catgttgaat  | 960  |
| gttgaaacat | gtccacatta | cctagctttc | tcagccgaag  | agatctccga  | aggttgatact | 1020 |
| cgtttcaaat | gtctccctcc | tatacgtgat | gcggcaaatc  | gagaaaaaat  | gtgggaagct  | 1080 |
| ttgatggaag | gagacattga | tatgctgagc | tctgatcatc  | cacctacaaa  | gcctgaaacc  | 1140 |
| aaaactttag | gtgatggcaa | cttcttgaaa | gcttgggggt  | ggatatcttc  | tttacagatt  | 1200 |
| gttcttctta | tcacatggct | ttatggaaaa | aagtatggag  | taacgtctga  | gcaggttaact | 1260 |
| tcttggtgga | gtgataggcc | ttccaaactc | gctcgactac  | actctaaggg  | agcggttaag  | 1320 |
| gttggaaaac | acgcagatct | tggttgtgtg | gaacctgaag  | ccgaatttga  | tgtagatgaa  | 1380 |
| gatcatccaa | ttcacttcaa | acacctagct | atctcagctt  | atttgggaag  | aagattatca  | 1440 |
| ggcaaatgtg | tttcgacatt | tgtagagagg | aacttgggtt  | ttggagaagg  | caagcatgct  | 1500 |
| tctgatgctt | gcgggtctct | gcaacttgca | actacttaac  | ttaaaaaggg  | atttaaaaga  | 1560 |
| tcttgatctg | caccatttaa | acaaatgtaa | atatgogatt  | aagagttgct  | ctcatgttgc  | 1620 |
| aagatgggtg | atgtaatgag | tgagctcttt | ttgccaatg   | taaggttaag  | actctatata  | 1680 |
| tcttgttgtt | ggctttaaag | ttagtggact | catstataat  | ttgtyatgac  | aaataattta  | 1740 |
| tatcgcttaa | gtaaatgatg | tatatattgt | ttagtgcaaat | gaattaaaag  | tatac       |      |

(2) INFORMATION FOR SEQ ID NO:1620:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 512 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..512  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Asp | Gln | Glu | Arg | Asp | Met | Glu | Arg | Thr | Leu | Leu | Gln | Trp | Arg | Leu |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Leu | Pro | Leu | Leu | Ala | Leu | Ile | Val | Ala | Leu | Phe | Ser | Phe | Phe | Phe | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ser | Pro | Arg | Ser | Leu | Gln | Gly | Asn | Asn | Lys | Cys | Ser | Leu | Leu | Pro | His |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asp | His | Tyr | Trp | Ile | Ser | Ser | Lys | Arg | Ile | Val | Thr | Pro | Asn | Gly | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Ser | Gly | Ser | Val | Glu | Val | Lys | Gly | Gly | Ile | Ile | Val | Ser | Val | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  | Lys | Glu | Val | Asp | Trp | 70  | His | Lys | Ser | Gln | Arg | 75  | Ser | Arg | Val | Lys | Val | 80  | Ile |
|     |     |     |     |     |     | 85  | Val | Leu | Met | Pro | Gly | 90  | Leu | Ile | Asp | Val | His | 95  | Val |
| Asp | Tyr | Gly | Glu | Ala | Val | 100 | Leu | Met | Pro | Gly | Leu | 105 | Ile | Asp | Val | His | 110 | Val |     |
| His | Leu | Asp | Asp | Pro | Gly | 115 | Arg | Ser | Glu | Trp | Glu | 120 | Gly | Phe | Pro | Ser | 125 | Gly |     |
| Thr | Lys | Ala | Ala | Ala | Ala | 130 | Gly | Gly | Ile | Thr | Thr | 135 | Leu | Val | Asp | Met | 140 | Pro |     |
| Leu | Asn | Ser | Phe | Pro | Ser | 145 | Thr | Val | Ser | Pro | Glu | 150 | Thr | Leu | Lys | Leu | 155 | Lys |     |
| Ile | Glu | Ala | Ala | Lys | Asn | 165 | Arg | Ile | His | Val | Asp | 170 | Val | Gly | Phe | Trp | 175 | Gly |     |
| Gly | Leu | Val | Pro | Asp | Asn | 180 | Ala | Leu | Asn | Ser | Ser | 185 | Ala | Leu | Glu | Ser | 190 | Leu |     |
| Leu | Asp | Ala | Gly | Val | Leu | 195 | Gly | Leu | Lys | Ser | Phe | 200 | Met | Cys | Pro | Ser | 205 | Gly |     |
| Ile | Asn | Asp | Phe | Pro | Met | 210 | Thr | Asn | Ile | Thr | His | 215 | Ile | Lys | Glu | Gly | 220 | Leu |     |
| Ser | Val | Leu | Ala | Lys | Tyr | 225 | Lys | Arg | Pro | Leu | Leu | 230 | Val | His | Ala | Glu | 235 | Ile |     |
| Glu | Arg | Asp | Leu | Glu | Ile | 240 | Glu | Asp | Gly | Ser | Glu | 245 | Asn | Asp | Pro | Arg | 250 | Ser |     |
| Tyr | Leu | Thr | Tyr | Leu | Lys | 255 | Thr | Arg | Pro | Thr | Ser | 260 | Trp | Glu | Glu | Gly | 265 | Ala |     |
| Ile | Arg | Asn | Leu | Leu | Ser | 270 | Val | Thr | Glu | Asn | Thr | 275 | Arg | Ile | Gly | Gly | 280 | Ser |     |
| Ala | Glu | Gly | Ala | His | Leu | 285 | His | Ile | Val | His | Leu | 290 | Ser | Asp | Ala | Ser | 295 | Ser |     |
| Ser | Leu | Asp | Leu | Ile | Lys | 300 | Glu | Ala | Lys | Gly | Lys | 305 | Gly | Asp | Ser | Val | 310 | Thr |     |
| Val | Glu | Thr | Cys | Pro | His | 315 | Tyr | Leu | Ala | Phe | Ser | 320 | Ala | Glu | Glu | Ile | 325 | Pro |     |
| Glu | Gly | Asp | Thr | Arg | Phe | 330 | Lys | Cys | Ser | Pro | Pro | 335 | Ile | Arg | Asp | Ala | 340 | Ala |     |
| Asn | Arg | Glu | Lys | Leu | Trp | 345 | Glu | Ala | Leu | Met | Glu | 350 | Gly | Asp | Ile | Asp | 355 | Met |     |
| Leu | Ser | Ser | Asp | His | Ser | 360 | Pro | Thr | Lys | Pro | Glu | 365 | Leu | Lys | Leu | Met | 370 | Ser |     |
| Asp | Gly | Asn | Phe | Leu | Lys | 375 | Ala | Trp | Gly | Gly | Ile | 380 | Ser | Ser | Leu | Gln | 385 | Phe |     |
| Val | Leu | Pro | Ile | Thr | Trp | 390 | Ser | Tyr | Gly | Lys | Lys | 395 | Tyr | Gly | Val | Thr | 400 | Leu |     |
| Glu | Gln | Val | Thr | Ser | Trp | 405 | Trp | Ser | Asp | Arg | Pro | 410 | Ser | Lys | Leu | Ala | 415 | Arg |     |
| Leu | His | Ser | Lys | Gly | Ala | 420 | Val | Thr | Val | Gly | Lys | 425 | His | Ala | Asp | Leu | 430 | Val |     |
| Val | Trp | Glu | Pro | Glu | Ala | 435 | Glu | Phe | Asp | Val | Asp | 440 | Glu | Asp | His | Pro | 445 | Ile |     |
| His | Phe | Lys | His | Pro | Ser | 450 | Ile | Ser | Ala | Tyr | Leu | 455 | Gly | Arg | Arg | Leu | 460 | Ser |     |
| Gly | Lys | Val | Val | Ser | Thr | 465 | Phe | Val | Arg | Gly | Asn | 470 | Leu | Val | Phe | Gly | 475 | Glu |     |
| Gly | Lys | His | Ala | Ser | Asp | 485 | Ala | Cys | Gly | Ser | Leu | 490 | Gln | Leu | Ala | Thr | 495 | Thr |     |
|     |     |     |     |     |     | 500 |     |     |     |     |     | 505 |     |     |     |     | 510 |     |     |

- (2) INFORMATION FOR SEQ ID NO:1621:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 506 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..506  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500760  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Thr | Leu | Leu | Gln | Trp | Arg | Leu | Leu | Pro | Leu | Leu | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Val | Ala | Leu | Phe | Ser | Phe | Phe | Phe | Ala | Ser | Pro | Arg | Ser | Leu | Gln |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Gly | Asn | Asn | Lys | Cys | Ser | Leu | Leu | Pro | His | Asp | His | Tyr | Trp | Ile | Ser |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Ser | Lys | Arg | Ile | Val | Thr | Pro | Asn | Gly | Leu | Ile | Ser | Gly | Ser | Val | Glu |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Val | Lys | Gly | Gly | Ile | Ile | Val | Ser | Val | Val | Lys | Glu | Val | Asp | Trp | His |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 80  |     |
| Lys | Ser | Gln | Arg | Ser | Arg | Val | Lys | Val | Ile | Asp | Tyr | Gly | Glu | Ala | Val |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Met | Pro | Gly | Leu | Ile | Asp | Val | His | Val | His | Leu | Asp | Asp | Pro | Gly |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Arg | Ser | Glu | Trp | Glu | Gly | Phe | Pro | Ser | Gly | Thr | Lys | Ala | Ala | Ala | Ala |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Gly | Gly | Ile | Thr | Thr | Leu | Val | Asp | Met | Pro | Leu | Asn | Ser | Phe | Pro | Ser |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |
| Thr | Val | Ser | Pro | Glu | Thr | Leu | Lys | Leu | Lys | Ile | Glu | Ala | Ala | Lys | Asn |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     |     | 160 |     |
| Arg | Ile | His | Val | Asp | Val | Gly | Phe | Trp | Gly | Gly | Leu | Val | Pro | Asp | Asn |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Leu | Asn | Ser | Ser | Ala | Leu | Glu | Ser | Leu | Leu | Asp | Ala | Gly | Val | Leu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Gly | Leu | Lys | Ser | Phe | Met | Cys | Pro | Ser | Gly | Ile | Asn | Asp | Phe | Pro | Met |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| Thr | Asn | Ile | Thr | His | Ile | Lys | Glu | Gly | Leu | Ser | Val | Leu | Ala | Lys | Tyr |
|     |     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |
| Lys | Arg | Pro | Leu | Leu | Val | His | Ala | Glu | Ile | Glu | Arg | Asp | Leu | Glu | Ile |
|     |     |     |     | 225 |     |     |     | 230 |     |     |     |     |     | 240 |     |
| Glu | Asp | Gly | Ser | Glu | Asn | Asp | Pro | Arg | Ser | Tyr | Leu | Thr | Tyr | Leu | Lys |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Thr | Arg | Pro | Thr | Ser | Trp | Glu | Glu | Gly | Ala | Ile | Arg | Asn | Leu | Leu | Ser |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Val | Thr | Glu | Asn | Thr | Arg | Ile | Gly | Gly | Ser | Ala | Glu | Gly | Ala | His | Leu |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |
| His | Ile | Val | His | Leu | Ser | Asp | Ala | Ser | Ser | Ser | Leu | Asp | Leu | Ile | Lys |
|     |     |     |     | 290 |     |     |     | 295 |     |     |     |     |     | 300 |     |
| Glu | Ala | Lys | Gly | Lys | Gly | Asp | Ser | Val | Thr | Val | Glu | Thr | Cys | Pro | His |
|     |     |     |     | 305 |     |     |     | 310 |     |     |     |     |     | 320 |     |
| Tyr | Leu | Ala | Phe | Ser | Ala | Glu | Glu | Ile | Pro | Glu | Gly | Asp | Thr | Arg | Phe |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Lys | Cys | Ser | Pro | Pro | Ile | Arg | Asp | Ala | Ala | Asn | Arg | Glu | Lys | Leu | Trp |
|     |     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |
| Glu | Ala | Leu | Met | Glu | Gly | Asp | Ile | Asp | Met | Leu | Ser | Ser | Asp | His | Ser |
|     |     |     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |
| Pro | Thr | Lys | Pro | Glu | Leu | Lys | Leu | Met | Ser | Asp | Gly | Asn | Phe | Leu | Lys |
|     |     |     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |
| Ala | Trp | Gly | Gly | Ile | Ser | Ser | Leu | Gln | Phe | Val | Leu | Pro | Ile | Thr | Trp |
|     |     |     |     | 385 |     |     |     | 390 |     |     |     |     |     | 400 |     |
| Ser | Tyr | Gly | Lys | Lys | Tyr | Gly | Val | Thr | Leu | Glu | Gln | Val | Thr | Ser | Trp |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |
| Trp | Ser | Asp | Arg | Pro | Ser | Lys | Leu | Ala | Arg | Leu | His | Ser | Lys | Gly | Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Val | Gly | Lys | His | Ala | Asp | Leu | Val | Val | Trp | Glu | Pro | Glu | Ala |
| 435 |     |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Glu | Phe | Asp | Val | Asp | Glu | Asp | His | Pro | Ile | His | Phe | Lys | His | Pro | Ser |
| 450 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Ile | Ser | Ala | Tyr | Leu | Gly | Arg | Arg | Leu | Ser | Gly | Lys | Val | Val | Ser | Thr |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Phe | Val | Arg | Gly | Asn | Leu | Val | Phe | Gly | Glu | Gly | Lys | His | Ala | Ser | Asp |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Ala | Cys | Gly | Ser | Leu | Gln | Leu | Ala | Thr | Thr |     |     |     |     |     |     |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1500761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Leu | Ile | Asp | Val | His | Val | His | Leu | Asp | Asp | Pro | Gly | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Glu | Trp | Glu | Gly | Phe | Pro | Ser | Gly | Thr | Lys | Ala | Ala | Ala | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ile | Thr | Thr | Leu | Val | Asp | Met | Pro | Leu | Asn | Ser | Phe | Pro | Ser | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ser | Pro | Glu | Thr | Leu | Lys | Leu | Lys | Ile | Glu | Ala | Ala | Lys | Asn | Arg |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | His | Val | Asp | Val | Gly | Phe | Trp | Gly | Gly | Leu | Val | Pro | Asp | Asn | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Asn | Ser | Ser | Ala | Leu | Glu | Ser | Leu | Leu | Asp | Ala | Gly | Val | Leu | Gly |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Lys | Ser | Phe | Met | Cys | Pro | Ser | Gly | Ile | Asn | Asp | Phe | Pro | Met | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ile | Thr | His | Ile | Lys | Glu | Gly | Leu | Ser | Val | Leu | Ala | Lys | Tyr | Lys |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Leu | Leu | Val | His | Ala | Glu | Ile | Glu | Arg | Asp | Leu | Glu | Ile | Glu |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asp | Gly | Ser | Glu | Asn | Asp | Pro | Arg | Ser | Tyr | Leu | Thr | Tyr | Leu | Lys | Thr |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |     |
| Arg | Pro | Thr | Ser | Trp | Glu | Glu | Gly | Ala | Ile | Arg | Asn | Leu | Leu | Ser | Val |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Glu | Asn | Thr | Arg | Ile | Gly | Gly | Ser | Ala | Glu | Gly | Ala | His | Leu | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Val | His | Leu | Ser | Asp | Ala | Ser | Ser | Ser | Leu | Asp | Leu | Ile | Lys | Glu |
|     |     |     | 195 |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Lys | Gly | Lys | Gly | Asp | Ser | Val | Thr | Val | Glu | Thr | Cys | Pro | His | Tyr |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Ala | Phe | Ser | Ala | Glu | Glu | Ile | Pro | Glu | Gly | Asp | Thr | Arg | Phe | Lys |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |     |
| Cys | Ser | Pro | Pro | Ile | Arg | Asp | Ala | Ala | Asn | Arg | Glu | Lys | Leu | Trp | Glu |
|     |     |     |     | 245 |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ala | Leu | Met | Glu | Gly | Asp | Ile | Asp | Met | Leu | Ser | Ser | Asp | His | Ser | Pro |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Thr | Lys | Pro | Glu | Leu | Lys | Leu | Met | Ser | Asp | Gly | Asn | Phe | Leu | Lys | Ala |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Gly | Gly | Ile | Ser | Ser | Leu | Gln | Phe | Val | Leu | Pro | Ile | Thr | Trp | Ser |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |



20 25 30  
Leu Pro Tyr Leu Thr Cys Gly Gly Gly Val Gly Gly Val Ile Gly Tyr  
35 40 45  
His Val Thr Trp Leu Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg  
50 55 60  
Ser Trp Lys Thr Lys Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu  
65 70 75 80  
Phe Thr Met Gly Glu Ser Trp His Asn Asn His His Ala Phe Glu Ser  
85 90 95  
Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr  
100 105 110  
Leu Ile Arg Leu Phe Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu  
115 120 125  
Pro Ser Glu Phe Gln Lys Gln Lys Leu Ala Leu Thr Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met Thr Ile Gly Phe His Val Leu Met Phe Trp Thr Val Leu Tyr Leu  
1 5 10 15  
Tyr Gly Gly Leu Pro Tyr Leu Thr Cys Gly Gly Gly Val Gly Gly Val  
20 25 30  
Ile Gly Tyr His Val Thr Trp Leu Val Asn Ser Ala Cys His Ile Trp  
35 40 45  
Gly Ser Arg Ser Trp Lys Thr Lys Asp Thr Ser Arg Asn Val Trp Trp  
50 55 60  
Leu Ser Leu Phe Thr Met Gly Glu Ser Trp His Asn Asn His His Ala  
65 70 75 80  
Phe Glu Ser Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp Ile  
85 90 95  
Thr Trp Tyr Leu Ile Arg Leu Phe Glu Val Leu Gly Leu Ala Thr Asp  
100 105 110  
Val Lys Leu Pro Ser Glu Phe Gln Lys Gln Lys Leu Ala Leu Thr Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Phe Trp Thr Val Leu Tyr Leu Tyr Gly Gly Leu Pro Tyr Leu Thr  
1 5 10 15  
Cys Gly Gly Gly Val Gly Gly Val Ile Gly Tyr His Val Thr Trp Leu  
20 25 30

Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg Ser Trp Lys Thr Lys  
35 40 45  
Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu Phe Thr Met Gly Gly  
50 55 60  
Ser Trp His Asn Asn His His Ala Phe Glu Ser Ser Ala Arg Gln Gly  
65 70 75 80  
Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr Leu Ile Arg Leu Phe  
85 90 95  
Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu Pro Ser Glu Phe Gln  
100 105 110  
Lys Gln Lys Lys Ala Leu Thr Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

|             |            |            |            |             |             |      |
|-------------|------------|------------|------------|-------------|-------------|------|
| acaagtcaaca | accccaacct | gcagtgcata | tctcttcgt  | tatcctcaat  | attctttttc  | 60   |
| ctcttctcca  | catcaacct  | tttgatttct | ccggtacaac | ccacaacctc  | taagctctcg  | 120  |
| gcaccacggc  | ccacagaga  | gctctccgcc | gattactact | ccaagaaatg  | tcttcagttt  | 180  |
| gaaactctcg  | tcggttcctg | cactctcag  | cggttcaaa  | aagtcctcat  | ctcagctcca  | 240  |
| gccaccattc  | gcctcttctt | tcaagactgc | ttcgttgagg | gttgatgagg  | gtcgatattg  | 300  |
| atagaaacaa  | agaaaggga  | caagaaatta | gcagagagag | aagcatatga  | gaataaggaa  | 360  |
| ttgagagagg  | aaggatttga | tagtatcatc | aaggcgaagg | ccttggttga  | gtctcattgc  | 420  |
| ctttctctcg  | tctcttctc  | tgatattctc | gctattgccg | ctcgagattt  | cattcatctg  | 480  |
| gcaggtaggg  | cttactatca | agtgaaaaaa | ggaagggtgg | acggaaaaaa  | atcaaacggca | 540  |
| aagaacgtcc  | ctccaaacat | acctcgatca | aactccaccg | ttgatcaact  | catcaagctc  | 600  |
| ttcgcgcca   | aaggactaac | cgtagaggaa | ctcgtcgtec | tttctggttc  | ccacaccatc  | 660  |
| ggttcgccca  | ttgtaaaaat | ttccttggtc | gtctctacga | ctacaaaggc  | acaaaacgac  | 720  |
| ccgacccgac  | tcttgaccaa | agattactaa | aagagctccg | gatgtcttgt  | cttttttccg  | 780  |
| gcggaagctc  | tggagtcgtc | cttcgctcgc | acgctacaac | tcggttttgt  | tttgataatg  | 840  |
| gatatttcac  | aggtctagga | accaacatgg | gcctctctcg | gtcggaccac  | gctttgttcc  | 900  |
| ttgacccgag  | gacgaagccc | attgcacttg | agatggcaag | agataagcag  | aagtttctca  | 960  |
| aggcgttttg  | agacgctatg | gataaaatgg | gttcctattg | tgtaaaagaga | gggaagagac  | 1020 |
| atggggaaat  | acgtacggat | tgtcgaagtc | ttttatagat | ttctcttatg  | ctctgtctcg  | 1080 |
| atggtttttg  | tcttgatctt | gatgtgtctt | gtgtcatgtg | tcctttaatt  | tattagcatt  | 1140 |
| ttcgtgtatg  | ttttgtttat | agtataaggt | attttttt   |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | His | Asn | Pro | Thr | Met | His | Val | Ile | Ser | Leu | Ser | Leu | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ile | Phe | Phe | Phe | Leu | Phe | Leu | Thr | Ser | Thr | Ile | Leu | Ile | Ser | Pro | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gln | Pro | Thr | Thr | Ser | Lys | Pro | Pro | Ala | Pro | Arg | Pro | His | Arg | Glu | Leu |

35 40 45  
Ser Ala Asp Tyr Tyr Ser Lys Lys Cys Pro Gln Leu Glu Thr Leu Val  
50 55 60  
Gly Ser Val Thr Ser Gln Arg Phe Lys Glu Val Pro Ile Ser Ala Pro  
65 70 75 80  
Ala Thr Ile Arg Leu Phe Phe His Asp Cys Phe Val Glu Gly Cys Asp  
85 90 95  
Gly Ser Ile Leu Ile Glu Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu  
100 105 110  
Arg Glu Ala Tyr Glu Asn Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser  
115 120 125  
Ile Ile Lys Ala Lys Ala Leu Val Glu Ser His Cys Pro Ser Leu Val  
130 135 140  
Ser Xaa Ser Asp Ile Leu Ala Ile Ala Ala Arg Asp Phe Ile His Leu  
145 150 155 160  
Ala Gly Gly Pro Tyr Tyr Gln Val Lys Lys Gly Arg Trp Asp Gly Lys  
165 170 175  
Arg Ser Thr Ala Lys Asn Val Pro Pro Asn Ile Pro Arg Ser Asn Ser  
180 185 190  
Thr Val Asp Gln Leu Ile Lys Leu Phe Ala Ser Lys Gly Leu Thr Val  
195 200 205  
Glu Glu Leu Val Val Leu Ser Gly Ser His Thr Ile Gly Ser Pro Ile  
210 215 220  
Val Lys Ile Ser Leu Val Val Ser Thr Thr Thr Lys Ala Gln Asn Asp  
225 230 235 240  
Pro Thr Arg Val Leu Thr Lys Asp Tyr  
245

(2) INFORMATION FOR SEQ ID NO:1629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1500780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1629:

Met His Val Ile Ser Leu Ser Leu Ser Ser Ile Phe Phe Phe Leu Phe  
1 5 10 15  
Leu Thr Ser Thr Ile Leu Ile Ser Pro Val Gln Pro Thr Thr Ser Lys  
20 25 30  
Pro Pro Ala Pro Arg Pro His Arg Glu Leu Ser Ala Asp Tyr Tyr Ser  
35 40 45  
Lys Lys Cys Pro Gln Leu Glu Thr Leu Val Gly Ser Val Thr Ser Gln  
50 55 60  
Arg Phe Lys Glu Val Pro Ile Ser Ala Pro Ala Thr Ile Arg Leu Phe  
65 70 75 80  
Phe His Asp Cys Phe Val Glu Gly Cys Asp Gly Ser Ile Leu Ile Glu  
85 90 95  
Thr Lys Lys Gly Ser Lys Lys Leu Ala Glu Arg Glu Ala Tyr Glu Asn  
100 105 110  
Lys Glu Leu Arg Glu Glu Gly Phe Asp Ser Ile Ile Lys Ala Lys Ala  
115 120 125  
Leu Val Glu Ser His Cys Pro Ser Leu Val Ser Xaa Ser Asp Ile Leu  
130 135 140  
Ala Ile Ala Ala Arg Asp Phe Ile His Leu Ala Gly Gly Pro Tyr Tyr  
145 150 155 160  
Gln Val Lys Lys Gly Arg Trp Asp Gly Lys Arg Ser Thr Ala Lys Asn  
165 170 175

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Pro | Asn | Ile | Pro | Arg | Ser | Asn | Ser | Thr | Val | Asp | Gln | Leu | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Leu | Phe | Ala | Ser | Lys | Gly | Leu | Thr | Val | Glu | Glu | Leu | Val | Val | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Gly | Ser | His | Thr | Ile | Gly | Ser | Pro | Ile | Val | Lys | Ile | Ser | Leu | Val |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Val | Ser | Thr | Thr | Thr | Lys | Ala | Gln | Asn | Asp | Pro | Thr | Arg | Val | Leu | Thr |
|     |     |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Lys | Asp | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

|             |            |            |            |             |            |      |
|-------------|------------|------------|------------|-------------|------------|------|
| aaaacaacaa  | acgtaacaag | gattcgagct | ctctctagac | gatgcaagcc  | aaaatcaatt | 60   |
| ctttctctcaa | gcctctctct | tcttcttcta | tcgctgcctc | agtaacaaca  | gacacagacg | 120  |
| atrgstttag  | ctgtctggga | gaacaatcgg | aacgccatcg | tcaaacaccta | ccagcgctga | 180  |
| ttctgcgatta | ccgaaagaag | tgaagtgcct | aaaggatgca | tcgaaaaagac | gctgaagaaa | 240  |
| ggatcttctt  | ctgtacctaa | aaatcacaaa | aagaagcgta | attatacaca  | attccacata | 300  |
| cggttggggc  | aatctgattt | tcttctcaga | cattgcgcag | aatgtggagc  | taagtatgct | 360  |
| cttggaagatg | aattagatga | gaagaacatc | caaagtttct | acaaggacta  | tatgtatgga | 420  |
| ctccctttta  | agggttggca | gaacgagaaa | gcgtttacat | cacctttgtt  | catcaagaac | 480  |
| cgcatcgtaa  | tggatcaga  | aaatgattcc | cctgcacaca | gaacaagggt  | gcaagaggtt | 540  |
| gtgaaaatga  | tggaggttga | gttgggtgag | gattggattc | ttcaccaaca  | ttgtaaggtt | 600  |
| tatctattca  | tatccttcca | gaggatctct | ggatgtctag | ttgctgaacc  | aattaaggaa | 660  |
| gcatttaagc  | tcatagcttc | tctgatgat  | gaaagacagt | tacaaaaaga  | gagctcatcc | 720  |
| tcgccttcaa  | ctctcatcca | gtttggaaac | attgttctac | aaagagaggt  | atcgaaaaga | 780  |
| tgtcgaaatc  | cagatgatag | attagataac | ggagtcattg | tatgtgaaga  | agaagctaaa | 840  |
| ccagctgttt  | gtgggattag | agcgatttgg | gtctcacctt | ctaataagaag | aaaaggcata | 900  |
| gccacatggt  | tactcgatac | cacgagggaa | agctttcgca | acaattgggtg | catgctggag | 960  |
| aaaatctcagt | tagcattttc | acaaccaacc | tccataggaa | gatcttttgg  | atctaaatat | 1020 |
| tttggaaact  | gttcattctt | actttacaaa | gtcagctaaa | tgtatactca  | cttttcttaa | 1080 |
| acggcatagg  | tttcatcaca | tcacaacatc | catcttcact | gtc         |            |      |

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1500786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Gly | Leu | Pro | Phe | Lys | Gly | Trp | Gln | Asn | Glu | Lys | Ala | Phe | Thr |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Leu | Phe | Ile | Lys | Asn | Arg | Ile | Val | Met | Val | Ser | Glu | Asn | Asp |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Pro | Ala | His | Arg | Asn | Lys | Val | Gln | Glu | Val | Val | Lys | Met | Met | Glu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Val | Glu | Leu | Gly | Glu | Asp | Trp | Ile | Leu | His | Gln | His | Cys | Lys | Val | Tyr |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |

Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val Ala Glu Pro  
65 70 75 80  
Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp Glu Arg Gln  
85 90 95  
Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile Gln Phe Gly  
100 105 110  
Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg Thr Ser Asp  
115 120 125  
Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu Ala Lys Pro  
130 135 140  
Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser Asn Arg Arg  
145 150 155 160  
Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu Ser Phe Arg  
165 170 175  
Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe Ser Gln Pro  
180 185 190  
Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly Thr Cys Ser  
195 200 205  
Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe Ser  
210 215 220

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Met Val Ser Glu Asn Asp Ser Pro Ala His Arg Asn Lys Val Gln Glu  
1 5 10 15  
Val Val Lys Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His  
20 25 30  
Gln His Cys Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly  
35 40 45  
Cys Leu Val Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser  
50 55 60  
Pro Asp Asp Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Pro Ser  
65 70 75 80  
Thr Ser Ile Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys  
85 90 95  
Arg Cys Arg Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys  
100 105 110  
Glu Glu Glu Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val  
115 120 125  
Ser Pro Ser Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr  
130 135 140  
Thr Arg Glu Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln  
145 150 155 160  
Leu Ala Phe Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys  
165 170 175  
Tyr Phe Gly Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp  
180 185 190  
Thr His Phe Ser  
195

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..177  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500788  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

```
Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His Gln His Cys
1      5      10      15
Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val
20      25      30
Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp
35      40      45
Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile
50      55      60
Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg
65      70      75      80
Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu
85      90      95
Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser
100     105     110
Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu
115     120     125
Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe
130     135     140
Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly
145     150     155     160
Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe
165     170     175
ser
```

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1452 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1452  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500793  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

```
aagcattttg catctctgtt tcttggtttt gtgttttagt tttagagaaa aatgggacag      60
attccgaggt ttcttttctt gaggaatatg ttggctctct cgttggccat caacttcaag      120
ttgattctaa agattttgaa gggatagata gaacgaggag attcatggga cagaaacagc      180
tatgttagca tatggccggt ggtatccacc acggcttcag aatctctctc gtgtcttcca      240
gcattcttga actatagcaa gattgaagaa gacgatgata gaattatcaa tctcaaattt      300
ggtagtccaa cgggtgatga gagatattgg caggaaaaat gagaggtgac aacaattggt      360
atacctggat ggcaatctct tagctatttt tcagatgaaa acaacctctg ttggtttctt      420
gagccagagc ttgccaaaaga gattgtgagg gtgcataagg ttgttgggaa tgctgttaac      480
caagaccgct tcattgttgt tggcactggc tcaacacaaat tgcatacagg tgctctctat      540
gctctctccc cacatgatga ctccggctccc attaatgtgc tgctacggcg accctattat      600
agtagacagt cgttgattac agactgcctc aaatcaggtt tatatcgatg ggttgagat      660
gcaaaagcgt acaaaagaaga ttgtccatac attgaaactg ttacatctcc aaacaacctc      720
gatgggttct tgagagaatc agtagtgaac agtaactgaag gtatatgtat ccatgatttg      780
gcttactatt gggccacagta tacaccgata acataaccag ctgatcacga tgttatgtct      840
ttcaactgctt caaagagcac ttggcatgca gggatacggg ttggvtgggc ttgtgtgaaa      900
gacagagaga cggctaggaa aatgatagag tacattgaac tcaacacgat tggggtttca      960
```

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| aaggactcac | agcttagagt | agccaaggtt | cttaaggttg | tgtcagacag | ttgtgggaat | 1020 |
| gtaacgggca | aatctttctt | tgaccatagt | tatgatgcta | tgatgagag  | gtggaaacta | 1080 |
| ttgaacaag  | cagcaagga  | tactaaacgt | ttcagtggtc | ctgatttcgt | ctctcaacgt | 1140 |
| tgcaatttct | ttggcagggt | ctttgagcca | caaccagcat | ttgcatgtgt | taagtgtgaa | 1200 |
| gaagggtag  | tggtattgtg | gaagtttctt | agagaggaga | agaagattct | aactaaaagt | 1260 |
| ggaagtgact | tcggagatga | gctaagtaat | gtgaggataa | gcatgttgga | tagagatact | 1320 |
| aactttaata | ttttccttca | caggattaca | tcttccttta | attcaacttt | gtaagtgcac | 1380 |
| atgcatgtga | ttatgatcga | ttgtcataac | ttgcaacaag | tgttttgtct | cataaatatt | 1440 |
| attggaatt  | tg         |            |            |            |            |      |

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1500794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Gln | Ile | Pro | Arg | Phe | Leu | Ser | Trp | Arg | Asn | Met | Leu | Val | Leu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ser | Leu | Ala | Ile | Asn | Phe | Ser | Leu | Ile | Leu | Lys | Ile | Leu | Lys | Gly | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Glu | Arg | Gly | Asp | Ser | Trp | Asp | Arg | Thr | Ala | Tyr | Val | Ser | Ile | Trp |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Pro | Val | Val | Ser | Thr | Thr | Ala | Ser | Glu | Ser | Ser | Ser | Leu | Ser | Ser | Ala |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Ser | Cys | Asn | Tyr | Ser | Lys | Ile | Glu | Glu | Asp | Asp | Asp | Arg | Ile | Ile | Asn |  |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |  |
| Leu | Lys | Phe | Gly | Asp | Pro | Thr | Val | Tyr | Glu | Arg | Tyr | Trp | Gln | Glu | Asn |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | Glu | Val | Thr | Thr | Met | Val | Ile | Pro | Gly | Trp | Gln | Ser | Leu | Ser | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Ser | Asp | Glu | Asn | Asn | Leu | Cys | Trp | Phe | Leu | Glu | Pro | Glu | Leu | Ala |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Lys | Glu | Ile | Val | Arg | Val | His | Lys | Val | Val | Gly | Asn | Ala | Val | Thr | Gln |  |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |  |
| Asp | Arg | Phe | Ile | Val | Val | Gly | Thr | Gly | Ser | Thr | Gln | Leu | Tyr | Gln | Ala |  |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |  |
| Ala | Leu | Tyr | Ala | Leu | Ser | Pro | His | Asp | Asp | Ser | Gly | Pro | Ile | Asn | Val |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Val | Ser | Ala | Ala | Pro | Tyr | Tyr | Ser | Thr | Tyr | Pro | Leu | Ile | Thr | Asp | Cys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Lys | Ser | Gly | Leu | Tyr | Arg | Trp | Gly | Gly | Asp | Ala | Lys | Thr | Tyr | Lys |  |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |  |
| Glu | Asp | Gly | Pro | Tyr | Ile | Glu | Leu | Val | Thr | Ser | Pro | Asn | Asn | Pro | Asp |  |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |  |
| Gly | Phe | Leu | Arg | Glu | Ser | Val | Val | Asn | Ser | Thr | Glu | Gly | Ile | Leu | Ile |  |
|     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |  |
| His | Asp | Leu | Ala | Tyr | Trp | Trp | Pro | Gln | Tyr | Thr | Pro | Ile | Thr |     |     |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1500795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Leu | Ser | Leu | Ala | Ile | Asn | Phe | Ser | Leu | Ile | Leu | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Gly | Asp | Arg | Glu | Arg | Gly | Asp | Ser | Trp | Asp | Arg | Thr | Ala | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Ser | Ile | Trp | Pro | Val | Val | Ser | Thr | Ala | Ser | Glu | Ser | Ser | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Ser | Ser | Ala | Ser | Cys | Asn | Tyr | Ser | Lys | Ile | Glu | Glu | Asp | Asp | Asp |
|     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Ile | Asn | Leu | Lys | Phe | Gly | Asp | Pro | Thr | Val | Tyr | Glu | Arg | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Gln | Glu | Asn | Gly | Glu | Val | Thr | Thr | Met | Val | Ile | Pro | Gly | Trp | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Ser | Tyr | Phe | Ser | Asp | Glu | Asn | Asn | Leu | Cys | Trp | Phe | Leu | Glu |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Pro | Glu | Leu | Ala | Lys | Glu | Ile | Val | Arg | Val | His | Lys | Val | Val | Gly | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Ala | Val | Thr | Gln | Asp | Arg | Phe | Ile | Val | Val | Gly | Thr | Gly | Ser | Thr | Gln |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Leu | Tyr | Gln | Ala | Ala | Leu | Tyr | Ala | Leu | Ser | Pro | His | Asp | Asp | Ser | Gly |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Pro | Ile | Asn | Val | Val | Ser | Ala | Ala | Pro | Tyr | Ser | Thr | Tyr | Pro | Leu |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ile | Thr | Asp | Cys | Leu | Lys | Ser | Gly | Leu | Tyr | Arg | Trp | Gly | Gly | Asp | Ala |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Lys | Thr | Tyr | Lys | Glu | Asp | Gly | Pro | Tyr | Ile | Glu | Leu | Val | Thr | Ser | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asn | Asn | Pro | Asp | Gly | Phe | Leu | Arg | Glu | Ser | Val | Val | Asn | Ser | Thr | Glu |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Ile | Leu | Ile | His | Asp | Leu | Ala | Tyr | Tyr | Trp | Pro | Gln | Tyr | Thr | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1500796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Thr | Ala | Ser | Lys | Ser | Thr | Gly | His | Ala | Gly | Ile | Arg | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Trp | Ala | Leu | Val | Lys | Asp | Arg | Glu | Thr | Ala | Arg | Lys | Met | Ile | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ile | Glu | Leu | Asn | Thr | Ile | Gly | Val | Ser | Lys | Asp | Ser | Gln | Leu | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ala | Lys | Val | Leu | Lys | Val | Val | Ser | Asp | Ser | Cys | Gly | Asn | Val | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Gly | Lys | Ser | Phe | Phe | Asp | His | Ser | Tyr | Asp | Ala | Met | Tyr | Glu | Arg | Trp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Leu | Leu | Lys | Gln | Ala | Ala | Lys | Asp | Thr | Lys | Arg | Phe | Ser | Val | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Phe | Val | Ser | Gln | Arg | Cys | Asn | Phe | Phe | Gly | Arg | Val | Phe | Glu | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |  |  |  |  |
| Gln | Pro | Ala | Phe | Ala | Trp | Phe | Lys | Cys | Glu | Glu | Gly | Ile | Val | Asp | Cys |  |  |  |  |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Glu | Lys | Phe | Leu | Arg | Glu | Glu | Lys | Lys | Ile | Leu | Thr | Lys | Ser | Gly | Lys |  |  |  |  |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |  |  |  |
| Tyr | Phe | Gly | Asp | Glu | Leu | Ser | Asn | Val | Arg | Ile | Ser | Met | Leu | Asp | Arg |  |  |  |  |
|     | 145 |     |     |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |  |  |  |  |
| Asp | Thr | Asn | Phe | Asn | Ile | Phe | Leu | His | Arg | Ile | Thr | Ser | Ser | Phe | Asn |  |  |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |  |  |  |  |
| Ser | Thr | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:1638:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1235  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| aactaaatca  | gaagattact | actaaacaga  | gtcttttttg | acttgccaaa  | aacacatctg  | 60   |
| tctctctctc  | tctttgcgga | tctgaaatgg  | cgattctctg | tatcgatttc  | tccaaactca  | 120  |
| atggtgaaga  | aagagagaag | acactgtctg  | aaatcgctag | agcttgcgaa  | gagtggggat  | 180  |
| tttttcagct  | gggtgaacct | ggtattccat  | ttgagcttct | aaataaggtg  | aagaagctga  | 240  |
| gctcagattg  | ctacaataca | gagagagaag  | aagcattcaa | gacttcta    | cccgtaga    | 300  |
| tgctcaacga  | attggttcaa | aagaactctg  | gcgagaagct | agaaaacgtg  | gactgggaag  | 360  |
| atgtcttcac  | tctcttggac | cataaccaaa  | tcgaatggcc | atccaaaatt  | aaagagacta  | 420  |
| tgaggagaata | cagagaagaa | gtgaggaagc  | tagcgagcaa | gatgatggaa  | gtgatggatg  | 480  |
| agaatttggg  | tttgctataa | ggttacataa  | agaaaagctt | caatgaagga  | atggaagatg  | 540  |
| gagaagagac  | agctttcttt | gggactaaag  | tcagccatta | ccctccttgt  | cctcatcctg  | 600  |
| agctagtcaa  | tgccctctga | ggcactatct  | atgcaggagg | tgctgttttg  | cttttccaag  | 660  |
| acgatgaata  | tgatggcctt | caggtcttga  | aagacggcga | gtggatcgat  | gttcagccctc | 720  |
| tacctaatgc  | cattgtttac | aacactgggtg | atcagattga | agttctttagc | aacggaaggt  | 780  |
| acaagagtgc  | gtggcacagg | gtggtggcga  | gggaggaagg | aaacagaagg  | tctatagctt  | 840  |
| ccttctacaa  | tccgtctgac | aaggcggcga  | tagggccagc | cacggtggcg  | gaagaggaag  | 900  |
| gaagtgaaga  | gaagtataca | aagtttgtgt  | ttggagatta | catggatgtt  | tatgcaaac   | 960  |
| agaagtctat  | gcttaaaag  | cctcgttttc  | tagctgtaaa | gtctctctaa  | atgtactatt  | 1020 |
| ttatktattt  | ttacagact  | atcactgttt  | tatctacacc | cattatgtat  | tttctcttaa  | 1080 |
| gctataaatg  | ccaatttata | tagttaaaaa  | ttggcactct | gctctccagg  | ctttatattt  | 1140 |
| ttttgttttt  | ttttgtttg  | ccatgtgatg  | tatgaatctt | tcttgtgtga  | cctatgttct  | 1200 |
| tagtttttga  | atataaatg  | gtgtgccttt  | ttctt      |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1639:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 307 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..307  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Ala | Ile | Pro | Val | Ile | Asp | Phe | Ser | Lys | Leu | Asn | Gly | Glu | Glu | Arg |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |  |  |
| Glu | Lys | Thr | Leu | Ser | Glu | Ile | Ala | Arg | Ala | Cys | Glu | Glu | Trp | Gly | Phe |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |  |  |
| Phe | Gln | Leu | Val | Asn | His | Gly | Ile | Pro | Leu | Glu | Leu | Leu | Asn | Lys | Val |  |  |  |  |

[illegible]

Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val  
115 120 125  
Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn  
130 135 140  
Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu  
145 150 155 160  
Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp  
165 170 175  
Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala  
180 185 190  
Val Lys Ser Leu  
195

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1500800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Met Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile  
1 5 10 15  
Lys Lys Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe  
20 25 30  
Phe Gly Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu  
35 40 45  
Val Asn Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu  
50 55 60  
Phe Gln Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu  
65 70 75 80  
Trp Ile Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly  
85 90 95  
Asp Gln Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His  
100 105 110  
Arg Val Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe  
115 120 125  
Tyr Asn Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu  
130 135 140  
Glu Glu Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr  
145 150 155 160  
Met Asp Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe  
165 170 175  
Leu Ala Val Lys Ser Leu  
180

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

acaccggcgt ttggctgmsa tcatcgagat gatacacact gcaagcttga tacacgacga

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| tgtgttagac | gagagtgcac  | tgccaagagg  | aaagggaaac  | gttcgatgac | ttttcggcac | 120 |
| aagagtagcg | gtgctagctg  | gagatttcat  | gtttgctcaa  | gcgtcatggt | acttagcaaa | 180 |
| tctcgagaat | cttgaagtta  | ttaaagctcat | cagtcagggtg | atcaaagact | ttgcaagcgg | 240 |
| agagataaag | caggcgctcca | gctttatttga | ctgcgacacc  | aagctcgagc | agtacttact | 300 |
| caaaagtctc | tacaagacag  | cctcttttagt | ggctgcgagc  | accaaaggag | ctgccatttt | 360 |
| cagcagagtt | gagcctgatg  | tgacagaaca  | aatgtacgag  | tttgggaaga | atctcggctc | 420 |
| ctctttccag | atagttgatg  | atattttggg  | tttcaactcag | tcgacagagc | agctcgggaa | 480 |
| gccagcaggg | agtgattttg  | ctaaaggtaa  | cttaacagca  | cctgtgattt | tcgctctgga | 540 |
| gagggtgcc  | aggctaagag  | agatcattga  | gtcagagttt  | tgtgaggcgg | gttctctgga | 600 |
| agaagcgatt | gaagcgggtg  |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Arg | Arg | Leu | Ala | Xaa | Ile | Ile | Glu | Met | Ile | His | Thr | Ala | Ser | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | His | Asp | Asp | Val | Leu | Asp | Glu | Ser | Asp | Met | Arg | Arg | Gly | Lys | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Thr | Val | His | Glu | Leu | Phe | Gly | Thr | Arg | Val | Ala | Val | Leu | Ala | Gly | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Met | Phe | Ala | Gln | Ala | Ser | Trp | Tyr | Leu | Ala | Asn | Leu | Glu | Asn | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Val | Ile | Lys | Leu | Ile | Ser | Gln | Val | Ile | Lys | Asp | Phe | Ala | Ser | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Glu | Ile | Lys | Gln | Ala | Ser | Ser | Leu | Phe | Asp | Cys | Asp | Thr | Lys | Leu | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Glu | Tyr | Leu | Leu | Lys | Ser | Phe | Tyr | Lys | Thr | Ala | Ser | Leu | Val | Ala | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Thr | Lys | Gly | Ala | Ala | Ile | Phe | Ser | Arg | Val | Glu | Pro | Asp | Val | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Gln | Met | Tyr | Glu | Phe | Gly | Lys | Asn | Leu | Gly | Leu | Ser | Phe | Gln | Ile |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Val | Asp | Asp | Ile | Leu | Asp | Phe | Thr | Gln | Ser | Thr | Glu | Gln | Leu | Gly | Lys |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |
| Pro | Ala | Gly | Ser | Asp | Leu | Ala | Lys | Gly | Asn | Leu | Thr | Ala | Pro | Val | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Phe | Ala | Leu | Glu | Arg | Glu | Pro | Arg | Leu | Arg | Glu | Ile | Ile | Glu | Ser | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Phe | Cys | Glu | Ala | Gly | Ser | Leu | Glu | Glu | Ala | Ile | Glu | Ala | Val |     |     |
|     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Leu Asp Glu Ser

[illegible]

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1776

(D) OTHER INFORMATION: / Ceres Seq. ID 1500805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
gtctcatcac ttccacttt cctctctgca tttgttgct ctctctcctg aaaacccttg      60
aattttgcta cagcatctct gaaacgtgtc ttttgactg acttcaatct tttttatcac      120
ttaccgtttc tgggttttat gaagcaactg agctttcttc ttgaactcgg      180
aagaagaaaa aaacacagat ctttatttgt taaagcttcc aaattcgaga agagaatttg      240
aaacagacaaa ttctcaggata ttctgttctt cgtctacttt ggtctctctc ttctctcttt      300
cgaaaagggtt ttattctgtc ttaaagaaaa cttttttgag agggtaaaaa aagcttcaat      360
tttcagagaaa acacaaaagg cagaaaacaga gaaaaacaaa tcatctaat catgaaaacag      420
ggttcaatga atagactcgt tctctgtagt gtcttaatca ccatctgctc gatttgtggg      480
gcttactcca tttgcaatgc ttatcttgct aaagacttta aagagaagtt ggtgaagtgt      540
gaaatcaact ataatgatga taacagtact gataagatgc agaattgcaac aacaaccagt      600
acatgcagaa atttcaataa gccagtgggt actgaagcac taccgcaagg aattatcgag      660
aaaacatcga acctggaaac acaacatcta tggaactacg atgacacaaa aaagagaagg      720
cctaaccatt cgatgagttt gttagccatt cgggtcggtt tcaagcaaaa ggagctagtt      780
aacaagaatt tcacaagaat tctctctcga gatttcggg tcatgctttt tcatatgat      840
gggtgtgtgc atgaactggaa cgaagtatca tggaaataat atgcgattca tgtttcctgt      900
atgaatcaaa caaaatgggt gttcccaag cgattcttgc atcccgatc agtgcacag      960
tacgagtata ttcttctttg ggacgaagat cttggtgttg gtcattcaa tcttcaacga      1020
tatctatcta ttgtcaaaaa gagaggggctt gagatatcgc aacctgtctc tgacacttgc      1080
aaatcagaaa tgcatactcc tataaccgct cgtcaaaaaa aatcaaaagt tcatagaaga      1140
atgtataaat acaaaggtag cggggcagtg gatgaccata gatgaccata gcaccaatcc      1200
gggtgggtgg aaatgatggc acctgttttc tctagagctg catggagatg ttcttggtat      1260
atgattcaga atgatttgat ccatgcttgg ggtctggata cgcagcttgg ttatttgtgt      1320
caaggtgacc tgaagaaaaa tgcgtgtgtt gttgatgcgg agtacaatat tcatatgggt      1380
cttccaacac tgggtgtgtt tgaaaocgct tcaagcgctt tgcggaatga gacagactcg      1440
aaatcaacgg aatcattaga gtctcgtgaa gtggataata gaccagaagt gaggatgaaa      1500
tggttggttg agatcgaagg attcaaggaa cgttggaaga aagctgtgag ggatgataca      1560
tttctcctgt tgagtgtgct ttgtgggtcca ttgtatacca ttattttggt acatagattt      1620
tgatttactt cgagaaaaat tagtgtattt atgtgtttta tggaccacag tgtagattta      1740
acattttgga gcatataaca aaagtgtttt tgtgcc
```

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1500806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

```
Met Lys Gln Gly Ser Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile
1      5      10      15
Thr Thr Ala Leu Ile Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu
      20      25      30
Ala Lys Asp Phe Lys Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys
      35      40      45
Met His Asn Ser Thr Asp Lys Met Gln Asn Ala Thr Thr Thr Ser Thr
```

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Cys Lys Asn Phe Asn Lys Pro Val Gly Thr Glu Ala Leu Pro Gln Gly |     |     |
| 65                                                              | 70  | 75  |
| Ile Ile Glu Lys Thr Ser Asn Leu Glu Thr Gln His Leu Trp Asn Tyr |     |     |
|                                                                 | 85  | 90  |
| Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala |     |     |
|                                                                 | 100 | 105 |
| Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln |     |     |
|                                                                 | 115 | 120 |
| Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly |     |     |
|                                                                 | 130 | 135 |
| Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His |     |     |
| 145                                                             | 150 | 155 |
| Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu |     |     |
|                                                                 | 165 | 170 |
| His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu |     |     |
|                                                                 | 180 | 185 |
| Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val |     |     |
|                                                                 | 195 | 200 |
| Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys |     |     |
|                                                                 | 210 | 215 |
| Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val |     |     |
| 225                                                             | 230 | 235 |
| His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His |     |     |
|                                                                 | 245 | 250 |
| Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val |     |     |
|                                                                 | 260 | 265 |
| Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp |     |     |
|                                                                 | 275 | 280 |
| Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln |     |     |
|                                                                 | 295 | 300 |
| Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile |     |     |
| 305                                                             | 310 | 315 |
| His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala |     |     |
|                                                                 | 325 | 330 |
| Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg |     |     |
|                                                                 | 340 | 345 |
| Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met |     |     |
|                                                                 | 355 | 360 |
| Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys |     |     |
|                                                                 | 370 | 375 |
| Trp Val Asp Pro Tyr                                             |     | 380 |
| 385                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1648:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 384 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..384
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1500807
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:
 

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile Thr Thr Ala Leu Ile |    |    |
| 1                                                               | 5  | 10 |
| Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu Ala Lys Asp Phe Lys |    |    |
|                                                                 | 20 | 25 |
| Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys Met His Asn Ser Thr |    |    |
|                                                                 | 35 | 40 |
|                                                                 |    | 45 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asp | Lys | Met | Gln | Asn | Ala | Thr | Thr | Thr | Ser | Thr | Cys | Lys | Asn | Phe | Asn |  |
| 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Lys | Pro | Val | Gly | Thr | Glu | Ala | Leu | Pro | Gln | Gly | Ile | Ile | Glu | Lys | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Asn | Leu | Glu | Thr | Gln | His | Leu | Trp | Asn | Tyr | Asp | Asp | Thr | Lys | Lys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Arg | Pro | Asn | His | Ser | Met | Ser | Leu | Leu | Ala | Met | Ala | Val | Gly | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Gln | Lys | Glu | Leu | Val | Asn | Lys | Val | Ile | Gln | Lys | Phe | Pro | Pro | Arg |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Phe | Ala | Val | Met | Leu | Phe | His | Tyr | Asp | Gly | Val | Val | Asp | Asp | Trp |  |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Lys | Gln | Tyr | Pro | Trp | Asn | Asn | His | Ala | Ile | His | Val | Ser | Val | Met | Asn |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Gln | Thr | Lys | Trp | Trp | Phe | Ala | Lys | Arg | Phe | Leu | His | Pro | Asp | Ile | Val |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Glu | Tyr | Glu | Tyr | Ile | Phe | Leu | Trp | Asp | Glu | Asp | Leu | Gly | Val | Gly |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| His | Phe | Asn | Pro | Gln | Arg | Tyr | Leu | Ser | Ile | Val | Lys | Glu | Glu | Gly | Leu |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Ile | Ser | Gln | Pro | Ala | Leu | Asp | Thr | Ser | Lys | Ser | Glu | Val | His | His |  |
| 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Pro | Ile | Thr | Ala | Arg | Gln | Lys | Lys | Ser | Lys | Val | His | Arg | Arg | Met | Tyr |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |  |
| Lys | Tyr | Lys | Gly | Ser | Gly | Arg | Cys | Asp | Asp | His | Ser | Thr | Asn | Pro | Pro |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Cys | Ile | Gly | Trp | Val | Glu | Met | Met | Ala | Pro | Val | Phe | Ser | Arg | Ala | Ala |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Trp | Arg | Cys | Ser | Trp | Tyr | Met | Ile | Gln | Asn | Asp | Leu | Ile | His | Ala | Trp |  |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Gly | Leu | Asp | Thr | Gln | Leu | Gly | Tyr | Cys | Ala | Gln | Gly | Asp | Arg | Lys | Lys |  |
| 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Asn | Val | Gly | Val | Val | Asp | Ala | Glu | Tyr | Ile | Ile | His | Tyr | Gly | Leu | Pro |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Thr | Leu | Gly | Val | Val | Glu | Thr | Ala | Ser | Ser | Ala | Leu | Arg | Asn | Glu | Thr |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |  |
| Asp | Ser | Lys | Ser | Thr | Glu | Ser | Leu | Glu | Ser | Arg | Glu | Val | Asp | Asn | Arg |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Pro | Glu | Val | Arg | Met | Lys | Ser | Phe | Val | Glu | Met | Lys | Arg | Phe | Lys | Glu |  |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Arg | Trp | Lys | Lys | Ala | Val | Arg | Asp | Asp | Thr | Cys | Trp | Val | Asp | Pro | Tyr |  |
| 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Asn | Ser | Thr | Asp | Lys | Met | Gln | Asn | Ala | Thr | Thr | Thr | Ser | Thr |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Cys | Lys | Asn | Phe | Asn | Lys | Pro | Val | Gly | Thr | Glu | Ala | Leu | Pro | Gln | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Ile | Glu | Lys | Thr | Ser | Asn | Leu | Glu | Thr | Gln | His | Leu | Trp | Asn | Tyr |  |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala |     |     |
| 50                                                              | 55  | 60  |
| Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln |     |     |
| 65                                                              | 70  | 75  |
| Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly |     |     |
| 85                                                              | 90  | 95  |
| Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His |     |     |
| 100                                                             | 105 | 110 |
| Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu |     |     |
| 115                                                             | 120 | 125 |
| His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu |     |     |
| 130                                                             | 135 | 140 |
| Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val |     |     |
| 145                                                             | 150 | 155 |
| Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys |     |     |
| 165                                                             | 170 | 175 |
| Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Ser Lys Val     |     |     |
| 180                                                             | 185 | 190 |
| His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His |     |     |
| 195                                                             | 200 | 205 |
| Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val |     |     |
| 210                                                             | 215 | 220 |
| Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp |     |     |
| 225                                                             | 230 | 235 |
| Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln |     |     |
| 245                                                             | 250 | 255 |
| Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile |     |     |
| 260                                                             | 265 | 270 |
| His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala |     |     |
| 275                                                             | 280 | 285 |
| Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg |     |     |
| 290                                                             | 295 | 300 |
| Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met |     |     |
| 305                                                             | 310 | 315 |
| Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys |     |     |
| 325                                                             | 330 | 335 |
| Trp Val Asp Pro Tyr                                             |     |     |
| 340                                                             |     |     |

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..543

- (D) OTHER INFORMATION: / Ceres Seq. ID 1500809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

|            |             |            |             |            |             |     |
|------------|-------------|------------|-------------|------------|-------------|-----|
| aacctccact | gttaataaac  | tcaaacctct | gcaattgtct  | tcttctcttc | aactccatca  | 60  |
| tctccaccac | cggtattctc  | gccggaatcc | aatggagctt  | accagcttcc | atcgctcttc  | 120 |
| tctcttattc | ctcatctcac  | taacattgat | catctctccg  | acgacaacaa | cttcaatcgg  | 180 |
| agttaactac | gggtcaaatcg | gagacaacct | ccctccccc   | accgacgtaa | tcccaactaa  | 240 |
| aaaatcaatc | ggagcaacaa  | aagtaaaact | ctacgacgca  | aatccacaaa | tctcaaaagc  | 300 |
| tttctccaac | accggaatcg  | aattcatcat | cggactcggc  | aacgaatacc | tctccaaaaa  | 360 |
| gaaagatctc | tcaaaagcct  | taacatggat | caacacaaaac | gttactccat | ttttacctgc  | 420 |
| gactaacatc | acatgcataa  | ctatcggtaa | cgaatactctc | gtctccaacg | actcttctact | 480 |
| cactaccaat | ctctctccag  | cgatgcaagg | agtttactct  | gctttaatca | ccgcgggtct  | 540 |
| ctc        |             |            |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Thr | Val | Asn | Lys | Leu | Lys | Pro | Leu | Gln | Leu | Ser | Ser | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Leu | His | His | Leu | His | His | Arg | His | Ser | Arg | Arg | Asn | Pro | Met | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Leu | Thr | Ser | Phe | His | Arg | Ser | Ser | Leu | Phe | Leu | Ile | Ser | Ser | Leu | Thr |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Ile | Ile | Leu | Pro | Thr | Thr | Thr | Thr | Ser | Ile | Gly | Val | Asn | Tyr | Gly |
|     |     |     |     | 50  |     |     | 55  |     |     | 60  |     |     |     |     |     |
| Gln | Ile | Gly | Asp | Asn | Leu | Pro | Ser | Pro | Thr | Asp | Val | Ile | Pro | Leu | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ser | Ile | Gly | Ala | Thr | Lys | Val | Lys | Leu | Tyr | Asp | Ala | Asn | Pro | Gln |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Leu | Lys | Ala | Phe | Ser | Asn | Thr | Gly | Ile | Glu | Phe | Ile | Ile | Gly | Leu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Asn | Glu | Tyr | Leu | Ser | Lys | Met | Lys | Asp | Pro | Ser | Lys | Ala | Leu | Thr |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Ile | Lys | Gln | Asn | Val | Thr | Pro | Phe | Leu | Pro | Ala | Thr | Asn | Ile | Thr |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Cys | Ile | Thr | Ile | Gly | Asn | Glu | Ile | Leu | Ala | Lys | Asn | Asp | Ser | Ser | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Thr | Thr | Asn | Leu | Leu | Pro | Ala | Met | Gln | Gly | Val | His | Ser | Ala | Leu | Ile |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Ala | Gly | Leu |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 180 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Thr | Ser | Phe | His | Arg | Ser | Ser | Leu | Leu | Phe | Leu | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Leu | Ile | Ile | Leu | Pro | Thr | Thr | Thr | Ser | Ile | Gly | Val | Asn |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Tyr | Gly | Gln | Ile | Gly | Asp | Asn | Leu | Pro | Ser | Pro | Thr | Asp | Val | Ile | Pro |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Ile | Lys | Ser | Ile | Gly | Ala | Thr | Lys | Val | Lys | Leu | Tyr | Asp | Ala | Asn |
|     |     |     |     | 50  |     |     | 55  |     |     | 60  |     |     |     |     |     |
| Pro | Gln | Ile | Leu | Lys | Ala | Phe | Ser | Asn | Thr | Gly | Ile | Glu | Phe | Ile | Ile |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Gly | Leu | Gly | Asn | Glu | Tyr | Leu | Ser | Lys | Met | Lys | Asp | Pro | Ser | Lys | Ala |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Thr | Trp | Ile | Lys | Gln | Asn | Val | Thr | Pro | Phe | Leu | Pro | Ala | Thr | Asn |

100 105 110  
Ile Thr Cys Ile Thr Ile Gly Asn Glu Ile Leu Ala Leu Asn Asp Ser  
115 120 125  
Ser Leu Thr Thr Asn Leu Leu Pro Ala Met Gln Gly Val His Ser Ala  
130 135 140  
Leu Ile Thr Ala Gly Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

caagtgatca aacaaaaaav gaccaagtct ttttggtwtt tcagatcgag aaaaaatgtg 60  
gttgcaagggt ttgaagtaat ctgcaatgg attctttgac tggatttaga atgggaaccca 120  
aatggcaaat tgatctctcag ctctctcttgg ttggtccaaa gattgggtgaa ggaagctcatg 180  
ctaaagtcta tgagggaataa tacaagaatc agacagttgc tataaagata gttcacagag 240  
gagaacaccc agaagagatt gctaaaaagag attcaagatt ccttagagaa gtagaaatgc 300  
tctcacgtgt tcaacacaag aatttgggtca agttcatggg tgcttgcaag gagcctgtaa 360  
tggtgatagt tacagaactt ctcaaggcgg gtacattggc taaatattcta ttaaaacttga 420  
gccgcgcatg ttggagactt cgtgtgggcta tcggttttgc gcttgatatt gctcgttgta 480  
tggaaatgctt gcaatccatc gggatcattc accgtgatct caaacccgag aacttgccttt 540  
taactgcaga ccataaaaaca gtaaaactag cagattttgg attagccaaga gaagagtcac 600  
tgactggagt gatgacggct gagacaggaa cataccgatg gatggcacct gagttgtaca 660  
gcacgggt

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

Met Asp Ser Leu Thr Gly Phe Arg Met Glu Pro Lys Trp Gln Ile Asp  
1 5 10 15  
Pro Gln Leu Leu Phe Val Gly Pro Lys Ile Gly Glu Gly Ala His Ala  
20 25 30  
Lys Val Tyr Glu Gly Lys Tyr Lys Asn Gln Thr Val Ala Ile Lys Ile  
35 40 45  
Val His Arg Gly Glu Thr Pro Glu Glu Ile Ala Lys Arg Asp Ser Arg  
50 55 60  
Phe Leu Arg Glu Val Glu Met Leu Ser Arg Val Gln His Lys Asn Leu  
65 70 75 80  
Val Lys Phe Ile Gly Ala Cys Lys Glu Pro Val Met Val Ile Val Thr  
85 90 95  
Glu Leu Leu Gln Gly Gly Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg  
100 105 110  
Pro Ala Cys Leu Glu Thr Arg Val Ala Ile Gly Phe Ala Leu Asp Ile  
115 120 125  
Ala Arg Gly Met Glu Cys Leu His Ser His Gly Ile Ile His Arg Asp  
130 135 140

Leu Lys Pro Glu Asn Leu Leu Leu Thr Ala Asp His Lys Thr Val Lys  
145 150 155 160  
Leu Ala Asp Phe Gly Leu Ala Arg Glu Glu Ser Leu Thr Glu Met Met  
165 170 175  
Thr Ala Glu Thr Gly Thr Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser  
180 185 190  
Thr

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1500822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Glu Pro Lys Trp Gln Ile Asp Pro Gln Leu Leu Phe Val Gly Pro  
1 5 10 15  
Lys Ile Gly Glu Gly Ala His Ala Lys Val Tyr Glu Gly Lys Tyr Lys  
20 25 30  
Asn Gln Thr Val Ala Ile Lys Ile Val His Arg Gly Glu Thr Pro Glu  
35 40 45  
Glu Ile Ala Lys Arg Asp Ser Arg Phe Leu Arg Glu Val Glu Met Leu  
50 55 60  
Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala Cys Lys  
65 70 75 80  
Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly Thr Leu  
85 90 95  
Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr Arg Val  
100 105 110  
Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys Leu His  
115 120 125  
Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu  
130 135 140  
Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu Ala Arg  
145 150 155 160  
Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr Tyr Arg  
165 170 175  
Trp Met Ala Pro Glu Leu Tyr Ser Thr  
180 185

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Leu Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala  
1 5 10 15  
Cys Lys Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly  
20 25 30  
Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr

|                                                                 |                     |     |
|-----------------------------------------------------------------|---------------------|-----|
| 35                                                              | 40                  | 45  |
| Arg Val Ala Ile Gly Phe Ala Leu Asp Ile Ala                     | Arg Gly Met Glu Cys |     |
| 50                                                              | 55                  | 60  |
| Leu His Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu |                     |     |
| 65                                                              | 70                  | 75  |
| Leu Leu Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu |                     | 80  |
|                                                                 | 85                  | 90  |
| Ala Arg Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr |                     | 95  |
|                                                                 | 100                 | 105 |
| Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser Thr                     |                     | 110 |
|                                                                 | 115                 | 120 |

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1887
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| cacacattct  | tcgagaaggt  | ttagaataca  | caaagcataa  | ctcacctacc  | cctaaaccaa  | 60   |
| ctccaaatttc | tctctccctc  | tattaaatct  | tctctcaatca | ctttctcttg  | agtccttttg  | 120  |
| cttggaatcc  | tgatcatggc  | gtctctctct  | acttcccaat  | ccattctctcg | gatgacccaa  | 180  |
| accgcctctc  | tcttcttttc  | tatccgtcgg  | agctccgtcg  | ctctctctct  | ccgcgcgttc  | 240  |
| agatatctct  | ccattccaaa  | accaggaaga  | acttccggca  | gtcgtgggga  | gttaagaaga  | 300  |
| gtgatctgat  | gctaaaaggt  | tctgagattc  | gtcctgtgaa  | gggtgaggct  | tctgtttcca  | 360  |
| cggcggagaa  | agcttcggag  | attgtgcttc  | aacctcattg  | agaaatctcg  | ggcttcatta  | 420  |
| agcttctcgg  | ctccaaagct  | ctctctaatt  | gaattctgct  | tctcgtctgt  | ctatctgagg  | 480  |
| gaactactgt  | agtggacaac  | ttgttgaaca  | gtgatgacat  | caattacatg  | cttgatgcgt  | 540  |
| tgaagataat  | gggacttaat  | gtggaaaact  | acagtgaaaa  | caatcgtgct  | gtagtttgaag | 600  |
| gatgtggcgg  | ggtatttcca  | gtctccattg  | attccaagag  | tgatactgaa  | ctttacctcg  | 660  |
| gcaatgcagg  | aacagcaaat  | cgctccactta | ccgccgcagt  | tactgctgca  | gggtgcaacg  | 720  |
| caagttatgt  | ccttgatggg  | gtgcctcaga  | tgagagagag  | acctataggg  | gatttgggtg  | 780  |
| ttggtcttaa  | gcagcttggt  | gtgatgtttg  | aatgtactct  | tggcactaac  | tgccctcctg  | 840  |
| tctgtgtcaa  | cgctaatggg  | ggccttccgt  | gtggaaaggt  | gaagctttct  | ggatctatta  | 900  |
| gtagtacgta  | cttgaccgct  | ctgctcatgg  | cagctccctt  | agctcttgga  | gacgtcgaaa  | 960  |
| ttgaaaattg  | cgataaattg  | atttctgttc  | cgatgttga   | aatgacattg  | aagttgatgg  | 1020 |
| aacgtttttg  | ggtaagtgtc  | gagcatagtg  | aaagctggga  | tcgtttcttt  | gttaagggtg  | 1080 |
| ggcaaaaata  | caagtcgcgg  | ggtaatgctt  | acgtagaagg  | tgatctctct  | attgtactgt  | 1140 |
| atttctctgc  | tggtgctgcc  | attaccggtg  | aaactgtcac  | tgttgaaggt  | tgtggaacga  | 1200 |
| ccagttttga  | gggagatgtg  | aaatttgccg  | aggttcttga  | gaaaatggga  | gttaaaagtt  | 1260 |
| acttgacaga  | gaacagatgtg | actgtgacag  | ggcgtcttag  | agatgctttt  | ggaatggagac | 1320 |
| ccttgcggcc  | tattgatgtc  | aaatgaacca  | aaatgcctga  | tgtagcaatg  | actcttgccc  | 1380 |
| tcgttgcctc  | ctttgcagat  | gggtcaaccca | ccattagaga  | tgtggctagc  | tggagagttaa | 1440 |
| aggagacaga  | aaggatgatt  | ggcattttga  | cagagcttag  | aaaactggga  | gctacagttg  | 1500 |
| aagaaggttc  | agattattgt  | gtgattactc  | cgccgaaaaa  | ggtgaaaccc  | gcagagattg  | 1560 |
| atacatatga  | tgatcataga  | atggcaatgg  | cattctctct  | tgacgctgtg  | gctgatgttc  | 1620 |
| caatcaccat  | caatgacccc  | gggtgcacca  | ggaaaaacct  | ccccgactac  | ttccaaagttc | 1680 |
| ttgaaagaat  | cacaaagcat  | taaaacaaaa  | aactctaaaa  | ctccactagt  | ttttctctct  | 1740 |
| gatccaagct  | tatctgtttc  | catttttctt  | gtctctgtaa  | cattattaga  | aagcaagagt  | 1800 |
| agtgttttgt  | ttgtgtgacc  | tgaactgagt  | gagatttgag  | atgcaatcat  | tgaatcggct  | 1860 |
| ttggtatata  | attttactct  | gtttttcc    |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1500829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Gly | Ser | Glu | Ile | Arg | Pro | Val | Lys | Val | Arg | Ala | Ser | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Ala | Glu | Lys | Ala | Ser | Glu | Ile | Val | Leu | Gln | Pro | Ile | Arg | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Gly | Leu | Ile | Lys | Leu | Pro | Gly | Ser | Lys | Ser | Leu | Ser | Asn | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Leu | Leu | Leu | Ala | Ala | Leu | Ser | Glu | Gly | Thr | Thr | Val | Val | Asp | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Leu | Asn | Ser | Asp | Asp | Ile | Asn | Tyr | Met | Leu | Asp | Ala | Leu | Lys | Ile |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Gly | Leu | Asn | Val | Glu | Thr | His | Ser | Glu | Asn | Asn | Arg | Ala | Val | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Gly | Cys | Gly | Gly | Val | Phe | Pro | Ala | Ser | Ile | Asp | Ser | Lys | Ser | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Glu | Leu | Tyr | Leu | Gly | Asn | Ala | Gly | Thr | Ala | Met | Arg | Pro | Leu | Thr |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Ala | Ala | Val | Thr | Ala | Ala | Gly | Gly | Asn | Ala | Ser | Tyr | Val | Val | Leu | Asp |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Val | Pro | Gln | Met | Arg | Glu | Arg | Pro | Ile | Gly | Asp | Leu | Val | Val | Gly | Leu |
|     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |
| Lys | Gln | Leu | Gly | Ala | Asp | Val | Glu | Cys | Thr | Leu | Gly | Thr | Asn | Cys | Pro |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Pro | Val | Arg | Val | Asn | Ala | Asn | Gly | Gly | Leu | Pro | Gly | Gly | Lys | Val | Lys |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Leu | Ser | Gly | Ser | Ile | Ser | Ser | Gln | Tyr | Leu | Thr | Ala | Leu | Leu | Met | Ala |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ala | Pro | Leu | Ala | Leu | Gly | Asp | Val | Glu | Ile | Glu | Ile | Val | Asp | Lys | Leu |
|     |     | 210 |     |     | 215 |     |     |     |     |     |     | 220 |     |     |     |
| Ile | Ser | Val | Pro | Tyr | Val | Glu | Met | Thr | Leu | Lys | Leu | Met | Glu | Arg | Phe |
|     |     | 225 |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Val | Ser | Ala | Glu | His | Ser | Glu | Ser | Trp | Asp | Arg | Phe | Phe | Val | Lys |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Gly | Gln | Lys | Tyr | Lys | Ser | Pro | Gly | Asn | Ala | Tyr | Val | Glu | Gly | Asp |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Ser | Ser | Ala | Ser | Tyr | Phe | Leu | Ala | Gly | Ala | Ala | Ile | Thr | Gly | Glu |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Thr | Val | Thr | Val | Glu | Gly | Cys | Gly | Thr | Thr | Ser | Leu | Gln | Gly | Asp | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Phe | Ala | Glu | Val | Leu | Glu | Lys | Met | Gly | Cys | Lys | Val | Ser | Trp | Thr |
|     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Asn | Ser | Val | Thr | Val | Thr | Gly | Pro | Ser | Arg | Asp | Ala | Phe | Gly | Met |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Arg | His | Leu | Arg | Ala | Ile | Asp | Val | Asn | Met | Asn | Lys | Met | Pro | Asp | Val |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ala | Met | Thr | Leu | Ala | Val | Val | Ala | Leu | Phe | Ala | Asp | Gly | Pro | Thr | Thr |
|     |     | 355 |     |     |     |     |     | 360 |     |     |     | 365 |     |     |     |
| Ile | Arg | Asp | Val | Ala | Ser | Trp | Arg | Val | Lys | Glu | Thr | Glu | Arg | Met | Ile |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Ile | Cys | Thr | Glu | Leu | Arg | Lys | Leu | Gly | Ala | Thr | Val | Glu | Glu | Gly |
|     |     | 385 |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Ser | Asp | Tyr | Cys | Val | Ile | Thr | Pro | Pro | Lys | Lys | Val | Lys | Pro | Ala | Glu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     | 415 |     |     |
| Ile | Asp | Thr | Tyr | Asp | Asp | His | Arg | Met | Ala | Met | Ala | Phe | Ser | Leu | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ala | Cys | Ala | Asp | Val | Pro | Ile | Thr | Ile | Asn | Asp | Pro | Gly | Cys | Thr | Arg |

(2) INFORMATION FOR SEQ ID NO:1659:

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..391
      (D) OTHER INFORMATION: / Ceres Seq. ID 1500830
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

|          |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1 | Leu<br>Glu | Asp<br>Asn | Ala<br>Asn | Leu<br>Arg | Lys<br>Ala | Ile<br>Val | Leu<br>Val | Gly<br>Glu | Leu<br>Gly | Asn<br>Cys | Val<br>Gly | Glu<br>Val | Thr<br>Phe | His<br>Pro | Ser<br>Ala |
|          |            |            |            | 5          |            |            |            | 25         |            | 10         |            |            | 30         |            |            |
| Ser      | Ile        | Asp        | Ser        | Lys        | Ser        | Asp        | Ile        | Glu        | Leu        | Tyr        | Leu        | Gly        | Asn        | Ala        | Gly        |
| Thr      | Ala        | Met        | Arg        | Pro        | Leu        | Thr        | Ala        | Ala        | Val        | Thr        | Ala        | Ala        | Gly        | Gly        | Asn        |
| Ala      | Ser        | Tyr        | Val        | Leu        | Asp        | Gly        | Val        | Pro        | Gln        | Met        | Arg        | Glu        | Arg        | Pro        | Ile        |
| 65       |            |            |            |            | 70         |            |            |            |            | 75         |            |            |            |            | 80         |
| Gly      | Asp        | Leu        | Val        | Val        | Gly        | Leu        | Lys        | Gln        | Leu        | Gly        | Ala        | Asp        | Val        | Glu        | Cys        |
|          |            |            |            | 85         |            |            |            |            | 90         |            |            |            |            | 95         |            |
| Thr      | Leu        | Gly        | Thr        | Asn        | Cys        | Pro        | Pro        | Val        | Arg        | Val        | Asn        | Ala        | Asn        | Gly        | Gly        |
|          |            |            |            | 100        |            |            |            | 105        |            |            |            |            | 110        |            |            |
| Leu      | Pro        | Gly        | Gly        | Lys        | Val        | Lys        | Leu        | Ser        | Gly        | Ser        | Ile        | Ser        | Ser        | Gln        | Tyr        |
|          |            |            |            | 115        |            |            | 120        |            |            |            |            | 125        |            |            |            |
| Leu      | Thr        | Ala        | Leu        | Leu        | Met        | Ala        | Ala        | Pro        | Leu        | Ala        | Leu        | Gly        | Asp        | Val        | Glu        |
|          |            |            |            | 130        |            | 135        |            |            |            |            | 140        |            |            |            |            |
| Ile      | Glu        | Ile        | Val        | Asp        | Lys        | Leu        | Ile        | Ser        | Val        | Pro        | Tyr        | Val        | Glu        | Met        | Thr        |
| 145      |            |            |            |            | 150        |            |            |            |            | 155        |            |            |            |            | 160        |
| Leu      | Lys        | Leu        | Met        | Glu        | Arg        | Phe        | Gly        | Val        | Ser        | Ala        | Glu        | His        | Ser        | Glu        | Ser        |
|          |            |            |            | 165        |            |            |            | 170        |            |            |            |            |            | 175        |            |
| Trp      | Asp        | Arg        | Phe        | Val        | Lys        | Gly        | Gly        | Gln        | Lys        | Tyr        | Lys        | Ser        | Pro        | Gly        |            |
|          |            |            |            | 180        |            |            | 185        |            |            |            |            |            | 190        |            |            |
| Asn      | Ala        | Tyr        | Val        | Glu        | Gly        | Asp        | Ala        | Ser        | Ser        | Ala        | Ser        | Tyr        | Phe        | Leu        | Ala        |
|          |            |            |            | 195        |            |            | 200        |            |            |            |            | 205        |            |            |            |
| Gly      | Ala        | Ala        | Ile        | Thr        | Gly        | Glu        | Thr        | Val        | Thr        | Val        | Glu        | Gly        | Cys        | Gly        | Thr        |
|          |            |            |            | 210        |            | 215        |            |            |            |            | 220        |            |            |            |            |
| Thr      | Ser        | Leu        | Gln        | Gly        | Asp        | Val        | Lys        | Phe        | Ala        | Glu        | Val        | Leu        | Glu        | Lys        | Met        |
| 225      |            |            |            |            | 230        |            |            |            |            | 235        |            |            |            |            | 240        |
| Gly      | Cys        | Lys        | Val        | Ser        | Trp        | Thr        | Glu        | Asn        | Ser        | Val        | Thr        | Val        | Thr        | Gly        | Pro        |
|          |            |            |            | 245        |            |            |            |            | 250        |            |            |            |            | 255        |            |
| Ser      | Arg        | Asp        | Ala        | Phe        | Gly        | Met        | Arg        | His        | Leu        | Arg        | Ala        | Ile        | Asp        | Val        | Asn        |
|          |            |            |            | 260        |            |            |            | 265        |            |            |            |            | 270        |            |            |
| Met      | Asn        | Lys        | Met        | Pro        | Asp        | Val        | Ala        | Met        | Thr        | Leu        | Ala        | Val        | Val        | Ala        | Leu        |
|          |            |            |            | 275        |            |            | 280        |            |            |            |            | 285        |            |            |            |
| Phe      | Ala        | Asp        | Gly        | Pro        | Thr        | Ile        | Arg        | Asp        | Val        | Ala        | Ser        | Trp        | Arg        | Val        |            |
|          |            |            |            | 290        |            | 295        |            |            |            | 300        |            |            |            |            |            |
| Lys      | Glu        | Thr        | Glu        | Arg        | Met        | Ile        | Ala        | Ile        | Cys        | Thr        | Glu        | Leu        | Arg        | Lys        | Leu        |
| 305      |            |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            | 320        |
| Gly      | Ala        | Thr        | Val        | Glu        | Glu        | Gly        | Ser        | Asp        | Tyr        | Cys        | Val        | Ile        | Thr        | Pro        | Pro        |
|          |            |            |            | 325        |            |            |            |            | 330        |            |            |            |            | 335        |            |
| Lys      | Lys        | Val        | Lys        | Pro        | Ala        | Glu        | Ile        | Asp        | Thr        | Tyr        | Asp        | Asp        | His        | Arg        | Met        |
|          |            |            |            | 340        |            |            |            | 345        |            |            |            |            | 350        |            |            |

Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile  
355 360 365  
Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val  
370 375 380  
Leu Glu Arg Ile Thr Lys His  
385 390

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser  
1 5 10 15  
Tyr Val Leu Asp Gly Val Pro Gln Met Arg Glu Arg Pro Ile Gly Asp  
20 25 30  
Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu  
35 40 45  
Gly Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro  
50 55 60  
Gly Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr  
65 70 75 80  
Ala Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu  
85 90 95  
Ile Val Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys  
100 105 110  
Leu Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Glu Ser Trp Asp  
115 120 125  
Arg Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala  
130 135 140  
Tyr Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala  
145 150 155 160  
Ala Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser  
165 170 175  
Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys  
180 185 190  
Lys Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg  
195 200 205  
Asp Ala Phe Gly Met Arg His Leu Arg Ala Ile Asp Val Asn Met Asn  
210 215 220  
Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala  
225 230 235 240  
Asp Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu  
245 250 255  
Thr Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala  
260 265 270  
Thr Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Lys Lys  
275 280 285  
Val Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met  
290 295 300  
Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile Asn Asp  
305 310 315 320  
Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu  
325 330 335  
Arg Ile Thr Lys His

340

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

```
aacgaggctg tggagaaaaa aaccaaagg t gactgttgtt agagatgagg aatgcagagc 60
tcacatctcat cccaacacca acgtgttggtc atcttgttcc gttctctgaa ttgtctaggc 120
gtctcattga gcaggatgat aaaaatccgta tcaccttcc tcttgatgaag caacaaggctc 180
agtctcactt ggattcctat gtaagacaaa ttctctcgtc tctgccgttt gttagattta 240
ttgatgtccc tggatttaga gagaacacaa cacttggtag acagtctgtg gaagcctatg 300
gtgtacgatt ttattgaaac aaatgtccctt ctgtgcaaaa atataatcat gggatcctta 360
tcttctcctg cattttgatgg agttacgggtc aagggtattg ttgtgtattt ttctgtcttc 420
ccgatgattg attgttcaaa agatgcaagt ctctcttttt atgtgttctt gactctaaat 480
tcgggatccc tagctatgat gcagtatctg gcataatggac ataagaaaaga taccctagtt 540
ttgcaagaaa accctgaaga aatgtgtgta atctctggat ttgtaaaccc tgtcccgacc 600
aaagtacgtc cgctacgtct gttatttaga gatggttatg atgtcagct taaactggct 660
atatgtgtta caaaggctaa ttgaatccta gtgaatacct cctttgatat tgagcctacc 720
tctctgaatc attttcttga agaagagaaat taccctctctg tttatgctgt tggccccata 780
tttaaccgga agggccatccc tcatccagat caagaactcg cctgtgtgtg cgagctcgatg 840
aaaatgcttg atgtctcaacc cgaggcatca ttgttatccc ttgtttttgg gagtatgggt 900
agcttaagag gtctcttagt gaaggaaata gcacatggag ttgagctatg tcagtataga 960
tctctctggg cactccgcac agaagaagtg acaaatgatg atcttttggc agadggatgc 1020
atgggacgtg tcagtggagc gggaaatgata tgcggttggt ctctcaggt ggaataactg 1080
gcccataaag cagtgggagg tttgttttct cattgtggat ggaactcaat agtagagagt 1140
ttatggtttg gtgtgccaat tgtgacatgg cccaatgtat gcagagcaac agctcaatgc 1200
gtttctgatg gtgaaggaaac tgaagctcgc agtggagctg aaactcgatt atagtgtaca 1260
tagtggtgag attgtaaagt caaacgagat agagacagcg atttcttgtg taatgaacaa 1320
gataataat gttgtgagga acagagtatg ggatatctcg cagatgatcc agagagctac 1380
gaagaatggt ggaatctcgt ttgccgcaat tgagaaatcc atacatgacg tgataggaac 1440
caggacttag cctttcttat cggattctcc ataaactgta acctgattat gcaacagctcc 1500
tttgaatctg ctttgtttct aatatttttt tctattcttt tgtcatcagc ttgtccttta 1560
actttgtctg tgttgattcc ttatctacc aagctgtgag ttctttttgt agccaatgct 1620
gcatttcttc tgttatggat ttgttcaaaa attgggtaca tctcttattc ttt
```

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

```
Met Val Tyr Asp Phe Ile Glu Thr Asn Val Pro Leu Val Gln Asn Ile
1 5 10 15
Ile Met Gly Ile Leu Ser Ser Pro Ala Phe Asp Gly Val Thr Val Lys
20 25 30
Gly Phe Val Ala Asp Phe Phe Cys Leu Pro Met Ile Asp Val Ala Lys
35 40 45
Asp Ala Ser Leu Pro Phe Tyr Val Phe Leu Thr Ser Asn Ser Gly Phe
50 55 60
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ala | Met | Met | Gln | Tyr | Leu | Ala | Tyr | Gly | His | Lys | Lys | Asp | Thr | Ser |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Val | Phe | Ala | Arg | Asn | Ser | Glu | Glu | Met | Leu | Ser | Ile | Pro | Gly | Phe | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Asn | Pro | Val | Pro | Ala | Lys | Val | Leu | Pro | Ser | Ala | Leu | Phe | Ile | Glu | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Gly | Tyr | Asp | Ala | Asp | Val | Lys | Leu | Ala | Ile | Leu | Phe | Thr | Lys | Ala | Asn |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Gly | Ile | Leu | Val | Asn | Thr | Ser | Phe | Asp | Ile | Glu | Pro | Thr | Ser | Leu | Asn |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| His | Phe | Leu | Glu | Glu | Glu | Asn | Tyr | Pro | Ser | Val | Tyr | Ala | Val | Gly | Pro |  |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Ile | Phe | Asn | Pro | Lys | Ala | His | Pro | His | Pro | Asp | Gln | Asp | Leu | Ala | Cys |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Cys | Asp | Glu | Ser | Met | Lys | Trp | Leu | Asp | Ala | Gln | Pro | Gly | Ala | Ser | Val |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Phe | Leu | Cys | Phe | Gly | Ser | Met | Gly | Ser | Leu | Arg | Gly | Pro | Leu | Val |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Lys | Glu | Ile | Ala | His | Gly | Leu | Glu | Leu | Cys | Gln | Tyr | Arg | Phe | Leu | Trp |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |
| Ser | Leu | Arg | Thr | Glu | Glu | Val | Thr | Asn | Asp | Asp | Leu | Leu | Pro | Xaa | Gly |  |
|     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |  |
| Phe | Met | Asp | Arg | Val | Ser | Gly | Arg | Gly | Met | Ile | Cys | Gly | Trp | Ser | Pro |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |  |
| Gln | Val | Glu | Ile | Leu | Ala | His | Lys | Ala | Val | Gly | Gly | Phe | Val | Ser | His |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |  |
| Cys | Gly | Trp | Asn | Ser | Ile | Val | Glu | Ser | Leu | Trp | Phe | Gly | Val | Pro | Ile |  |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |  |
| Val | Thr | Trp | Pro | Asn | Val | Cys | Arg | Ala | Thr | Ala | Gln | Cys | Val | Ser | Asp |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Gly | Glu | Gly | Thr | Glu | Ala | Arg | Ser | Gly | Ala | Glu | Thr | Arg | Leu |     |     |  |
|     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1500834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Ile | Leu | Ser | Ser | Pro | Ala | Phe | Asp | Gly | Val | Thr | Val | Lys | Gly |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Val | Ala | Asp | Phe | Phe | Cys | Leu | Pro | Met | Ile | Asp | Val | Ala | Lys | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ser | Leu | Pro | Phe | Tyr | Val | Phe | Leu | Thr | Ser | Asn | Ser | Gly | Phe | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ala | Met | Met | Gln | Tyr | Leu | Ala | Tyr | Gly | His | Lys | Lys | Asp | Thr | Ser | Val |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Ala | Arg | Asn | Ser | Glu | Glu | Met | Leu | Ser | Ile | Pro | Gly | Phe | Val | Asn |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Pro | Val | Pro | Ala | Lys | Val | Leu | Pro | Ser | Ala | Leu | Phe | Ile | Glu | Asp | Gly |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Asp | Ala | Asp | Val | Lys | Leu | Ala | Ile | Leu | Phe | Thr | Lys | Ala | Asn | Gly |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Leu | Val | Asn | Thr | Ser | Phe | Asp | Ile | Glu | Pro | Thr | Ser | Leu | Asn | His |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Phe | Leu | Glu | Glu | Glu | Asn | Tyr | Pro | Ser | Val | Tyr | Ala | Val | Gly | Pro | Ile |  |

|                                                                 |                                         |     |
|-----------------------------------------------------------------|-----------------------------------------|-----|
| 130                                                             | 135                                     | 140 |
| Phe Asn Pro Lys Ala His                                         | Pro His Pro Asp Gln Asp Leu Ala Cys Cys |     |
| 145                                                             | 150                                     | 155 |
| Asp Glu Ser Met Lys Trp                                         | Leu Asp Ala Gln Pro Glu Ala Ser Val Val | 160 |
|                                                                 | 165                                     | 170 |
| Phe Leu Cys Phe Gly Ser Met Gly Ser Leu Arg Gly Pro Leu Val Lys |                                         | 175 |
|                                                                 | 180                                     | 185 |
| Glu Ile Ala His Gly Leu Glu Leu Cys Gln Tyr Arg Phe Leu Trp Ser |                                         | 190 |
|                                                                 | 195                                     | 200 |
| Leu Arg Thr Glu Glu Val Thr Asn Asp Asp Leu Leu Pro Xaa Gly Phe |                                         | 205 |
|                                                                 | 210                                     | 215 |
| Met Asp Arg Val Ser Gly Arg Gly Met Ile Cys Gly Trp Ser Pro Gln |                                         | 220 |
|                                                                 | 225                                     | 230 |
| Val Glu Ile Leu Ala His Lys Ala Val Gly Gly Phe Val Ser His Cys |                                         | 235 |
|                                                                 | 240                                     | 245 |
| Gly Trp Asn Ser Ile Val Glu Ser Leu Trp Phe Gly Val Pro Ile Val |                                         | 250 |
|                                                                 | 255                                     | 260 |
| Thr Trp Pro Asn Val Cys Arg Ala Thr Ala Gln Cys Val Ser Asp Gly |                                         | 265 |
|                                                                 | 270                                     | 275 |
| Glu Gly Thr Glu Ala Arg Ser Gly Ala Glu Thr Arg Leu             |                                         | 280 |
|                                                                 | 285                                     | 290 |
|                                                                 | 295                                     | 300 |

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1500835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Ile Asp Val Ala Lys Asp Ala Ser Leu Pro Phe Tyr Val Phe Leu |     |
| 1                                                               | 5   |
| Thr Ser Asn Ser Gly Phe Leu Ala Met Met Gln Tyr Leu Ala Tyr Gly | 10  |
|                                                                 | 15  |
|                                                                 | 20  |
| His Lys Lys Asp Thr Ser Val Phe Ala Arg Asn Ser Glu Glu Met Leu | 25  |
|                                                                 | 30  |
|                                                                 | 35  |
| Ser Ile Pro Gly Phe Val Asn Pro Val Pro Ala Lys Val Leu Pro Ser | 40  |
|                                                                 | 45  |
|                                                                 | 50  |
| Ala Leu Phe Ile Glu Asp Gly Tyr Asp Ala Asp Val Lys Leu Ala Ile | 55  |
|                                                                 | 60  |
|                                                                 | 65  |
| Leu Phe Thr Lys Ala Asn Gly Ile Leu Val Asn Thr Ser Phe Asp Ile | 70  |
|                                                                 | 75  |
|                                                                 | 80  |
|                                                                 | 85  |
| Glu Pro Thr Ser Leu Asn His Phe Leu Glu Glu Asn Tyr Pro Ser     | 90  |
|                                                                 | 95  |
|                                                                 | 100 |
| Val Tyr Ala Val Gly Pro Ile Phe Asn Pro Lys Ala His Pro His Pro | 105 |
|                                                                 | 110 |
|                                                                 | 115 |
| Asp Gln Asp Leu Ala Cys Cys Asp Glu Ser Met Lys Trp Leu Asp Ala | 120 |
|                                                                 | 125 |
|                                                                 | 130 |
| Gln Pro Glu Ala Ser Val Val Phe Leu Cys Phe Gly Ser Met Gly Ser | 135 |
|                                                                 | 140 |
|                                                                 | 145 |
| Leu Arg Gly Pro Leu Val Lys Glu Ile Ala His Gly Leu Glu Leu Cys | 150 |
|                                                                 | 155 |
|                                                                 | 160 |
|                                                                 | 165 |
| Gln Tyr Arg Phe Leu Trp Ser Leu Arg Thr Glu Glu Val Thr Asn Asp | 170 |
|                                                                 | 175 |
|                                                                 | 180 |
| Asp Leu Leu Pro Xaa Gly Phe Met Asp Arg Val Ser Gly Arg Gly Met | 185 |
|                                                                 | 190 |
|                                                                 | 195 |
| Ile Cys Gly Trp Ser Pro Gln Val Glu Ile Leu Ala His Lys Ala Val | 200 |
|                                                                 | 205 |
|                                                                 | 210 |
|                                                                 | 215 |
|                                                                 | 220 |

Gly Gly Phe Val Ser His Cys Gly Trp Asn Ser Ile Val Glu Ser Leu  
225 230 235 240  
Trp Phe Gly Val Pro Ile Val Thr Trp Pro Asn Val Cys Arg Ala Thr  
245 250 255  
Ala Gln Cys Val Ser Asp Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala  
260 265 270  
Glu Thr Arg Leu  
275

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..566

(D) OTHER INFORMATION: / Ceres Seq. ID 1500836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| atacgaatt   | tagcacatag  | ccggagctcc  | gatactgtca | tcttgctccg | acgaagcgat | 60  |
| tcccgcccaa  | ccaatcgctc  | tgggtgtg    | tcaactttg  | ctagattact | tagtcacagt | 120 |
| ggcgctcttt  | ccaattcccg  | atcaaaaagt  | ccgaggcaca | agcttcaagg | tccaaggagt | 180 |
| tggttaacact | gggaatgctt  | taacatgtgt  | tgctcgtttg | ggtttgcctt | gtcgaatctt | 240 |
| ggctaagggt  | gctgatgatt  | ctcacggcgc  | atatatggta | gaagaactcg | aatctagcgg | 300 |
| tgtggatact  | tgtttttgta  | tgagtgtctaa | agatggagct | tcacatttta | attacgtcat | 360 |
| tgtagataac  | caaacgaata  | ctcgtacttg  | tatttacact | ccaggatatt | ctctttgtct | 420 |
| accagatgac  | cttactggaat | cttactctct  | agatgttctt | gatggagtaa | gagttctata | 480 |
| tgtaaatgga  | aggtcccggt  | aagccgaatt  | gcttcttgcc | caaaaggcac | atagcaagaa | 540 |
| atataaccaat | cttaattaat  | gcagag      |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..174

(D) OTHER INFORMATION: / Ceres Seq. ID 1500837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ser | Cys | Ser | Asp | Glu | Ala | Ile | Pro | Gly | Gln | Pro | Ile | Val | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Gly | Cys | Gly | Gln | Leu | Cys | Leu | Asp | Tyr | Leu | Val | Thr | Val | Ala | Ser | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Pro | Ile | Pro | Asp | Gln | Lys | Ile | Arg | Gly | Thr | Ser | Phe | Lys | Val | Gln | Gly |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Val | Gly | Asn | Thr | Gly | Asn | Ala | Leu | Thr | Cys | Val | Ala | Arg | Leu | Gly | Leu |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Cys | Arg | Ile | Leu | Ala | Lys | Val | Ala | Asp | Asp | Ser | His | Gly | Arg | Tyr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Met | Val | Glu | Glu | Leu | Glu | Ser | Ser | Gly | Val | Asp | Thr | Ser | Phe | Cys | Met |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Ala | Lys | Asp | Gly | Ala | Ser | His | Phe | Asn | Tyr | Val | Ile | Val | Asp | Asn |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Gln | Thr | Asn | Thr | Arg | Thr | Cys | Ile | Tyr | Thr | Pro | Gly | Tyr | Pro | Pro | Leu |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Pro | Asp | Asp | Leu | Thr | Glu | Ser | Leu | Leu | Leu | Asp | Val | Leu | Asp | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | Arg | Val | Leu | Tyr | Val | Asn | Gly | Arg | Ser | Arg | Glu | Ala | Glu | Leu | Leu |  |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Asn | Lys | Lys | Leu | Ile | Gln | Gln | Asp | Pro | Ala | Met | Ser | Ser | Thr | Ala |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Asn | Ile | Ser | Gly | Ser | Gly | Asn | Arg | Lys | Ser | Ser | Arg | Leu | Gln | Arg |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Arg | Ala | Pro | Pro | Pro | Leu | Lys | Ile | Asn | Pro | Cys | Glu | Arg | Xaa | Trp | Lys |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Val | Ala | Ile | Pro | Leu | Leu | Ser | Pro | Thr | Glu | Ser | Pro | Pro | Gln | Lys | Pro |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Ala | Val | Met | Lys | Arg | Glu | Glu | Gln | Arg | Trp | Gly | Lys | Glu | Ala | Glu |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Lys | Pro | Pro | Xaa | Phe | Lys | Lys | Trp | Gln | His | Pro | Ala | Ala | Pro | Phe | Tyr |  |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Gln | Pro | Ala | Pro | Ser | Ser | Asn | Gln | Pro | Phe | Ala | Trp | Pro | Asn |     |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Ser | Thr | Ala | Arg | Asn | Ile | Ser | Gly | Ser | Gly | Asn | Arg | Lys | Ser |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |
| Ser | Arg | Leu | Gln | Arg | Arg | Ala | Pro | Pro | Pro | Leu | Lys | Ile | Asn | Pro | Cys |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Glu | Arg | Xaa | Trp | Lys | Val | Ala | Ile | Pro | Leu | Leu | Ser | Pro | Thr | Glu | Ser |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Pro | Pro | Gln | Lys | Pro | Pro | Ala | Val | Met | Lys | Arg | Glu | Glu | Gln | Arg | Trp |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Lys | Glu | Ala | Glu | Lys | Pro | Pro | Xaa | Phe | Lys | Lys | Trp | Gln | His | Pro |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |  |
| Ala | Ala | Pro | Phe | Tyr | Gln | Pro | Ala | Pro | Ser | Ser | Asn | Gln | Pro | Phe |     |  |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |

Ala Trp Pro Asn  
100

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| gcataatcag  | ctgtcaggtc  | agattccccg  | agatcttggt  | gagctctcct  | ttctgtcaac  | 60  |
| catgaacttc  | gccacaaca   | atctcgaagg  | tccaatgcc   | cgcggaacac  | aatttcaaa   | 120 |
| ccaaaactgt  | tcttcattca  | tggacaaacc  | caagctttac  | ggctctgatg  | atatctcgag  | 180 |
| aaaaactcat  | gtcccaaatc  | ctagaccaca  | agaattagag  | aaagtatcac  | agccgggaaga | 240 |
| agagcaagtg  | attaaactgga | catcagcagc  | aatagcgtat  | ggacctgggtg | tgttttgcgg  | 300 |
| attagtgtat  | ggacatatct  | tcatcttcga  | taagcaggag  | tggttaatag  | aaaagtcttcg | 360 |
| tagaacaacg  | ccagaggttg  | tcatcagaag  | cgctcgttga  | acacgtgcat  | atgtatgtgt  | 420 |
| ttgtgaaaaa  | ctcttttcgt  | tgcggttgtaa | tggttctaata | tatggttttg  | taataaaacgt | 480 |
| cttttggtggc | ggtacgtatt  | tgatacatat  | tggttttg    |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Asn | Gln | Leu | Ser | Gly | Gln | Ile | Pro | Arg | Asp | Leu | Gly | Glu | Leu | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Leu | Ser | Thr | Met | Asn | Phe | Ala | His | Asn | Asn | Leu | Glu | Gly | Pro | Met |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Arg | Gly | Thr | Gln | Phe | Gln | Ser | Gln | Asn | Cys | Ser | Ser | Phe | Met | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Lys | Leu | Tyr | Gly | Leu | Asp | Asp | Ile | Cys | Arg | Lys | Thr | His | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Asn | Pro | Arg | Pro | Gln | Glu | Leu | Glu | Lys | Val | Ser | Glu | Pro | Glu | Glu |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Gln | Val | Ile | Asn | Trp | Thr | Ser | Ala | Ala | Ile | Ala | Tyr | Gly | Pro | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Phe | Cys | Gly | Leu | Val | Ile | Gly | His | Ile | Phe | Ile | Ser | His | Lys | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Trp | Leu | Met | Glu | Lys | Phe | Arg | Arg | Asn | Lys | Pro | Arg | Val | Val | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Arg | Ser | Ala | Arg |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Phe | Ala | His | Asn | Asn | Leu | Glu | Gly | Pro | Met | Pro | Arg | Gly | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Phe | Gln | Ser | Gln | Asn | Cys | Ser | Ser | Phe | Met | Asp | Asn | Pro | Lys | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Gly | Leu | Asp | Asp | Ile | Cys | Arg | Lys | Thr | His | Val | Pro | Asn | Pro | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Gln | Glu | Leu | Glu | Lys | Val | Ser | Glu | Pro | Glu | Glu | Glu | Gln | Val | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Trp | Thr | Ser | Ala | Ala | Ile | Ala | Tyr | Gly | Pro | Gly | Val | Phe | Cys | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Val | Ile | Gly | His | Ile | Phe | Ile | Ser | His | Lys | Gln | Glu | Trp | Leu | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Lys | Phe | Arg | Arg | Asn | Lys | Pro | Arg | Val | Val | Ile | Arg | Ser | Ala | Arg |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..101  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500857  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:  
Met Pro Arg Gly Thr Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met  
1 5 10 15  
Asp Asn Pro Lys Leu Tyr Gly Leu Asp Asp Ile Cys Arg Lys Thr His  
20 25 30  
Val Pro Asn Pro Arg Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu  
35 40 45  
Glu Glu Gln Val Ile Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro  
50 55 60  
Gly Val Phe Cys Gly Leu Val Ile Gly His Ile Phe Ile Ser His Lys  
65 70 75 80  
Gln Glu Trp Leu Met Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val  
85 90 95  
Ile Arg Ser Ala Arg  
100

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 615 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..615  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500862  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:  
gataaatattt cattttcrtc gtttctttct ttctaagttt cgaatgtcagt tcctaatactc 60  
tatggcggttc atgatagcca aatggtaact ttggtagcct aatgtatgtc acgtaaaatta 120  
tccacgtggc actcaactttt ttgcactcttt ctcaaaatat atcaaaaggag acttcataaa 180  
gaaagaatct ttagtgtgga gagactaaaa ggacaccaca agcttatttc ataagaaact 240  
tcaaattaga atcagaaaaca agagcatcct tcttcattta cacaggtaaa ttagggtgtaa 300  
aaatggtgat gagaagtgtg gatctacgat cagataccgt tactagaccg acagatgcga 360  
tgcgagaagc aatgtgtaac gcagagggtg atgatgacgt cctcggtatat gacccaacgg 420  
ctagacgtct tgaagaggag atggctaaga tgatggggaa agaggctgct ctgttcgtgc 480  
catccgggac aatgggggaat ctgatcagcg tgatggttca ctgcgacggt agaggcagcg 540  
aggtgattct tggcgacaat tgtcacatcc atgtttacga gaatggaggg atatcgacta 600  
tcgggggagt gcatc

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500863  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:  
Met Val Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro  
1 5 10 15  
Thr Asp Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp

20 25 30  
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala  
35 40 45  
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met  
50 55 60  
Gly Asn Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu  
65 70 75 80  
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly  
85 90 95  
Ile Ser Thr Ile Gly Gly Val His

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1500864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro Thr Asp  
1 5 10 15  
Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Val Leu  
20 25 30  
Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala Lys Met  
35 40 45  
Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn  
50 55 60  
Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile  
65 70 75 80  
Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser  
85 90 95  
Thr Ile Gly Gly Val His  
100

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1500865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Val Leu Gly  
1 5 10 15  
Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala Lys Met Met  
20 25 30  
Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn Leu  
35 40 45  
Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile Leu  
50 55 60  
Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser Thr  
65 70 75 80  
Ile Gly Gly Val His  
85

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

```
attttttagg ttgttcagc tgttttacgg agtcgctttt gagatatcga tcttacgaag      60
aagcaaaaaa ggcgggtccc ttgcttacca agaaggtgtt gaagaagagg tctactaagt      120
tcatacagacc ccagagtgcac cgtagaatca ccgtcaagga aagctggagg aggccaaaagg      180
gtattgtattc aaggatgaga aaaaagtcca aaggtgtgac ttgatgcccc aatgttggtt      240
acggatcttca caagaagact cgtcactatc ttcccaatgg attcaagaaa ttcgttgttc      300
acaacacaaag tgagctcgag ttgttgatga tgcacaacag gacttactgt gctgagattg      360
ctcacaacgt ctccactaag aagagaaaag caattgttga gagagcttct cagctagacg      420
ttgttggttac caacagcgctt gctaggtccc gttagcacaaga agacgagtga agaagaattc      480
tgccgactac ttagtgtgtt ctctgtgttt gttgcatttc cttttgttta taagacgatt      540
tttgattact gctgtgtgtt tgtttggagt gaacaaacat gagttttggt tttagtatga      600
aacagatcaa gttaaagacc ttgttaaag ctatttcgga ttc
```

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

```
Phe Leu Gly Leu Phe Ser Cys Phe Thr Glu Ser Leu Leu Arg Tyr Arg
1      5      10      15
Ser Tyr Glu Glu Ala Lys Met Ala Val Pro Leu Leu Thr Lys Lys Val
20      25      30
Val Lys Lys Arg Ser Thr Lys Phe Ile Arg Pro Gln Ser Asp Arg Arg
35      40      45
Ile Thr Val Lys Glu Ser Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg
50      55      60
Met Arg Arg Lys Phe Lys Gly Val Thr Leu Met Pro Asn Val Gly Tyr
65      70      75      80
Gly Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Gly Phe Lys Lys
85      90      95
Phe Val Val His Asn Thr Ser Glu Leu Glu Leu Leu Met Met His Asn
100      105      110
Arg Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Lys Lys Arg
115      120      125
Lys Ala Ile Val Glu Arg Ala Ser Gln Leu Asp Val Val Val Thr Asn
130      135      140
Arg Leu Ala Arg Leu Arg Ser Gln Glu Asp Glu
145      150      155
```

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Val | Pro | Leu | Leu | Thr | Lys | Lys | Val | Val | Lys | Lys | Arg | Ser | Thr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Phe | Ile | Arg | Pro | Gln | Ser | Asp | Arg | Arg | Ile | Thr | Val | Lys | Glu | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Trp | Arg | Arg | Pro | Lys | Gly | Ile | Asp | Ser | Arg | Met | Arg | Arg | Lys | Phe | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Val | Thr | Leu | Met | Pro | Asn | Val | Gly | Tyr | Gly | Ser | Asp | Lys | Lys | Thr |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | His | Tyr | Leu | Pro | Asn | Gly | Phe | Lys | Lys | Phe | Val | Val | His | Asn | Thr |  |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Ser | Glu | Leu | Glu | Leu | Met | Met | His | Asn | Arg | Thr | Tyr | Cys | Ala | Glu |     |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ile | Ala | His | Asn | Val | Ser | Thr | Lys | Lys | Arg | Lys | Ala | Ile | Val | Glu | Arg |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Ala | Ser | Gln | Leu | Asp | Val | Val | Val | Thr | Asn | Arg | Leu | Ala | Arg | Leu | Arg |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Ser | Gln | Glu | Asp | Glu |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1500869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Arg | Lys | Phe | Lys | Gly | Val | Thr | Leu | Met | Pro | Asn | Val | Gly | Tyr |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Ser | Asp | Lys | Lys | Thr | Arg | His | Tyr | Leu | Pro | Asn | Gly | Phe | Lys | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Phe | Val | Val | His | Asn | Thr | Ser | Glu | Leu | Glu | Leu | Leu | Met | Met | His | Asn |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Thr | Tyr | Cys | Ala | Glu | Ile | Ala | His | Asn | Val | Ser | Thr | Lys | Lys | Arg |  |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Lys | Ala | Ile | Val | Glu | Arg | Ala | Ser | Gln | Leu | Asp | Val | Val | Val | Thr | Asn |  |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Arg | Leu | Ala | Arg | Leu | Arg | Ser | Gln | Glu | Asp | Glu |     |     |     |     |     |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1500877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

tacctacccc ctgcgcttgc aaaaaatcct tcttgatccg cacaggaagg tggaaggtcc

cggcagaga acttgccggc gaaaggcga aaccgacgtg ctcccrggcg ggcggcgaca 120  
cggcattggag cgagagcgcnc aggcagtgcc gaggaacagg aaggtggtgc tgcgcgggta 180  
catcgaccgc gcgcccaggg aggaagacat ggagctcgtc gacggcrgcg ccgtggagct 240  
gcgcgtcccc gadggcggcg gcggccccgc ggtgctggtg aagaacctct acctatctcg 300  
cgacccttac atgcgcggca ggatgcggga ctcccgcaac tcctacatcc cgccctccaa 360  
acctggatca cctattgang gggttgccgt ggggarggtg gtcgactcca ctcatccagg 420  
attcagtgcc ggtgacgttg ttccgggat gactggatgg gaggactaca gtctgatcac 480  
caatcctgaa cag

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

Thr Tyr Pro Leu Arg Leu His Lys Ile Leu Leu Asp Pro His Arg Lys  
1 5 10 15  
Val Glu Gly Pro Gly Arg Arg Thr Trp Arg Ala Lys Gly Glu Thr Asp  
20 25 30  
Val Leu Xaa Gly Gly Arg Arg His Gly Met Glu Arg Glu Xaa Gln Ala  
35 40 45  
Val Ala Arg Asn Arg Lys Val Val Leu Arg Gly Tyr Ile Asp Arg Ala  
50 55 60  
Pro Arg Glu Glu Asp Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu  
65 70 75 80  
Arg Val Pro Xaa Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu  
85 90 95  
Tyr Leu Ser Cys Asp Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg  
100 105 110  
Asn Ser Tyr Ile Pro Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe  
115 120 125  
Gly Val Gly Xaa Val Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly  
130 135 140  
Asp Val Val Ser Gly Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr  
145 150 155 160  
Asn Pro Glu Gln

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1500879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

Met Glu Arg Glu Xaa Gln Ala Val Ala Arg Asn Arg Lys Val Val Leu  
1 5 10 15  
Arg Gly Tyr Ile Asp Arg Ala Pro Arg Glu Glu Asp Met Glu Leu Val  
20 25 30  
Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly Gly Gly Gly Pro  
35 40 45  
Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp Pro Tyr Met Arg

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |
| Gly | Arg | Met | Arg | Asp | Phe | Arg | Asn | Ser | Tyr | Ile | Pro | Pro | Phe | Lys | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Ser | Pro | Ile | Xaa | Gly | Phe | Gly | Val | Gly | Xaa | Val | Val | Asp | Ser | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| His | Pro | Gly | Phe | Ser | Ala | Gly | Asp | Val | Val | Ser | Gly | Met | Thr | Gly | Trp |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Glu | Asp | Tyr | Ser | Leu | Ile | Thr | Asn | Pro | Glu | Gln |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..95  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Val | Asp | Gly | Xaa | Ala | Val | Glu | Leu | Arg | Val | Pro | Xaa | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Gly | Pro | Ala | Val | Leu | Val | Lys | Asn | Leu | Tyr | Leu | Ser | Cys | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Tyr | Met | Arg | Gly | Arg | Met | Arg | Asp | Phe | Arg | Asn | Ser | Tyr | Ile | Pro |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Phe | Lys | Pro | Gly | Ser | Pro | Ile | Xaa | Gly | Phe | Gly | Val | Gly | Xaa | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Asp | Ser | Thr | His | Pro | Gly | Phe | Ser | Ala | Gly | Asp | Val | Val | Ser | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Thr | Gly | Trp | Glu | Asp | Tyr | Ser | Leu | Ile | Thr | Asn | Pro | Glu | Gln |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..535  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| aagtcagcag  | gacatctgat  | tgggggaacta | cagaaaaagg | tcggaatcga | atccgtgggt | 60  |
| cactcagccct | tcctcccacca | cagagccgcg  | cgcgcgcgcg | gaggactccg | gcgaaatgcg | 120 |
| tcgccgctgc  | cctcggggcct | cctccgcgcg  | cgcgcgcgcg | ccacactaag | cctcttaagg | 180 |
| atcttatgcac | atgtcagaag  | ctcacacagt  | caactttctg | ctcttggttc | tgtacacatt | 240 |
| gaatgctcaa  | atctcgcgag  | aagatgctat  | tactttacct | atccctctcc | atgcataatc | 300 |
| tggtgattgt  | ctatttgtct  | agacacacga  | gacaaagttt | aggtcgtgtg | gcacctcatg | 360 |
| gttgaaactc  | caactcttgc  | aactctttaa  | agaaaacctg | agacagatct |            | 420 |
| gaggtcgtat  | aacctatagc  | gcgagattga  | actgataagg | tcacatatga | tgtgcgaagt | 480 |
| ctctgargct  | gtgttattga  | aaagctcatt  | gctgataag  | gcgcacacat | tactc      |     |

(2) INFORMATION FOR SEQ ID NO:1688

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1500882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

```
Val Arg Gly Thr Leu His Trp Gly Thr Thr Glu Lys Gly Pro Asn Arg
1      5      10      15
Ile Arg Gly Ala Leu Pro Leu Pro Pro Gln Ala Ala Ala Ala Ala
20      25      30
Val Arg Thr Pro Ala Asn Gly Val Pro Arg Arg Leu Gly Pro Pro Pro
35      40      45
Pro Pro Arg Arg Arg His Thr Arg Pro Pro Lys Glu Leu Cys Thr Cys
50      55      60
Gln Lys Leu Gln Gln Ser Thr Phe Ser Phe Gly Phe Cys Tyr Ile
65      70      75
```

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

```
Met Ala Ser Arg Val Ala Ser Gly Leu Leu Arg Arg Arg Ala Gly Ala
1      5      10      15
Thr Leu Gly Leu Leu Arg Ser Tyr Ala His Val Arg Ser Tyr Asn Ser
20      25      30
Gln Leu Ser Ala Leu Val Ser Ala Thr Ser Glu Cys Ser Asn Leu Pro
35      40      45
Arg Arg Cys Tyr Tyr Leu Pro Asn Pro Ser Pro Tyr Gln Val Trp Ser
50      55      60
Arg Ser Phe Ala Ser Asp Asn Gly Asp Lys Phe Glu Ala Val Val Pro
65      70      75
Phe Met Gly Glu Ser Val Thr Asp Gly Thr Leu Ala Asn Phe Leu Lys
85      90      95
Lys Pro Gly Asp Arg Val Glu Ala Asp Glu Pro Ile Ala Gln Ile Glu
100      105      110
Thr Asp Lys Val Thr Ile Asp Val Ala Ser Pro Xaa Ala Gly Val Ile
115      120      125
Glu Lys Leu Ile Ala Ser Glu Gly Asp Thr Val Thr
130      135      140
```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1500884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

```
ataccgcaac cagctattga gctactgcct ctgaccaagt cccaagctgc gctgcgcctg 60
ctatgtcgtc gtccctcgccc gtatcggcgg tctcatcagc cactgcgcgc cagctcgttg 120
acgactgcct cggcatcgtg cagcttctta gcgatggcac cgtgacgcgc tccgsagacta 180
ctccgacatc cctctccttg gcgaggtgcc gtccaacctg cccgtccagt ggaaggacgt 240
```

cgtctacgac cccgcgcacg cgtctccgct ccgcatgtac aggccccaccg acaccgcagg 300  
cggcaggacg accaacaaca agctgccggt gctagtctac ttccacggcg gcggcttctg 360  
catctgcagc ttccgagatgc ccactttcca cgcggcgagg ctccgcctcg ccgcgcagct 420  
cccgcgctc gtgctctmcg ccgactacmg cctggggccc gaggaccgcc t

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

Ile Pro Gln Pro Ala Ile Glu Leu Leu Pro Leu Thr Lys Ser Gln Ala  
1 5 10 15  
Ala Leu Arg Leu Leu Cys Arg Arg Pro Arg Pro Tyr Arg Ser His  
20 25 30  
Gln Pro Leu Arg Arg Thr Ser Trp Thr Thr Ala Ser Ala Ser Cys Ser  
35 40 45  
Phe Leu Ala Met Ala Pro  
50

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

Met Ser Ser Ser Ser Pro Val Ser Ala Val Ser Ser Ala Thr Ala Pro  
1 5 10 15  
His Val Val Asp Asp Cys Leu Gly Ile Val Gln Leu Leu Ser Asp Gly  
20 25 30  
Thr Val Thr Arg Ser Xaa Thr Thr Pro Thr Ser Leu Ser Trp Ala Arg  
35 40 45  
Cys Arg Pro Thr Cys Pro Ser Ser Gly Arg Thr Ser Ser Thr Thr Pro  
50 55 60  
Arg Thr Arg Ser Ala Ser Ala Cys Thr Gly Pro Pro Thr Pro Thr Ala  
65 70 75 80  
Ala Gly Arg Pro Thr Thr Ser Cys Arg Cys  
85 90

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Tyr Arg Pro Thr Asp Thr Asp Gly Gly Arg Thr Thr Asn Asn Lys

|                                                                 |    |    |    |
|-----------------------------------------------------------------|----|----|----|
| 1                                                               | 5  | 10 | 15 |
| Leu Pro Val Leu Val Tyr Phe His Gly Gly Phe Cys Ile Cys Ser     |    |    |    |
|                                                                 | 20 | 25 | 30 |
| Phe Glu Met Pro His Phe His Ala Gly Gly Leu Arg Leu Ala Ala Glu |    |    |    |
|                                                                 | 35 | 40 | 45 |
| Leu Pro Ala Leu Val Leu Xaa Ala Asp Tyr Xaa Leu Gly Pro Glu His |    |    |    |
|                                                                 | 50 | 55 | 60 |

Arg  
65

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| cttccgcgtgc | ttttcctttc | tctctctctc | cccttctctc | ccccaaagcag | gcggggcgag  | 60  |
| cgagcccaagc | aggcgctctc | cctctcgtcc | atccgtttcc | tcctcccccct | gcttcccggc  | 120 |
| tcgctctccct | ccctccctcg | tcgctctctt | ttcatgcgcg | aggaggagacc | gtggggagacc | 180 |
| ccaccaccagc | caccaccacc | tccatccgtg | cgctctctgc | tctcgtgtgt  | ggtgctcctc  | 240 |
| ctctctctctc | tgctcccggg | gcgggcggcc | tccttttcca | cctcctgtgt  | gtcagggagc  | 300 |
| cgggaggcgcg | tmcgggaggt | ggcgcgcatg | gggtcgcgmg | gggaggggtc  | ggcggaacacm | 360 |
| gcmccactca  | gtaataatga | aaatrgcgcg | tmatattatg | gagttgcag   | ttctctgtgt  | 420 |
| aaaagagcat  | cgatggagga | cttctatgag | gcaagaatag | acgamtgtga  | tggagagaaaa | 480 |
| attgggaatgt | tcggtgtata | tgatggtcat | ggaggagctc | gagcagctga  | gtatgttaag  | 540 |
| cagcaccttt  | tcagcaattt | aatcaaacac | ccaaagtcca | tcactgatac  | c           |     |

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Leu Pro Leu Leu Phe Leu Ser Pro Leu Ser Pro Phe Leu Ser Pro Ser |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Arg Arg Gly Glu Arg Ala Gln Gln Ala Ser Leu Leu Ser Ser Ile Arg |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Phe Leu Leu Pro Leu Leu Pro Gly Ser Pro Pro Ser Pro Pro Cys Ala |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Pro Leu Phe Met Arg Glu Glu Gly Pro Trp Gly Pro Pro Pro Pro Ala |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Pro Pro Pro Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Leu Leu Leu Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Trp Cys Xaa Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Xaa Gly Xaa Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Xaa Arg Xaa Ile Tyr Gly Val Ala Ser Ser Pro Gly Lys Arg Ala Ser |     |     |     |
|                                                                 | 130 | 135 | 140 |

Met Glu Asp Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys  
145 150 155 160  
Ile Gly Met Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala  
165 170 175  
Glu Tyr Val Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys  
180 185 190  
Phe Ile Thr Asp Thr  
195

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1500890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Phe Arg Cys Phe Ser Phe Leu Leu Ser Pro Leu Ser Ser Pro Gln Ala  
1 5 10 15  
Gly Gly Ala Ser Glu Pro Ser Arg Arg Leu Ser Ser Arg Pro Ser Val  
20 25 30  
Ser Ser Ser Pro Cys Phe Pro Ala Arg Leu Pro Pro Leu Pro Val Arg  
35 40 45  
Leu Phe Ser Cys Ala Arg Arg Asp Arg Gly Asp His His Gln His  
50 55 60  
His His Leu His Pro Cys Ala Ser Arg Ser Arg Trp Trp Cys Ser Ser  
65 70 75 80  
Ser Ser Ser Cys Ser Arg Gly Gly Arg Pro Pro Phe Pro Pro Pro Ala  
85 90 95  
Gly Xaa Arg Ala Gly Arg Ala Xaa Arg Arg Trp Arg Ala Trp Gly Ser  
100 105 110  
Xaa Gly Xaa Gly Arg Arg Thr Xaa Xaa Thr Ser Val Ile Met Lys Xaa  
115 120 125  
Gly Gly Xaa Phe Met Glu Leu Arg Val Leu Leu Val Lys Glu His Arg  
130 135 140  
Trp Arg Thr Ser Met Arg Gln Glu  
145 150

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Arg Glu Glu Gly Pro Trp Gly Pro Pro Pro Pro Ala Pro Pro Pro  
1 5 10 15  
Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu Leu Leu Leu  
20 25 30  
Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys Trp Cys Xaa  
35 40 45  
Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu Xaa Gly Xaa  
50 55 60  
Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn Xaa Arg Xaa

65 70 75 80  
Ile Tyr Gly Val Ala Ser Ser Pro Gly Lys Arg Ala Ser Met Glu Asp  
85 90 95  
Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys Ile Gly Met  
100 105 110  
Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala Glu Tyr Val  
115 120 125  
Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys Phe Ile Thr  
130 135 140  
Asp Thr  
145

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..654  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

ctccgccgtc gctgtccac ttccccgtg cttctccgc gtcgaggccg cgtcccagtg 60  
cgaagagacc acgaactcaga tggccagccg ctgggtccgg cccgaggtgt acccgtgtgt 120  
cgccggcaacg ggcgtggccg tcggcatctg cggatttcag ctcttcggga acatcaccgg 180  
caaccgggaa gtcagggttaa accaaggcagg gagggcagct ggtgtgcttg agaaccatga 240  
ggaggggagg cgttacgccca tgcattggcct aacgcctacc ctctatggg ttctttcagc 300  
agcactggcc tcactatttc ttctaaatta ccaagattct cggacatgta cactctcaca 360  
atagcaagtg cggatccaca gtctatctct gcaaaccaagc cagtctcatt cactaagagc 420  
gtacacaagt ggtttacaaa ggaaggagtt cttgtggagg gccgtgtctg gaaggatgtc 480  
gagaagctga ttgatgacta caacagctgag cgcaagagta aatgaattgg tagctcgtgt 540  
ctctggccat ctggggagac atcgtgtgtc agagaaatcc gtcaaatgtt agcttaatat 600  
gaacaggcat ttctgtata ctgtaccggt tgaccagtga atgaatgatg ttct

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

Ser Ala Val Ala Cys Pro Leu Ser Pro Cys Phe Ser Ala Val Glu Ala  
1 5 10 15  
Ala Ser Gln Cys Glu Glu Thr Thr Thr Gln Met Ala Ser Arg Trp Val  
20 25 30  
Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala Thr Gly Val Ala Val Gly  
35 40 45  
Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile Thr Gly Asn Pro Glu Val  
50 55 60  
Arg Val Asn Lys Ala Gly Arg Ala Ala Gly Val Leu Glu Asn His Glu  
65 70 75 80  
Glu Gly Arg Arg Tyr Ala Met His Gly Leu Thr Pro Thr Leu Leu Trp  
85 90 95  
Val Leu Ser Ala Ala Leu Ala Ser Leu Phe Leu Leu Asn Tyr Gln Asp  
100 105 110  
Ser Arg Thr Cys Thr Leu Ser Gln

115 120  
(2) INFORMATION FOR SEQ ID NO:1700:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 94 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..94  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500902  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:  
Met Ala Ser Arg Trp Val Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala  
1 5 10 15  
Thr Gly Val Ala Val Gly Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile  
20 25 30  
Thr Gly Asn Pro Glu Val Arg Val Asn Lys Ala Gly Arg Ala Ala Gly  
35 40 45  
Val Leu Glu Asn His Glu Glu Gly Arg Arg Tyr Ala Met His Gly Leu  
50 55 60  
Thr Pro Thr Leu Leu Trp Val Leu Ser Ala Ala Leu Ala Ser Leu Phe  
65 70 75 80  
Leu Leu Asn Tyr Gln Asp Ser Arg Thr Cys Thr Leu Ser Gln  
85 90

(2) INFORMATION FOR SEQ ID NO:1701:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 79 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..79  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500903  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:  
Met Gly Ser Phe Ser Ser Thr Gly Leu Thr Ile Ser Ser Lys Leu Pro  
1 5 10 15  
Arg Phe Ser Asp Met Tyr Thr Leu Thr Ile Ala Ser Ala Asp Pro Gln  
20 25 30  
Ser Ile Ser Ala Asn Lys Pro Val His Phe Thr Lys Ser Val Thr Lys  
35 40 45  
Trp Phe Thr Lys Glu Gly Val Leu Val Glu Gly Leu Phe Trp Lys Asp  
50 55 60  
Val Glu Lys Leu Ile Asp Asp Tyr Asn Ser Glu Arg Lys Ser Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1702:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 465 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..465  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500907  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:  
acacaacacc agtaagcaag caccgccagc acgcacaagc aggcacaaagct ctcgaccatc 60  
gctctgaggg attaatggcg gcgggaggag gaggcggcgg catcgcgacg agaagggccc 120

tgctgctgag gcgttcggcg ggcacctgga ggcggcgagg atgacggagg cggaggagga 180  
acacagcgcg gtcgaagtccc ggctgtcggg tctgctgtgg caccggcggt cggcgtacga 240  
cgctgtgttc agctgcgcgt cgaaccaggt ggcgagggt ctgctgacgc tgccctactc 300  
gttcgcgcac tggggatgct garcggcggt ctgttcaccg tcttctacgg cctgctgggc 360  
agctggacgg cgtacctgat cagcatcctg tacctggagt accgcaccg tcgggagcgc 420  
gagaaggcgc cggacttcgc gaaccacgtg atccagtgtg tcgag

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Thr Thr Pro Val Ser Lys His Arg Gln His Ala Gln Ala Gly Lys Ala  
1 5 10 15  
Leu Asp His Arg Ser Glu Gly Leu Met Ala Ala Gly Gly Gly Gly  
20 25 30  
Gly Ile Ala Thr Arg Arg Pro Leu Leu Arg Arg Ser Ala Gly Thr  
35 40 45  
Trp Arg Arg Arg Arg  
50

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

Met Thr Glu Ala Glu Glu His Ser Gly Val Lys Ser Arg Leu Ser  
1 5 10 15  
Gly Leu Leu Trp His Gly Gly Ser Ala Tyr Asp Ala Trp Phe Ser Cys  
20 25 30  
Ala Ser Asn Gln Val Ala Gln Val Leu Leu Thr Leu Pro Tyr Ser Phe  
35 40 45  
Ala His Trp Gly Cys  
50

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1500910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

Met Leu Xaa Gly Val Leu Phe Gln Leu Phe Tyr Gly Leu Leu Gly Ser  
1 5 10 15  
Trp Thr Ala Tyr Leu Ile Ser Ile Leu Tyr Leu Glu Tyr Arg Thr Arg

Arg Glu Xaa Glu Lys Ala Ala Asp Phe Arg Asn His Val Ile Gln Trp  
35 40 45  
Phe Glu  
50

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..548
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

```
gttacatccc accatttgct gttcaccttc cctcccgttt gcctcctctc getgtctcgt      60
agcttcctttc ctccggcgac ggctggggcga gcggccgcga ctgcggccct tcgtcggcgga    120
cgagcatcca cctgcgcggc gccccatctt ccgctccttc ccttactcgc gctcggcaca    180
caggcgacgg cgccggcggc gctcaggatc gggctatcac cgacggggtc cggtctctcc    240
gcccgctctt cgccactcgc ctgcgccttc cgctccggtt cctccgcaca ccggccggcg    300
atcctgcaag ggttggatga tggggcagat ctgaaggatg ctgatttcta taagcagcaa    360
gctaaacttc tttcaagaa ctgtcaaaa gggcatcatg aagcttcaag gatgtaatt    420
gagacagggc cctactattt ccactacatt attgarggca gagtatgta tctgactatg    480
tgtgamcgct cttatccgaa gaaacttgca ttccagtacc tagaagatct gaaaaatgaa    540
tttgagag
```

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

```
Val Thr Ser His His Leu Leu Phe Thr Phe Pro Val Cys Leu Leu
1 5 10 15
Ser Leu Ser Arg Ser Phe Phe Pro Pro Ala Thr Ala Gly Arg Ala Ala
20 25 30
Ala Ser Arg Ala Leu Arg Arg Arg Ala Ser Thr Cys Ala Ala Pro
35 40 45
His Leu Pro Leu Leu Pro Leu Leu Ala Leu Gly Thr Gln Ala Thr Ala
50 55 60
Ala Ala Ala Leu Arg Ile Gly Leu Ser Pro Thr Gly Ser Gly Phe Ser
65 70 75 80
Ala Arg Leu Ser Pro Leu Ala Ser Arg Pro Arg Leu Arg Ser Ser Ala
85 90 95
His Arg Pro Ala Ile Leu Gln Gly Leu Asp Gly Arg Asp Leu Lys
100 105 110
Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys Leu Leu Phe Lys Asn Leu
115 120 125
Ser Lys Gly His His Glu Ala Ser Arg Met Xaa Ile Glu Thr Gly Pro
130 135 140
Tyr Tyr Phe His Tyr Ile Ile Xaa Gly Arg Val Cys Tyr Leu Thr Met
145 150 155 160
Cys Xaa Arg Ser Tyr Pro Lys Lys Leu Ala Phe Gln Tyr Leu Glu Asp
165 170 175
```

Leu Lys Asn Glu Phe Glu  
180

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Pro | Thr | Ile | Cys | Cys | Ser | Pro | Ser | Leu | Pro | Phe | Ala | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Cys | Leu | Val | Ala | Ser | Phe | Leu | Arg | Arg | Leu | Gly | Glu | Arg | Pro |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Pro | Val | Gly | Pro | Phe | Val | Gly | Asp | Glu | His | Pro | Ala | Arg | Arg | Pro |     |
|     |     |     | 35  |     |     | 40  |     | 45  |     |     |     |     |     |     |     |
| Ile | Phe | Arg | Ser | Phe | Pro | Tyr | Ser | Arg | Ser | Ala | His | Arg | Arg | Arg |     |
|     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |     |     |
| Arg | Arg | Arg | Ser | Gly | Ser | Gly | Tyr | His | Arg | Arg | Gly | Pro | Ala | Ser | Pro |
|     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |     |     |
| Pro | Ala | Ser | Arg | His | Ser | Pro | Arg | Ala | Leu | Ala | Ser | Gly | Pro | Pro | His |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Thr | Gly | Arg | Arg | Ser | Cys | Lys | Gly | Trp | Met | Met | Gly | Glu | Ile |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

|             |             |            |             |             |            |     |
|-------------|-------------|------------|-------------|-------------|------------|-----|
| atgctctacc  | ggagtagcgc  | aactccgcaa | gcaaatccctc | ctatctccaa  | gcctccaatc | 60  |
| tgtgaacggt  | gaaccccaat  | cgaatgacgc | cgacggsagc  | ctctctctcc  | agcctccccc | 120 |
| attcgtctct  | atctccgatg  | tgcgcgcgct | ccagctccccc | ccgcgcggcg  | gccaccggcc | 180 |
| tcgccccctgc | tggaaaggcct | tggagtgccg | ctccgtacag  | acgcggatgg  | tctctctctt | 240 |
| cgttggggagc | agaacacgcc  | cgagaaacgt | tatatgtgct  | tccctgttgc  | gagttggagc | 300 |
| tcccgaagca  | ctggtcattg  | gagtagtcgc | cttgttggtg  | ttcggcccca  | agggctagc  | 360 |
| agagtgatgcc | aggaattttg  | ggaagacttt | gcgtgcttcc  | caaccaacca  | ttagagagat | 420 |
| acaggatgta  | tcaaggaggt  | tcaggagcac | tcttgaacga  | gaaatcgga   | ttgatgaggt | 480 |
| ttcccagtcg  | acgaattata  | cacccacgac | catgaataac  | aaccaacaac  | ctgctgcgca | 540 |
| ctcaaatatc  | aagcctgcac  | ctgcacctta | caccagcgat  | gaacttgta   | aagtaactga | 600 |
| agaaacaaatt | gctgcacatg  | ctgctgcaga | gagttatcgt  | cagttgggtc  | gggtgttccg | 660 |
| cttaaaacttt | atttgtgggt  | ggttggtact | tttgtgtgtg  | ttattttttt  | ggacctcgta | 720 |
| atagtcggtc  | ggttcaatgt  | tatcgcggtc | actggcacaac | cttaagtgtat | acggtattct | 780 |
| tcctttcggg  |             |            |             |             |            |     |

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1500927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Ser | Thr | Gly | Val | Ala | Gln | Leu | Arg | Lys | Gln | Ile | Leu | Leu | Ser | Pro |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ser | Leu | Gln | Ser | Val | Asn | Gly | Glu | Pro | Gln | Ser | Asn | Asp | Ala | Asp | Xaa |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Leu | Leu | Leu | Pro | Ala | Pro | Pro | Phe | Val | Ser | Ile | Ser | Asp | Val | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Leu | Gln | Leu | Pro | Pro | Arg | Gly | Gly | His | Arg | Pro | Arg | Pro | Cys | Trp |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Lys | Gly | Leu | Glu | Cys | Gly | Ser | Val | Gln | Thr | Arg | Met | Val | Ser | Ser | Phe |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | Gly | Ser | Arg | Thr | Arg | Arg | Arg | Asn | Val | Ile | Cys | Ala | Ser | Leu | Phe |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gly | Val | Gly | Ala | Pro | Glu | Ala | Leu | Val | Ile | Gly | Val | Val | Ala | Leu | Leu |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Val | Phe | Gly | Pro | Lys | Gly | Leu | Ala | Glu | Val | Ala | Arg | Asn | Leu | Gly | Lys |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Thr | Leu | Arg | Ala | Phe | Gln | Pro | Thr | Ile | Arg | Glu | Ile | Gln | Asp | Val | Ser |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Arg | Glu | Phe | Arg | Ser | Thr | Leu | Glu | Arg | Glu | Ile | Gly | Ile | Asp | Glu | Val |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |  |
| Ser | Gln | Ser | Thr | Asn | Tyr | Thr | Pro | Thr | Thr | Met | Asn | Asn | Asn | Gln | Gln |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Pro | Ala | Ala | Asp | Ser | Asn | Ile | Lys | Pro | Ala | Pro | Ala | Pro | Tyr | Thr | Ser |  |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |     |  |
| Asp | Glu | Leu | Val | Lys | Val | Thr | Glu | Glu | Gln | Ile | Ala | Ala | Ser | Ala | Ala |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ala | Glu | Ser | Tyr | Arg | Gln | Leu | Val | Arg | Cys | Val | Arg | Leu | Asn | Phe | Ile |  |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |  |
| Cys | Gly | Trp | Leu | Val | Leu | Leu | Trp | Trp | Leu | Phe | Phe | Trp | Thr | Ser |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Ser | Ser | Phe | Val | Gly | Ser | Arg | Thr | Arg | Arg | Arg | Asn | Val | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Cys | Ala | Ser | Leu | Phe | Gly | Val | Gly | Ala | Pro | Glu | Ala | Leu | Val | Ile | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Val | Ala | Leu | Leu | Val | Phe | Gly | Pro | Lys | Gly | Leu | Ala | Glu | Val | Ala |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Asn | Leu | Gly | Lys | Thr | Leu | Arg | Ala | Phe | Gln | Pro | Thr | Ile | Arg | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ile | Gln | Asp | Val | Ser | Arg | Glu | Phe | Arg | Ser | Thr | Leu | Glu | Arg | Glu | Ile |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly | Ile | Asp | Glu | Val | Ser | Gln | Ser | Thr | Asn | Tyr | Thr | Pro | Thr | Thr | Met |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Asn | Asn | Gln | Gln | Pro | Ala | Ala | Asp | Ser | Asn | Ile | Lys | Pro | Ala | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |

Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile  
115 120 125  
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val  
130 135 140  
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Leu Trp Trp Leu Phe  
145 150 155 160  
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1500929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| aaggattttt  | gcaccgtgcc  | tctgcctcca | ggattgtgct | gcgcgcctc  | caccattttc | 60  |
| gcgcgcgcgc  | ccccgcaccc  | acctccaagg | atccttgccc | cgcccccctg | actcctcgcg | 120 |
| tcgcgatctc  | cgcgtccatt  | tccgtgcccc | gcgatgcgct | gcacagtgtc | gcgcgcctcg | 180 |
| gcgcgcgcgc  | gcgcattacm  | ccccccccca | tcaccacctc | gctgtggtgt | acccccgtcc | 240 |
| ttggcgcgcg  | caccccgcac  | cccgcccgag | attggctctt | ccaccgcctc | ccctggagat | 300 |
| gagcgctcgc  | ttagggttag  | gcgtccacag | gttgatccct | ccaccacaag | cgagaggaga | 360 |
| tcgctgggaag | agggggggctg | ggagacgaac | acgaacacgg | tcacatctg  | ggtgcmctcg | 420 |
| cmcccacctc  | tctcgaatcc  | tgamgcccac | acagcgctc  | cgcmtcctg  | agaccgcgac | 480 |

gc

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asp | Phe | Cys | Thr | Val | Pro | Leu | Pro | Gly | Leu | Ser | Cys | Arg | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Ile | Phe | Ala | Ala | Ala | Pro | Pro | Thr | Pro | Pro | Pro | Arg | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ala | Pro | Ala | Pro | Val | Leu | Leu | Ala | Ser | Ala | Ser | Pro | Ala | Pro | Phe |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Leu | Pro | Ala | Met | Arg | Ser | His | Val | Ser | Pro | Pro | Ser | Ala | Arg | Gly |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| Arg | Leu | Xaa | Pro | Ser | Pro | Ser | Pro | Pro | Arg | Cys | Gly | Val | Pro | Pro |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Leu | Ala | Pro | Pro | Pro | Arg | Thr | Pro | Ser | Glu | Ile | Gly | Ser | Ser | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Pro | Gly | Asp | Glu | Arg | Ser | Leu | Arg | Val | Arg | Arg | Pro | Thr | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Pro | Ser | Thr | Thr | Ser | Glu | Arg | Arg | Ser | Leu | Glu | Glu | Gly | Gly | Trp |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| Thr | Asn | Arg | Asn | Thr | Val | His | Ile | Trp | Val | Xaa | Ser | Xaa | Pro | Thr |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| Ser | Asn | Pro | Xaa | Ala | His | Thr | Ala | Pro | Pro | Xaa | Ser |     |     |     |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ile | Phe | Ala | Pro | Cys | Leu | Cys | Leu | Gln | Asp | Cys | Arg | Ala | Ala | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Phe | Ser | Pro | Pro | Arg | Pro | Arg | His | His | Leu | Gln | Gly | Ser | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Pro | Leu | Tyr | Ser | Ser | Arg | Pro | His | Leu | Pro | Leu | His | Phe | Arg |
|     |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Cys | Pro | Arg | Cys | Ala | Arg | Thr | Cys | Arg | Arg | Pro | Arg | Pro | Ala | Gly | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asp | Tyr | Xaa | Pro | Pro | His | His | His | Leu | Ala | Val | Val | Tyr | Pro | Arg | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Arg | Arg | His | Pro | Ala | Pro | Arg | Pro | Arg | Leu | Ala | Leu | Pro | Pro | Leu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Leu | Glu | Met | Ser | Ala | Arg | Leu | Gly | Leu | Gly | Val | Gln | Arg | Leu | Tyr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Pro | Pro | Gln | Ala | Arg | Gly | Asp | Arg | Trp | Lys | Arg | Gly | Ala | Gly | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Thr | Gly | Thr | Arg | Ser | Thr | Ser | Gly | Cys | Xaa | Arg | Xaa | Pro | Leu | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Arg | Ile | Leu | Xaa | Pro | Thr | Gln | Arg | Leu | Arg | Xaa | Arg | Glu | Thr | Ala | Thr |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1500932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | His | Val | Ser | Pro | Pro | Ser | Ala | Arg | Gly | Pro | Arg | Leu | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Pro | Ser | Pro | Pro | Arg | Cys | Gly | Val | Pro | Pro | Ser | Leu | Ala | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Pro | Arg | Thr | Pro | Ser | Glu | Ile | Gly | Ser | Ser | Thr | Ala | Pro | Pro | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Arg | Ser | Leu | Arg | Val | Arg | Arg | Pro | Thr | Val | Val | Pro | Ser | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Ser | Glu | Arg | Arg | Ser | Leu | Glu | Glu | Gly | Gly | Trp | Glu | Thr | Asn | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Thr | Val | His | Ile | Trp | Val | Xaa | Ser | Xaa | Pro | Thr | Leu | Ser | Asn | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Xaa | Ala | His | Thr | Ala | Pro | Pro | Xaa | Ser |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 463 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..463  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500945  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:  
aatcaacaca ccaccaccac cagcagcaca tcaattttagc tagttccagg aacacgcgag 60  
gaaaccgcag catggccaac aaccgcattct tcgacgagta caaccgccgc gtccgaatgga 120  
gcgcgtccga cgaggcggag gccgtccgga tctcgtctccc aggggttcaag agggaggaca 180  
tacgcgtgct ggtggacagc cagcgccacc tgcggacgcg cgccgagcgg cacatcgccg 240  
gcaacaggtg gaggcgcgttc cagacggacg tcgacctccc cgccaactgc aacgcgcgac 300  
gcattccgcg caagtttcgag aacgacaggc tcacctcac gctccccaag agcacctctc 360  
cggcgcccat tccggcgccg ccgcagagggc cgcacgtgaa ggcgccgtcg acgtcgtcgg 420  
(2) INFORMATION FOR SEQ ID NO:1717:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500946  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:  
Ser Thr His His His His Gln Gln His Ile Asn Leu Ala Ser Ser Arg  
1 5 10 15  
Asn Thr Arg Gly Asn Arg Ser Met Ala Asn Asn Arg Ile Phe Asp Glu  
20 25 30  
Tyr Asn Pro Ala Val Glu Trp Ser Arg Ser Asp Glu Ala Asp Ala Val  
35 40 45  
Arg Ile Ser Leu Pro Gly Phe Lys Arg Glu Asp Ile Arg Val Leu Val  
50 55 60  
Asp Ser His Gly His Leu Arg Thr Arg Gly Glu Arg His Ile Ala Gly  
65 70 75 80  
Asn Arg Trp Ser Arg Phe Gln Thr Asp Val Asp Leu Pro Ala Asn Cys  
85 90 95  
Asn Ala Asp Gly Ile Arg Ala Lys Phe Glu Asn Asp Arg Leu Thr Ile  
100 105 110  
Thr Leu Pro Lys Ser Thr Ser Ser Ala Pro Ile Pro Ala Pro Pro Gln  
115 120 125  
Arg Pro His Val Lys Ala Pro Ser Thr Ser Ser Ala Arg Leu Pro Pro  
130 135 140  
Val Thr Ala Arg Pro Val Ala Arg Pro  
145 150  
(2) INFORMATION FOR SEQ ID NO:1718:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500947  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:  
Met Ala Asn Asn Arg Ile Phe Asp Glu Tyr Asn Pro Ala Val Glu Trp  
1 5 10 15  
Ser Arg Ser Asp Glu Ala Asp Ala Val Arg Ile Ser Leu Pro Gly Phe  
20 25 30  
Lys Arg Glu Asp Ile Arg Val Leu Val Asp Ser His Gly His Leu Arg  
35 40 45  
Thr Arg Gly Glu Arg His Ile Ala Gly Asn Arg Trp Ser Arg Phe Gln  
50 55 60  
Thr Asp Val Asp Leu Pro Ala Asn Cys Asn Ala Asp Gly Ile Arg Ala  
65 70 75 80  
Lys Phe Glu Asn Asp Arg Leu Thr Ile Thr Leu Pro Lys Ser Thr Ser  
85 90 95  
Ser Ala Pro Ile Pro Ala Pro Pro Gln Arg Pro His Val Lys Ala Pro  
100 105 110  
Ser Thr Ser Ser Ala Arg Leu Pro Pro Val Thr Ala Arg Pro Val Ala  
115 120 125  
Arg Pro  
130

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1500948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

Met Glu Pro Leu Arg Arg Gly Gly Arg Arg Pro Asp Leu Ala Pro Arg  
1 5 10 15  
Val Gln Glu Gly Gly His Thr Arg Ala Gly Gly Gln Pro Arg Pro Pro  
20 25 30  
Ala Asp Ala Arg Arg Ala Ala His Arg Arg Gln Gln Val Glu Pro Leu  
35 40 45  
Pro Asp Gly Arg Arg Pro Pro Arg Gln Leu Gln Arg Arg Arg His Pro  
50 55 60  
Arg Gln Val Arg Glu Arg Gln Ala His His His Ala Pro Gln Glu His  
65 70 75 80  
Leu Leu Gly Ala His Ser Gly Ala Ala Ala Glu Ala Ala Arg Glu Gly  
85 90 95  
Ala Val Asp Val Val Gly Glu Ala Ser Ala Gly Asp Cys  
100 105  
110

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1500953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

ctcgcagcca gcaggacacc actcatcttc ttctccccc cctcgtttcc atcgccacca  
ccctcttctc ctgcggtcct ccccggtccc actcccaacc cctcgcctc cgctccact  
gcagctgcgc ccatgcagag cctctctctg cccaccgctg cctgtggccc ggtggcgctc

60  
120  
180

ccgtgcgga ggcggaatct cccgggacgc ctctccgtcc ggcctccgc gacgggtgga 240  
gcggcaccgc ggcgggagac ggcacccaag aagcgggtgg tgatcacggg gatggggctg 300  
gtctccgttt tcgggaacga tctagacgct tactacgacc gcctgctagt cggggagagc 360  
ggcaccgggc ccacgcacgc ctctcagcgt tctaagtccc ccacccgctt tgcgggtcag 420  
atccggggct tctctccga gggatacatc gacggaaaga acgacgcgmg ccttgatgat 480  
tgccctccgat actgcacgt cagtggaag aaggctctcg

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1500954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

Leu Ala Ala Ser Arg Thr Pro Leu Ile Phe Ser Pro Ala Ser Phe  
1 5 10 15  
Pro Ser Pro Pro Ser Ser Pro Ala Val Leu Pro Arg Pro Thr Pro  
20 25 30  
Thr Pro Leu Ala Ser Ala Ser Thr Ala Ala Ala Ala Met Gln Ser Leu  
35 40 45  
Leu Leu Pro Thr Ala Ala Val Ala Pro Val Ala Pro Pro Cys Gly Arg  
50 55 60  
Arg Asn Leu Pro Gly Arg Leu Ser Val Arg Ala Ser Ala Thr Val Val  
65 70 75 80  
Ala Ala Pro Arg Arg Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr  
85 90 95  
Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala Tyr Tyr  
100 105 110  
Asp Arg Leu Leu Val Gly Glu Ser Gly Ile Gly Pro Ile Asp Arg Phe  
115 120 125  
Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln Ile Arg Gly Phe  
130 135 140  
Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg Xaa Leu Asp Asp  
145 150 155 160  
Cys Leu Arg Tyr Cys Ile Val Ser Gly Lys Lys Ala Leu  
165 170

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

Arg Ser Gln Gln Asp Thr Thr His Leu Leu Leu Pro Arg Leu Val Ser  
1 5 10 15  
Ile Ala Thr Thr Leu Phe Ser Cys Gly Pro Pro Pro Ser His Ser His  
20 25 30  
Pro Pro Arg Leu Arg Leu His Cys Ser Cys Arg His Ala Glu Pro Pro  
35 40 45  
Pro Ala His Arg Cys Arg Gly Pro Gly Gly Ala Ser Val Arg Lys Ala  
50 55 60  
Glu Ser Pro Gly Thr Pro Leu Arg Pro Arg Leu Arg Asp Gly Gly Ser

65 70 75 80  
Gly Thr Ala Ala Gly Asp Gly Ser Gln Glu Ala Gly Gly Asp His Gly  
85 90 95  
Asp Gly Ala Gly Leu Arg Phe Arg Glu Arg Cys Arg Arg Leu Leu Arg  
100 105 110  
Pro Pro Ala Ser Arg Gly Glu Arg His Arg Ala His Arg Pro Leu Arg  
115 120 125  
Arg Phe  
130

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

Met Gln Ser Leu Leu Pro Thr Ala Ala Val Ala Pro Val Ala Pro  
1 5 10 15  
Pro Cys Gly Arg Arg Asn Leu Pro Gly Arg Leu Ser Val Arg Ala Ser  
20 25 30  
Ala Thr Val Val Ala Ala Pro Arg Arg Glu Thr Asp Pro Lys Lys Arg  
35 40 45  
Val Val Ile Thr Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val  
50 55 60  
Asp Ala Tyr Tyr Asp Arg Leu Leu Val Gly Glu Ser Gly Ile Gly Pro  
65 70 75 80  
Ile Asp Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln  
85 90 95  
Ile Arg Gly Phe Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg  
100 105 110  
Xaa Leu Asp Asp Cys Leu Arg Tyr Cys Ile Val Ser Gly Lys Lys Ala  
115 120 125  
Leu

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..485  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

aytctgtgag ctgcagcysr tgcgtgcgcg ctactccatc gtctattaat tctctgtgta 60  
gtctccagcgc tcggtcttaga caagcctctc caacatgaag ctctctgggtt ggaatgcaccg 120  
gaagttacga cagaacagta atgatgtgtt caaagagttc aacaacgctg gaggtgggac 180  
gtgcaactgc atcaccgggc tggcgcgcgc ggaccgcgcc acttctctcg ccaccgccaa 240  
cgaatacttc gccgcgcaca acgaattcac caacaatcat ccactgtcgc cgccgcgcga 300  
cctcttcacc ttgtgttgca gcggcctcct caccattggc acgctaggca tcgcgcgcgtc 360  
gcgtgtctgc agatgctgat gaagttgatt acgacgtcga cgccgatgct gactccgact 420  
ttgacgacaa cgacgacacc gccggtkatg acgaagacca ggtcgacagc gccgtcacgc 480  
ccacg

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 94 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..94  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1500964  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:  
Met Lys Leu Leu Gly Trp Met His Arg Lys Leu Arg Gln Asn Ser Asn  
1           5           10           15  
Asp Val Phe Lys Glu Phe Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys  
          20           25           30  
Ile Thr Gly Leu Ala Ala Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala  
          35           40           45  
Asn Glu Tyr Phe Ala Ala Asp Asn Asp Phe Thr Asn Asn His Pro Ser  
50           55           60  
Ser Pro Ala Ala Asp Leu Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr  
65           70           75           80  
Ile Gly Thr Leu Gly Ile Ala Pro Ser Arg Val Cys Arg Cys  
          85           90  
(2) INFORMATION FOR SEQ ID NO:1726:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 88 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..88  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500965  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:  
Met His Arg Lys Leu Arg Gln Asn Ser Asn Asp Val Phe Lys Glu Phe  
1           5           10           15  
Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys Ile Thr Gly Leu Ala Ala  
          20           25           30  
Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala Asn Glu Tyr Phe Ala Ala  
35           40           45  
Asp Asn Asp Phe Thr Asn Asn His Pro Ser Ser Pro Ala Ala Asp Leu  
50           55           60  
Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr Ile Gly Thr Leu Gly Ile  
65           70           75           80  
Ala Pro Ser Arg Val Cys Arg Cys  
          85  
(2) INFORMATION FOR SEQ ID NO:1727:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 68 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..68  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1500966  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:  
Met Met Cys Ser Lys Ser Ser Thr Thr Leu Glu Val Gly Arg Ala Thr  
1           5           10           15

Ala Ser Pro Gly Trp Pro Arg Arg Thr Arg Pro Leu Ser Ser Pro Pro  
20 25 30  
Pro Thr Asn Thr Ser Pro Pro Thr Thr Thr Ser Pro Thr Ile Ile His  
35 40 45  
Arg Arg Arg Pro Pro Thr Ser Ser Pro Leu Val Ala Ala Ala Ser Ser  
50 55 60  
Pro Leu Ala Arg  
65

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1500974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| tcggttcggy | tecttctctc  | ccctatctag | ctagccttc   | cgttctctga | tcgcggcgga | 60  |
| gatggggcgc | tecaccacgc  | cgctcgctgc | ggcggcgggc  | ctgctctctg | tgctgctgcg | 120 |
| gcgcgtcgcc | geggcgggcg  | acagcatgtc | gacgtctctc  | tacggcgagc | ggasmgdmn  | 180 |
| aggagggcgc | gcgggatgtac | gccgagtgga | tgcgggcgca  | cgcccgagcc | tacaacggcg | 240 |
| tcggsaggag | gagcgaggt   | tcgagtggtt | cagggacaac  | ctccgctacg | tcgacgccca | 300 |
| caacggcgcc | gcgcgagcgg  | gcgtccactc | cttcgcgcctc | gggtcaacc  | gcttcgccga | 360 |
| cctcaccaac | gacgagtacc  | gcccacmeta | cctcggcgctc | aggagcaggg |            |     |

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1500975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Arg Ser Xaa Pro Ser Ser Pro Tyr Leu Ala Ser Leu Pro Val Pro Ala | 1 5 10 15   |
| Ser Arg Arg Arg Trp Ala Pro Pro Pro Arg Arg Ser Arg Arg Arg Arg | 20 25 30    |
| Arg Cys Phe Cys Cys Cys Ser Arg Arg Ser Pro Arg Arg Arg Thr Ala | 35 40 45    |
| Cys Arg Ser Ser Pro Thr Ala Ser Gly Xaa Xaa Xaa Glu Ala Arg Arg | 50 55 60    |
| Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Asn Ala Val | 65 70 75 80 |
| Xaa Arg Arg Ser Ala Gly Ser Arg Cys Ser Gly Thr Thr Ser Ala Thr | 85 90 95    |
| Ser Thr Pro Thr Thr Pro Pro Pro Xaa Arg Ala Ser Thr Pro Ser Ala | 100 105 110 |
| Ser Gly Ser Thr Ala Ser Pro Thr Ser Pro Thr Thr Ser Thr Xaa Pro | 115 120 125 |
| Xaa Thr Ser Ala Ser Gly Ala Gly                                 | 130 135     |

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..116  
(D) OTHER INFORMATION: / Ceres Seq. ID 1500976  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:  
Met Gly Ala Ser Thr Thr Pro Leu Ala Ser Ala Ala Ala Leu Leu Leu  
1 5 10 15  
Leu Leu Leu Ala Pro Leu Ala Ala Ala Ala Asp Ser Met Ser Ile Val  
20 25 30  
Ser Tyr Gly Glu Arg Xaa Xaa Xaa Gly Gly Ala Ala Asp Val Arg Arg  
35 40 45  
Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg Arg Xaa Glu Glu  
50 55 60  
Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr Val Asp Ala His  
65 70 75 80  
Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg Leu Gly Leu Asn  
85 90 95  
Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa Xaa Tyr Leu Gly  
100 105 110  
Val Arg Ser Arg  
115

(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1500977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

Met Ser Ile Val Ser Tyr Gly Glu Arg Xaa Xaa Gly Gly Ala Ala  
1 5 10 15  
Asp Val Arg Arg Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg  
20 25 30  
Arg Xaa Glu Glu Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr  
35 40 45  
Val Asp Ala His Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg  
50 55 60  
Leu Gly Leu Asn Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa  
65 70 75 80  
Xaa Tyr Leu Gly Val Arg Ser Arg  
85

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1500985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

agcacatcga tcagtcgcgt gtctagggtt cctctctcac catagcgccc gctctgtcgc

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ccttcgttca | cctctccttc | ctctcctccc | tgcttgccag  | ggagagggga | agtcagaggc | 120 |
| acggagtggc | gcagagcaga | cgcacgtgaa | ccatngtag   | ctgtccctgt | cgctcgctgc | 180 |
| gtcgtcaacg | aatccacaca | aggaaaggat | ggagaagaag  | ccgaccatcc | tcatgaacag | 240 |
| gtacgagctc | ggcgccacgc | tcgggcaggg | caccttcgcc  | aagggtgacc | acggccggaa | 300 |
| cctcgcgctc | ggcgaaagcg | tgcccatcaa | ggatcatcgac | aaggagaag  | tgatgcgcgt | 360 |
| cggcatgac  | gaccagatca | agcgcgagat | ctccgtcatg  | cgctcgtcc  | gccaccccaa | 420 |
| cgctgctcag | ctgcacgagg | gtgatggcca | gcaagagcaa  | gatatacttc | gccatggagt | 480 |
| acgtc      |            |            |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1500986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | His | Arg | Ser | Val | Ala | Cys | Leu | Gly | Phe | Leu | Ser | His | Ser | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Arg | Ser | Val | Ala | Leu | Arg | Ser | Pro | Leu | Pro | Leu | Leu | Pro | Ala | Cys |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Gln | Gly | Glu | Gly | Lys | Ser | Glu | Ala | Arg | Ser | Gly | Ala | Glu | Gln | Thr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Val | Asn | His | Xaa |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 50  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1500987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Lys | Pro | Thr | Ile | Leu | Met | Asn | Arg | Tyr | Glu | Leu | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Leu | Gly | Gln | Gly | Thr | Phe | Ala | Lys | Val | Tyr | His | Gly | Arg | Asn | Leu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ala | Ser | Gly | Glu | Ser | Val | Ala | Ile | Lys | Val | Ile | Asp | Lys | Glu | Lys | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Met | Arg | Val | Gly | Met | Ile | Asp | Gln | Ile | Lys | Arg | Glu | Ile | Ser | Val | Met |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| Arg | Leu | Val | Arg | His | Pro | Asn | Val | Val | Gln | Leu | His | Glu | Gly | Asp | Gly |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     |     |     | 75  |     |
| Gln | Gln | Glu | Gln | Asp | Ile | Leu | Arg | His | Gly | Val | Arg |     |     | 80  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 85  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     | 90  |     |

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1500988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Arg | Tyr | Glu | Leu | Gly | Arg | Thr | Leu | Gly | Gln | Gly | Thr | Phe | Ala |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Val | Tyr | His | Gly | Arg | Asn | Leu | Ala | Ser | Gly | Glu | Ser | Val | Ala | Ile |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Val | Ile | Asp | Lys | Glu | Lys | Val | Met | Arg | Val | Gly | Met | Ile | Asp | Gln |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Ile | Lys | Arg | Glu | Ile | Ser | Val | Met | Arg | Leu | Val | Arg | His | Pro | Asn | Val |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Val | Gln | Leu | His | Glu | Gly | Asp | Gly | Gln | Gln | Glu | Gln | Asp | Ile | Leu | Arg |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |  |
| His | Gly | Val | Arg |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1500992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| aacatctcct | cacttcacac | cactcccgcc | attgtcctgc | gcctttctgc | accgccacac  | 60  |
| acaccccgct | ccaatccaat | ggcgctctgc | caagccgttc | tcgcggctgc | ggctcctgcgc | 120 |
| gcgctgctcc | cgctcgccct | ctctcgcggg | ctgcggcttg | gccaccaccg | ccagcccgca  | 180 |
| cccgaggccg | cacggtcacg | caccgctcgg | aggtggcgcg | tggtcctcgg | cccacgccac  | 240 |
| cttctacggc | ggcgggcgac | cgctccggac | catggggcga | cggtgtggga | cggaacacct  | 300 |
| tacagccagg | ggtagcgcac | caacacggcg | gcgctgagca | cgcgctctct | caacaacggc  | 360 |
| ctcagctcgc | ggcgctgctt | cgaggtgcgg | tgcgagmcgc | cgggggggcg | cgcccgctcg  | 420 |
| trcmtgcmgg | gctccgtcgt | ggtgacggcc | accaattctt | gc         |             |     |

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Asn | Ile | Ser | Ser | Leu | His | Thr | Thr | Pro | Ala | Ile | Val | Leu | Arg | Leu | Ser |  |
| 1   |     |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Ala | Pro | Pro | His | Thr | Pro | Arg | Ser | Asn | Pro | Met | Ala | Pro | Arg | Gln | Ala |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Leu | Ala | Val | Val | Val | Leu | Ala | Ala | Leu | Leu | Pro | Leu | Ala | Leu | Ser |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Arg | Gly | Leu | Arg | Leu | Gly | His | His | Arg | Pro | Ala | Ala | Pro | Glu | Ala | Ala |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Arg | Ser | Arg | Thr | Ala | Arg | Arg | Trp | Arg | Val | Val | Gly | Arg | Thr | Cys | Gly |  |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |  |
| Leu | Leu | Arg | Arg | Arg | Arg | Arg | Val | Arg | His | His | Gly | Leu | Arg | Pro |     |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Gly | Asn | Leu | Tyr | Ser | Gln | Gly | Tyr | Gly | Thr | Asn | Thr | Ala | Ala | Leu |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |

Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe Glu  
115 120 125  
Val Arg Cys Xaa Ala Ala Gly Gly Gly Arg Ser Xaa Xaa Xaa Gly  
130 135 140  
Ser Val Val Val Thr Ala Thr Asn Phe Cys  
145 150

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1500994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

His Leu Leu Thr Ser His His Ser Arg His Cys Pro Ala Pro Phe Cys  
1 5 10 15  
Thr Ala Thr His Thr Pro Leu Gln Ser Asn Gly Ala Ser Pro Ser Arg  
20 25 30  
Pro Arg Gly Arg Gly Pro Arg Arg Ala Ala Pro Ala Arg Pro Leu Ser  
35 40 45  
Arg Ala Ala Ala Trp Pro Pro Pro Ser Arg Thr Arg Gly Arg Thr  
50 55 60  
Val Thr His Arg Ser Glu Val Ala Arg Gly Pro Arg Pro Thr Pro Pro  
65 70 75 80  
Ser Thr Ala Ala Ala Thr Arg Pro Ala Pro Trp Ala Asp Val Trp Val  
85 90 95  
Arg Gln Pro Leu Gln Pro Gly Val Arg His Gln His Gly Gly Ala Glu  
100 105 110  
His Gly Ala Leu Gln Gln Arg Pro Gln Leu Arg Arg Leu Leu Arg Gly  
115 120 125  
Ala Val Arg Xaa Gly Gly Gly Arg Arg Pro Leu Xaa Xaa Gly Leu  
130 135 140  
Arg Arg Gly Asp Gly His Gln Leu Leu  
145 150

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1500995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Met Ala Pro Arg Gln Ala Val Leu Ala Val Val Leu Ala Ala Leu  
1 5 10 15  
Leu Pro Leu Ala Leu Ser Arg Gly Leu Arg Leu Gly His His Arg Pro  
20 25 30  
Ala Ala Pro Glu Ala Ala Arg Ser Arg Thr Ala Arg Arg Trp Arg Val  
35 40 45  
Val Leu Gly Pro Arg His Leu Leu Arg Arg Arg Arg Val Arg His  
50 55 60  
His Gly Arg Thr Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly  
65 70 75 80  
Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1742:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | His | Arg | Pro | Asn | Ala | Ala | Ala | Pro | Leu | Leu | Ala | Lys | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ala | Thr | Ala | Thr | Pro | Pro | Ala | Xaa | Ala | Xaa | Lys | Tyr | Pro | Phe | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ala | Val | Leu | Ala | Ser | Met | Thr | Ser | Val | Leu | Met | Gly | Tyr | Asn | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Val | Thr | Ser | Gly | Ala | Gln | Ile | Phe | Met | Ala | Glu | Asp | Leu | Gly | Met |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asp | Ala | Gln | Ile | Glu | Val | Leu | Ser | Gly | Val | Ile | Asn | Ile | Tyr | Ser |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Val | Gly | Ala | Leu | Leu | Ala | Gly | Trp | Thr | Ser | Asp | Arg | Leu | Gly | Arg |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Leu | Thr | Ile | Val | Leu | Ala | Asn | Ala | Phe | Phe | Leu | Val | Gly | Pro | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Val | Leu | Met | Gly | Tyr | Asn | Val | Ala | Val | Thr | Ser | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gln | Ile | Phe | Met | Ala | Glu | Asp | Leu | Gly | Met | Ser | Asp | Ala | Gln | Ile | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Ser | Gly | Val | Ile | Asn | Ile | Tyr | Ser | Leu | Val | Gly | Ala | Leu | Leu |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Trp | Thr | Ser | Asp | Arg | Leu | Gly | Arg | Arg | Leu | Thr | Ile | Val | Leu |
|     |     |     |     | 50  |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Asn | Ala | Phe | Phe | Leu | Val | Gly | Pro | Leu |     |     |     |     |     |     |
|     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..528
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| aagacttcgt  | cgctaccacaa | aaaataaagc | agaaaaaaac | agagagtagt | agactacgac  | 60  |
| agcgtccgctc | gaaccggagg  | gtcggaggcg | gaggcgaaga | tgaggaagaa | gctcggcacc  | 120 |
| cggttccccg  | cggtctgaat  | caaaaagata | atgcaagcag | atgagtagtg | tggaagagatt | 180 |
| gcattagcag  | tgctgtttt   | agtctcgagg | gctcttgaat | tgtttttaca | agattttaatt | 240 |
| gaccggactt  | atgaaattac  | tcttcaaaag | ggagcaaaag | cactgaattc | cttccacctg  | 300 |
| aagcaatgtg  | tgaagaggta  | cagttctttt | gatttcttaa | ctgaagttgt | cagcaaggtta | 360 |
| ccagatcttg  | gtgggtctga  | tcatgtgga  | gatgaaagag | tgttacctag | aagaagaaaag | 420 |
| tcaaatggca  | gtgaccacga  | gaatgatgaa | tcaagatcta | gtaaaatggc | tataaganat  | 480 |
| gcaaatacca  | nnccagagg   | gacgtgggar | gggtcgaggc | agagggcg   |             |     |

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Lys | Leu | Gly | Thr | Arg | Phe | Pro | Ala | Ala | Arg | Ile | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Gln | Ala | Asp | Glu | Asp | Val | Gly | Lys | Ile | Ala | Leu | Ala | Val | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Val | Ser | Arg | Ala | Leu | Glu | Leu | Phe | Leu | Gln | Asp | Leu | Ile | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Thr | Tyr | Glu | Ile | Thr | Leu | Gln | Ser | Gly | Ala | Lys | Thr | Leu | Asn | Ser |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | His | Leu | Lys | Gln | Cys | Val | Lys | Arg | Tyr | Ser | Ser | Phe | Asp | Phe | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Glu | Val | Val | Ser | Lys | Val | Pro | Asp | Leu | Gly | Gly | Ala | Asp | Ser | Cys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Asp | Glu | Arg | Val | Leu | Pro | Arg | Arg | Lys | Ser | Asn | Gly | Ser | Asp |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Pro | Glu | Asn | Asp | Glu | Ser | Arg | Ser | Ser | Lys | Met | Ala | Ile | Arg | Xaa | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Thr | Xaa | Xaa | Arg | Gly | Thr | Xaa | Xaa | Gly | Ser | Arg | Gln | Arg | Ala |     |
| 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1746:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ala | Asp | Glu | Asp | Val | Gly | Lys | Ile | Ala | Leu | Ala | Val | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Ser | Arg | Ala | Leu | Glu | Leu | Phe | Leu | Gln | Asp | Leu | Ile | Asp | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Tyr | Glu | Ile | Thr | Leu | Gln | Ser | Gly | Ala | Lys | Thr | Leu | Asn | Ser | Phe |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Leu | Lys | Gln | Cys | Val | Lys | Arg | Tyr | Ser | Ser | Phe | Asp | Phe | Leu | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Val | Val | Ser | Lys | Val | Pro | Asp | Leu | Gly | Gly | Ala | Asp | Ser | Cys | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Glu | Arg | Val | Leu | Pro | Arg | Arg | Arg | Lys | Ser | Asn | Gly | Ser | Asp | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asn | Asp | Glu | Ser | Arg | Ser | Ser | Lys | Met | Ala | Ile | Arg | Xaa | Ala | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Thr | Xaa | Xaa | Arg | Gly | Thr | Xaa | Xaa | Gly | Ser | Arg | Gln | Arg | Ala |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1747:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 538 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..538  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501023  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:  
atccgcctcc gaaccacaga ggccacgacc cactactaca tcagtcacc gccaccgcgc 60  
accgcgagtc cgcgacagac atccgcgccc cgccctcact ctcaactccc agtccccacc 120  
gtgcgcggcac aagcgacgcy acgcagccac gcaggagagc ggaatggccc acggccgcga 180  
ctgccacggc ggggagtaga gcagccgtgc tgcctgctct ctgcctggcg ctggcgctgg 240  
cgctcgggcc ctccgcagcc ggccggggcg gcgactgcca ctcccgccc gtgttcaact 300  
tcggcgactc caactcggac acggcgggcc tgcctcgtct ctccggccc gcaccggcg 360  
ccaacggcag gacctttctt gccatgccc cmggccgcta ctgcgatgt cgctctgta 420  
tcgacttcac cgctgaaacc tgggctgac tcacctcagt gcgtacctga actcgatcgg 480  
aagcaacttc acacagggag ccaactttgc aacagctggt tcactgatca gaagacag  
(2) INFORMATION FOR SEQ ID NO:1748:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 179 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..179  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1501024  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:  
Ile Arg Leu Arg Thr His Glu Ala Thr Thr His Tyr Tyr Ile Ser Pro  
1 5 10 15  
Pro Pro Pro Arg Thr Ala Ser Pro Arg Gln Thr Ser Ala Pro Arg Pro  
20 25 30  
His Ser His Ser Pro Val Pro Thr Val Pro Pro Gln Ala Thr Arg Arg  
35 40 45  
Ser His Ala Gly Arg Gly Lys Trp Pro Arg Pro Arg Leu Pro Arg Arg  
50 55 60  
Gly Val Glu Gln Pro Cys Cys Cys Ser Arg Trp Arg Trp Arg Trp  
65 70 75 80  
Arg Cys Gly Pro Pro Thr Pro Ala Arg Ala Ala Thr Ala Thr Ser Arg  
85 90 95  
Pro Cys Ser Thr Ser Ala Thr Pro Thr Arg Thr Arg Ala Ala Cys His  
100 105 110  
Arg Ser Ser Ala Pro His Arg Arg Pro Thr Ala Gly Pro Ser Ser Ala  
115 120 125  
Cys Pro Xaa Ala Ala Thr Ala Met Val Ala Ser Ser Ser Thr Ser Ser  
130 135 140  
Leu Lys Pro Gly Ala Asp Ser Pro Gln Cys Val Pro Glu Leu Asp Arg  
145 150 155 160  
Lys Gln Leu His Thr Gly Ser Gln Leu Cys Asn Ser Trp Phe Ile Asp  
165 170 175  
Gln Lys Thr  
(2) INFORMATION FOR SEQ ID NO:1749:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 148 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

Pro Pro Pro Asn Pro Arg Gly His Asp Pro Leu Leu His Gln Ser Thr  
1 5 10 15  
Ala Thr Ala His Arg Glu Ser Ala Thr Asp Ile Arg Ala Pro Ala Ser  
20 25 30  
Leu Ser Leu Pro Ser Pro His Arg Ala Ala Thr Ser Asp Ala Thr Gln  
35 40 45  
Pro Arg Arg Glu Arg Glu Met Ala Thr Ala Ala Thr Ala Thr Ala Gly  
50 55 60  
Ser Arg Ala Ala Val Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala  
65 70 75 80  
Leu Arg Pro Ser Asp Ala Gly Ala Gly Gly Asp Cys His Phe Pro Ala  
85 90 95  
Val Phe Asn Phe Gly Asp Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser  
100 105 110  
Leu Phe Gly Ala Ala Pro Pro Pro Asn Gly Arg Thr Phe Phe Gly Met  
115 120 125  
Pro Xaa Gly Arg Tyr Cys Asp Gly Arg Leu Val Ile Asp Phe Ile Ala  
130 135 140  
Glu Thr Trp Gly  
145

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

Met Ala Thr Ala Ala Thr Ala Thr Ala Gly Ser Arg Ala Ala Val Leu  
1 5 10 15  
Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala Leu Arg Pro Ser Asp Ala  
20 25 30  
Gly Ala Gly Gly Asp Cys His Phe Pro Ala Val Phe Asn Phe Gly Asp  
35 40 45  
Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser Leu Phe Gly Ala Ala Pro  
50 55 60  
Pro Pro Asn Gly Arg Thr Phe Phe Gly Met Pro Xaa Gly Arg Tyr Cys  
65 70 75 80  
Asp Gly Arg Leu Val Ile Asp Phe Ile Ala Glu Thr Trp Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1501027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

acccctccag tcaggccgtc ccggccggac gtcaacggag acgtgtccaac ggcggcggtg  
agaagaccca taaccttcta gatttttttc cgtgcctca atggtatctc gggagagggc

60  
120

ccggcgccctc gccggcgagg cgcggaacgg tcgcaggaac tctccgcgga ggccggccaag 180  
cgctcgctcgg cgctggtctc ggagacggcg aagaagtcca aggagatctt ctccgaaacc 240  
gcctccaagt cgcgggagat cgccgctgag gccaccaagc aggcgcgacct cctcgccggc 300  
cagatcaagc acctcgccctc cgacctccct gtgccttcga tcccgcccat ccccgcgatc 360  
ccgcctatcc ccgcgcgtgc ctgctcggtg cccgacggcg ccgagcttga gtgctacggc 420  
atcacgcagc acctccgcga gttcgtcaag ggcgatgacca taaacacctt ccgcgacttc 480  
ccactgc

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

Pro Ser Ser Gln Ala Val Pro Arg Arg Arg Gln Arg Arg Val Asn  
1 5 10 15  
Gly Gly Gly Glu Lys Thr His Asn Leu Leu Asp Phe Phe Pro Leu Pro  
20 25 30  
Gln Trp Ile Ser Gly Arg Gly Pro Gly Pro Ser Pro Ala Arg Arg Arg  
35 40 45  
Thr Val Ala Gly Thr Leu Arg Gly Gly Gly Gln Ala Leu Val Gly Ala  
50 55 60  
Gly Leu Gly Asp Gly Glu Glu Val Gln Gly Asp Leu Leu Arg Asn Arg  
65 70 75 80  
Leu Gln Val Ala Gly Asp Arg Arg  
85

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

Met Asp Leu Trp Glu Arg Ala Arg Ala Phe Ala Gly Glu Ala Ala Asn  
1 5 10 15  
Gly Arg Arg Asn Ser Pro Arg Arg Arg Pro Ser Ala Arg Arg Trp  
20 25 30  
Ser Arg Arg Arg Arg Arg Ser Pro Arg Arg Ser Ser Pro Lys Pro Pro  
35 40 45  
Pro Ser Arg Gly Arg Ser Pro Leu Arg Pro Pro Ser Arg Pro Thr Ser  
50 55 60  
Ser Pro Ala Arg Ser Ser Thr Ser Pro Pro Thr Ser Leu Cys Leu Arg  
65 70 75 80  
Ser Arg Pro Ser Pro Arg Ser Arg Leu Ser Pro Pro Leu Pro Arg Arg  
85 90 95  
Cys Pro Thr Arg Pro Ser Leu Ser Ala Thr Ala Ser Pro Thr Thr Ser  
100 105 110  
Ala Ser Ser Ser Arg Ala  
115

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

Met Val Asp Ala Phe Arg Met His Ile Met Gln Thr Lys Glu Leu Gly  
1 5 10 15

Thr Cys Pro Val Arg Gln Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg  
20 25 30  
Ile Ser Asn Val Tyr Ile Val Ile Val Val Ser Ser Asn Ala Asn Val  
35 40 45  
Ala Cys Xaa Phe Lys Phe Val Val Glu Ala Val Ala Leu Phe Lys Ser  
50 55 60  
Tyr Phe Gly Gly Ala Phe Asp Glu Asp Ala Ile Arg Asn Asn Phe Val  
65 70 75 80  
Leu Ile Tyr Glu Leu Leu Asp Glu Ile Met Asp Phe  
85 90

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1501040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

Met His Ile Met Gln Thr Lys Glu Leu Gly Thr Cys Pro Val Arg Gln  
1 5 10 15  
Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg Ile Ser Asn Val Tyr Ile  
20 25 30  
Val Ile Val Val Ser Ser Asn Ala Asn Val Ala Cys Xaa Phe Lys Phe  
35 40 45  
Val Val Glu Ala Val Ala Leu Phe Lys Ser Tyr Phe Gly Gly Ala Phe  
50 55 60  
Asp Glu Asp Ala Ile Arg Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu  
65 70 75 80  
Asp Glu Ile Met Asp Phe  
85

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 1501058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

accagtcctcc tttacatcca cacacaacgc gaaccacacc acaccacacc acccgacgccc 60  
aacgtccgag accaaaactcc gatccccact atgcgcggcg acgggggaggc gctggcgccg 120  
gccgtccact tctggggcgga gaacccggcc acggaggcg agttctact ggcgcacggc 180  
acggaggggcg agccctctcta ctaccaccag cccgacgcgg gcgcccgccg gctcttcacg 240  
cgcgctggga ggcgccgcgc gcccgadcg cccaggcgcc tcgtgttcat ggtccacggc 300  
tacggcaatg acatcagctg gacgttccag tccacggcg tcttctctgc gcgggtccggg 360  
ttcgctgct tcggggcgga cctccggggc caggccgct cccac

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501059  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:  
Thr Ser Pro Leu Tyr Ile His Thr Gln Arg Ala Pro His His Thr Thr  
1 5 10 15  
Pro Pro Asp Ala Asn Val Arg Asp Gln Thr Pro Ile Pro Thr Met Pro  
20 25 30  
Ala Asp Gly Glu Ala Leu Ala Pro Ala Val His Phe Trp Gly Glu His  
35 40 45  
Pro Ala Thr Glu Ala Glu Phe Tyr Ser Ala His Gly Thr Glu Gly Glu  
50 55 60  
Pro Ser Tyr Phe Thr Thr Pro Asp Ala Gly Ala Arg Arg Leu Phe Thr  
65 70 75 80  
Arg Ala Trp Arg Pro Arg Ala Pro Xaa Arg Pro Arg Ala Leu Val Phe  
85 90 95  
Met Val His Gly Tyr Gly Asn Asp Ile Ser Trp Thr Phe Gln Ser Thr  
100 105 110  
Ala Val Phe Leu Ala Arg Ser Gly Phe Ala Cys Phe Ala Ala Asp Leu  
115 120 125  
Pro Gly His Gly Arg Ser His  
130 135  
(2) INFORMATION FOR SEQ ID NO:1760:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501060  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:  
Pro Val Pro Phe Thr Ser Thr His Asn Ala His His Thr Thr Pro His  
1 5 10 15  
His Pro Thr Pro Thr Ser Glu Thr Lys Leu Arg Ser Pro Leu Cys Arg  
20 25 30  
Arg Thr Gly Arg Arg Trp Arg Arg Pro Ser Thr Ser Gly Ala Ser Thr  
35 40 45  
Arg Pro Arg Arg Arg Ser Ser Thr Arg Arg Thr Ala Arg Arg Ala Ser  
50 55 60  
Pro Pro Thr Ser Pro Arg Pro Thr Arg Ala Pro Gly Gly Ser Ser Arg  
65 70 75 80  
Ala Arg Gly Gly Pro Ala Arg Pro Xaa Gly Pro Gly Arg Ser Cys Ser  
85 90 95  
Trp Ser Thr Ala Thr Ala Met Thr Ser Ala Gly Arg Ser Ser Pro Arg  
100 105 110  
Arg Ser Ser Ser Arg Gly Pro Gly Ser Pro Ala Ser Arg Pro Thr Ser  
115 120 125  
Arg Ala Thr Ala Ala Pro  
130  
(2) INFORMATION FOR SEQ ID NO:1761:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

Met Pro Ala Asp Gly Glu Ala Leu Ala Pro Ala Val His Phe Trp Gly  
1 5 10 15  
Glu His Pro Ala Thr Glu Ala Glu Phe Tyr Ser Ala His Gly Thr Glu  
20 25 30  
Gly Glu Pro Ser Tyr Phe Thr Thr Pro Asp Ala Gly Ala Arg Arg Leu  
35 40 45  
Phe Thr Arg Ala Trp Arg Pro Arg Ala Pro Xaa Arg Pro Arg Ala Leu  
50 55 60  
Val Phe Met Val His Gly Tyr Gly Asn Asp Ile Ser Trp Thr Phe Gln  
65 70 75 80  
Ser Thr Ala Val Phe Leu Ala Arg Ser Gly Phe Ala Cys Phe Ala Ala  
85 90 95  
Asp Leu Pro Gly His Gly Arg Ser His  
100 105

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..503

(D) OTHER INFORMATION: / Ceres Seq. ID 1501090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

aaactcaacg agtcccatatt tgccgaaggct tcggaggtacc aaactggcga attgcgacgt 60  
tgccggaatt gtaatggcaa taattccttc ctcttcgtt cccatttct cctctttcta 120  
ggtttctacc cctcatcggt cctcgtccca cgccatggt gaggtgaag caggtaaa 180  
tctcggtaaa gaaggacgtg gattcgtaca caatccgcgg cactaacaag gtcgtccatg 240  
tgggcgactg cgtgctgatg cgggcgtcgg actcggacaa gcacgcgtat gtrgcgcggg 300  
tggaagaagt ggargccgac ggaacgggca gstgncgggt rcaggtrcgc tggtaactacc 360  
gccttgagga atccaaggcg ggtcgccggc agttccacgg cgccaaggag cttttcttt 420  
ccgatcattt cgacctacag arcgccacca ccatcgaggg gaaatgtgtt gtccactctt 480  
tcaagaacta cccaagcgtt gat

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

Met Val Arg Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp  
1 5 10 15  
Ser Tyr Thr Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys  
20 25 30  
Val Leu Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg  
35 40 45  
Val Gly Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa  
50 55 60  
Arg Trp Tyr Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe  
65 70 75 80  
His Gly Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa

85 90 95  
Ala His Thr Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr  
100 105 110  
Thr Lys Leu Asp  
115

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1501092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp Ser Tyr Thr  
1 5 10 15  
Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys Val Leu Met  
20 25 30  
Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg Val Glu Lys  
35 40 45  
Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa Arg Trp Tyr  
50 55 60  
Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe His Gly Ala  
65 70 75 80  
Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa Ala His Thr  
85 90 95  
Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr Thr Lys Leu  
100 105 110  
Asp

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1501093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg Val Glu  
1 5 10 15  
Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa Arg Trp  
20 25 30  
Tyr Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe His Gly  
35 40 45  
Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa Ala His  
50 55 60  
Thr Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr Thr Lys  
65 70 75 80  
Leu Asp

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 547 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..547  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501115  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:  
acgccaccgc caccctccacc tctcgaaaac cgccgcgacc gatcgagcga abwnccttc 60  
ccgcgcgcgac gccgaaaccc tagctcctct tacgccatgg ccaccgtgtc gctcactccg 120  
caggcggtct tctccaccga gtcgcggcgc gccctggett ctgccaccat cctcgcgttc 180  
ccgccaaact tcgtacgccca gctcagcacc aaggcacgac gcaactgcag caacatcggc 240  
gtcgcgcaga tcgtcgcgcg cgctgtgtcc gactgcctcg ctgctcgccg cctccgcggs 300  
cgcgngatgtc agcgcaattc ctaacgctaa ggttgccgas cgtccgcgtg cgtattggcc 360  
gagcgtaacc tgctcggtc cgcgcgcagc ctgcgcgtcc acgcggggga raggtckgga 420  
agaagggatag ccacgggatgc tatcaccacg ccggtagtga acacgtcgcc ctactgggtc 480  
aacaactcgc aagagctaat cgactttaan gaggggargc atgctagctt cgagtatggg 540  
aggtatk  
(2) INFORMATION FOR SEQ ID NO:1767:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501116  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:  
Thr Pro Pro Pro Pro Pro Pro Arg Asn Arg Arg Asp Arg Ser Ser  
1 5 10 15  
Glu Xaa Xaa Phe Pro Arg Arg Arg Arg Asn Pro Ser Ser Ser Tyr Ala  
20 25 30  
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser  
35 40 45  
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe  
50 55 60  
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly  
65 70 75 80  
Val Ala Gln Ile Val Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg  
85 90 95  
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser  
100 105  
(2) INFORMATION FOR SEQ ID NO:1768:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501117  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:  
Arg His Arg His Leu His Leu Leu Glu Thr Ala Ala Thr Asp Arg Ala  
1 5 10 15  
Xaa Xaa Pro Ser Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro  
20 25 30  
Trp Pro Pro Cys Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 35                                                              | 40  | 45  |
| Ala Ala Pro Trp Leu Leu Pro Ser Ser Ala Ser Arg Gln Thr Ser     |     |     |
| 50                                                              | 55  | 60  |
| Tyr Ala Ser Ser Ala Pro Arg His Asp Ala Thr Ala Thr Ser Ala     |     |     |
| 65                                                              | 70  | 75  |
| Ser Arg Arg Ser Ser Pro Pro Arg Gly Pro Thr Ala Ser Leu Leu Ala |     |     |
| 85                                                              | 90  | 95  |
| Ala Ser Ala Xaa Arg Xaa Val Ser Ala Ile Pro Asn Ala Lys Val Ala |     |     |
| 100                                                             | 105 | 110 |
| Xaa Arg Pro Pro Ser Tyr Trp Pro Ser Val Thr Cys Ser Ala Pro Thr |     |     |
| 115                                                             | 120 | 125 |
| Pro Ala Ser Pro Ser Thr Arg Gly Xaa Gly Xaa Glu Glu Gly         |     |     |
| 130                                                             | 135 | 140 |

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1501118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser |  |
| 1 5 10 15                                                       |  |
| Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe |  |
| 20 25 30                                                        |  |
| Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly |  |
| 35 40 45                                                        |  |
| Val Ala Gln Ile Val Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg     |  |
| 50 55 60                                                        |  |
| Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser                     |  |
| 65 70 75                                                        |  |

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 921 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1501119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| artagcttcc cwcerrcttc crggggctcc gcrctccgc tagtccgcgc cggcgccacg    | 60  |
| gcccggctcg gaggggcggtt tgggggaggc cgaacgganc gccagcggtt ccgtttggtt  | 120 |
| gcggtggagg cgaactgctg ctggagcggt acccggtttt cctccgttca ctagcgctcg   | 180 |
| cgactgtagt atgcttggtt agttgctctg ccagatcccc agcccagcgc cctccgcatt   | 240 |
| gatccacgcg gtgatggtga tcagcaccca ggccaaagccc cgcccttctca agttctacag | 300 |
| tttccagcca cccgagaagc atcaggacct cgtccgctgt gtcttccaat tactctctgc   | 360 |
| aaggcccgag agcgcgagca attttgtcaa ggtggaactc attctttggc cgggaaacaaa  | 420 |
| aatgtgtctac aagcattttg gccacactat actttgtttt tgtotttgat agctctcgaga | 480 |
| acgagcttgc catgctcgac ctgcgtacaag tgtttgttga aacattggac agatgcttca  | 540 |
| agaatgtatg cgagcttgac atcgtattta acttcaacaa cgtgcacacg attttggtgt   | 600 |
| agatgatatc ggggggacag gtgatcgaaa caagttcaga agctataatg aaattctgtg   | 660 |
| aagagattga aaggctggag aaacaatcga gcacaaccag ctctcatacc aagtcgatta   | 720 |
| cagagcggtt tacccgttga gtttccactc gtttccagaa caatgtgaga ttttaaggtgt  | 780 |
| gaacagaact gagataact attcagttcc attttagttc tccgataaga ccttgtatgc    | 840 |

ccccgcccc cggtctgtatt ctgtaagcct gtaacctgga tatgaatgcg gcactctgcag 900  
tccaataata ctgcctgcgt t

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1501120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Met Ile Xaa Ala Val Met Val Ile Ser Thr Gln Ala Lys Pro Arg Leu  
1 5 10 15  
Leu Lys Phe Tyr Ser Phe Gln Pro Pro Glu Lys His Gln Asp Leu Val  
20 25 30  
Arg Cys Val Phe Gln Leu Leu Ser Ala Arg Pro Glu Ser Ala Ser Asn  
35 40 45  
Phe Val Lys Val Asp Ser Ile Phe Gly Pro Gly Thr Lys Met Val Tyr  
50 55 60  
Lys His Leu Gly His Thr Ile Leu Cys Phe Cys Leu  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met Val Ile Ser Thr Gln Ala Lys Pro Arg Leu Leu Lys Phe Tyr Ser  
1 5 10 15  
Phe Gln Pro Pro Glu Lys His Gln Asp Leu Val Arg Cys Val Phe Gln  
20 25 30  
Leu Leu Ser Ala Arg Pro Glu Ser Ala Ser Asn Phe Val Lys Val Asp  
35 40 45  
Ser Ile Phe Gly Pro Gly Thr Lys Met Val Tyr Lys His Leu Gly His  
50 55 60  
Thr Ile Leu Cys Phe Cys Leu  
65 70

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1501122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

Met Leu Asp Leu Val Gln Val Phe Val Glu Thr Leu Asp Arg Cys Phe  
1 5 10 15  
Lys Asn Val Cys Glu Leu Asp Ile Val Phe Asn Phe Asn Lys Leu His

(2) INFORMATION FOR SEO ID NO:1774:

(A) LENGTH: 352 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..352  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501123

|            |             |             |             |             |              |     |
|------------|-------------|-------------|-------------|-------------|--------------|-----|
| acagagggat | cgtcatctgc  | ccccaccaca  | actgtctccag | atccaggcga  | ggcaccggcaac | 60  |
| ggcagccggc | ccgaacccaag | ccgcgtttct  | ctctctctct  | gtcgtctccct | catcgcgcgc   | 120 |
| gacgtgacaa | cgaacacgca  | cgcgcgcgcga | tattgacgtc  | gtccaaagca  | cgcaggaggccc | 180 |
| gcgaactaaa | tcgcgttcgt  | cgcgggtctg  | sgthggccgc  | aatgggctcc  | ctcgatcagc   | 240 |
| ctctggggca | gacggtgtgcc | ggcccgcgac  | cggactacgc  | cctagcgcaag | ctccgcgaagt  | 300 |
| actcgtctct | ctcgcctctc  | tgctctctgt  | cgtcatccat  | ctctagctcgc | gc           |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) **FEATURE:**

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501124

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gly | Ile | Val | Ile | Arg | Pro | Thr | His | Asn | Cys | Ser | Arg | Ser | Arg | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Thr | Ala | Arg | Gln | Pro | Gly | Gln | Pro | Lys | Pro | Val | Phe | Ser | Ser | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Ser | Val | Pro | His | Ser | Pro | Arg | Arg | Asp | Lys | Thr | Thr | Arg | Arg | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Xaa | Xaa | Xaa | Ser | Ser | Lys | Ala | Arg | Arg | Gly | Gln | Pro | Thr | Asn | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Arg | Pro | Gly | Leu | Val | Val | Ala | Gly | Met | Gly | Leu | Asp | Gln | Leu |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Trp | Asp | Glu | Thr | Val | Ala | Gly | Pro | Arg | Pro | Asp | Ser | Gly | Leu | Gly | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Leu | Arg | Lys | Tyr | Ser | Ser | Phe | Ser | Pro | Ser | Ser | Ser | Ser | Ser | Ser | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Leu | Ala | Pro |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1501137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acaaacgaac | aaggcattaa | tctcctccaa | tctccagtg  | atccgggga  | accaaataca | 60  |
| atcagccctt | tcttttgcta | cggttttgta | tttcatcgtg | tcgcccaga  | aaatcgaag  | 120 |
| aacgcgcgcg | cacggccgcg | aacaaagcaa | agcaggcctc | cggtcccctg | aactgaattc | 180 |
| agaagtccac | aacgcaccca | gcacagacag | aagaccctcg | ccggacgctc | gctctcgccg | 240 |
| gggacaaact | aatcccaggg | ccaggatggc | ccgctacgat | cgcgcgatca | ccgtgttctc | 300 |
| accgcacggc | cacctcttcc | aggtcgagta | cgcctcagag | gcgctccgca | agggcaaccg | 360 |
| cgctgtcggc | gtccgcggcg | tcgacaccgt | cgctctcggc | gtcgcagaag | agtcaccccc | 420 |
| caagctccag | gactccaggt | ccgtcgcgaa | gatcgtkagc | ctggacaccc | acategc    |     |

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Thr | Asn | Lys | Ala | Leu | Ile | Ser | Ser | Asn | Pro | Pro | Val | Ile | Pro | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Asn | Gln | Ile | Lys | Ser | Ala | Leu | Ser | Phe | Ala | Thr | Val | Leu | Tyr | Phe | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Val | Ser | Pro | Lys | Lys | Ile | Glu | Gly | Thr | Arg | Arg | His | Arg | Pro | Gln | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Lys | Ala | Gly | Leu | Arg | Leu | Pro | Glu | Leu | Thr | Ser | Glu | Val | Thr | Asn |

(2) INFORMATION FOR SEQ ID NO:1779:

(A) LENGTH: 442 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1501139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| atcaatgactt | cttctcaggcg | acggtagacc | gttttagact  | ctcaggcgac | tgcacacacg | 60  |
| ggccacgcgt  | tactccggcg  | cgcgcgccag | tctctgagct  | agtcagctac | ttaatgatca | 120 |
| gcattcagta  | gcattccgcga | gattacaagg | ngcgcgggcg  | atggcggtgg | cgcgcttccc | 180 |
| ctctcgcgcg  | ctcttcggcg  | ctctcttgct | agtagtaata  | aggagagcct | tctctcgggt | 240 |
| ggtgcgcatt  | ctctccgcag  | cccgcggtga | agctcccceag | aggaaagcct | tgcgccctcc | 300 |
| ttgcgcaggt  | caccgcggcg  | tgcgccactc | gctgcccccg  | cagaagcgcg | agactcttca | 360 |
| gtcgctcgat  | ctgtggggcg  | cggaacaact | cctgggtgct  | ctcaagcccg | tggagaggtc | 420 |
| ctgcgcagcc  | cagactacgt  | gc         |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1501140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1  | Ser | Cys | Ile | Leu | His | Gly | Asp | Gly | Asp | Gln | Phe | Glu | Leu | Leu | Arg | Gln |
|    |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
|    | Leu | Gln | Thr | Arg | Ala | Thr | Leu | Tyr | Cys | Pro | Ala | Gly | Gly | Ser | Ser | Arg |
|    |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
|    | Ser | Ser | Gln | Leu | Leu | Asn | Asp | Gln | Leu | Ala | Arg | Ala | Ser | Xaa | Arg | Leu |
|    |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
|    | Gln | Xaa | Ala | Ala | Gly | Met | Ala | Val | Ala | Ala | Phe | Pro | Ser | Cys | Gly | Ala |
|    |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| 65 | Phe | Ala | Pro | Pro | Cys | Leu | Val | Ser | Thr | Arg | Arg | Ala | Phe | Ser | Ser | Val |
|    |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
|    | Val | Ala | Met | Ala | Ser | Ala | Ala | Pro | Val | Arg | Ala | Pro | Ser | Arg | Lys | Pro |
|    |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
|    | Phe | Ala | Pro | Pro | Arg | Glu | Val | His | Arg | Pro | Val | Ala | His | Ser | Leu | Pro |
|    |     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
|    | Pro | Gln | Lys | Arg | Glu | Ile | Phe | Glu | Ser | Leu | Xaa | Ser | Trp | Ala | Ala | Asp |
|    |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Asn Ile Leu Val Leu Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln  
130 135 140  
Thr Thr Cys  
145

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Val | Ala | Ala | Phe | Pro | Ser | Cys | Gly | Ala | Phe | Ala | Pro | Pro | Cys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Val | Ser | Thr | Arg | Arg | Ala | Phe | Ser | Ser | Val | Val | Ala | Met | Ala | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Ala | Pro | Val | Arg | Ala | Pro | Ser | Arg | Lys | Pro | Phe | Ala | Pro | Pro | Arg |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Glu | Val | His | Arg | Pro | Val | Ala | His | Ser | Leu | Pro | Pro | Gln | Lys | Arg | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ile | Phe | Glu | Ser | Leu | Xaa | Ser | Trp | Ala | Ala | Asp | Asn | Ile | Leu | Val | Leu |  |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Lys | Pro | Val | Glu | Arg | Ser | Trp | Gln | Pro | Gln | Thr | Thr | Cys |     |     |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1501142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

|            |            |            |             |             |             |     |
|------------|------------|------------|-------------|-------------|-------------|-----|
| atgcccgcgn | gtcctctcct | ctcctccccg | gcctcttcac  | tcacacacg   | aaccccacgc  | 60  |
| aggcagcagc | acggcgcaac | gcaaggaagg | cacaaacact  | annngccggg  | catggcgagc  | 120 |
| cgggcgagac | tgagagaagg | cgggccggcg | aggaaggagc  | ccggcaagggt | gccgtcgccg  | 180 |
| ctgtaccgcg | agcagcargg | ggagcgggag | tnngtgccct  | ggctcgtccc  | cgctcatttc  | 240 |
| gtgcgcagca | tcaccgtctt | cgctcgtacc | atgtacgccca | acaactgcgc  | cgcgcgcgac  | 300 |
| accaacaagt | cgctgcggcg | cttcctcgmm | cgcttctcct  | tcacgcgcgt  | gcgacagaaac | 360 |
| ccgctcttcg | ggccctcttc | cgccacgctc | accaagatgg  | gggcctcggt  | gtgggagaag  | 420 |
| gtgggtgcac | gccaccaggg | ctggcgccct | ctctccagca  | tgtk        |             |     |

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1501143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Ile Ala Arg Xaa Pro Leu Leu Ser Ser Pro Ala Pro Ser Leu His Gln

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Arg Thr Pro Arg Arg Gln Gln His Ala Gln Xaa Gln Gly Arg His Lys | 20  | 25  | 30  |
| His Xaa Xaa Pro Gly Met Ala Thr Arg Ala Asp Val Glu Lys Gly Gly | 35  | 40  | 45  |
| Pro Ala Arg Lys Glu Pro Gly Lys Val Pro Ser Pro Leu Tyr Pro Gln | 50  | 55  | 60  |
| His Xaa Gly Glu Arg Glu Xaa Val Pro Trp Leu Val Pro Val Ile Phe | 65  | 70  | 75  |
| Val Ala Ser Ile Thr Val Phe Val Val Thr Met Tyr Ala Asn Asn Cys | 85  | 90  | 95  |
| Xaa Ala Arg Asp Thr Asn Lys Cys Val Ala Arg Phe Leu Xaa Arg Phe | 100 | 105 | 110 |
| Ser Phe Gln Pro Leu Arg Gln Asn Pro Leu Phe Gly Pro Ser Ser Ala | 115 | 120 | 125 |
| Thr Leu Thr Lys Met Gly Ala Leu Val Trp Glu Lys Val Val His Arg | 130 | 135 | 140 |
| His Gln Gly Trp Arg Leu Leu Ser Ser Met                         | 145 | 150 |     |

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Ser Pro Xaa Val Leu Ser Ser Pro Pro Arg Pro Leu His Ser Thr Asn | 1   | 5   | 10  | 15  |
| Glu Pro His Ala Gly Ser Ser Thr Arg Xaa Arg Lys Glu Gly Thr Asn | 20  | 25  | 30  | 35  |
| Thr Xaa Xaa Arg Ala Trp Arg Arg Gly Arg Thr Trp Arg Arg Ala Gly | 40  | 45  | 50  | 55  |
| Arg Arg Gly Arg Ser Pro Ala Arg Cys Arg Arg Arg Cys Thr Arg Ser | 60  | 65  | 70  | 75  |
| Thr Xaa Gly Ser Gly Ser Xaa Cys Pro Gly Ser Ser Pro Ser Ser Ser | 80  | 85  | 90  | 95  |
| Ser Pro Ala Ser Pro Ser Ser Ser Ser Pro Cys Thr Pro Thr Thr Xaa | 100 | 105 | 110 | 115 |
| Pro Arg Ala Thr Pro Thr Ser Ala Ser Pro Ala Ser Ser Xaa Ala Ser | 120 | 125 | 130 | 135 |
| Pro Ser Ser Arg Cys Asp Arg Thr Arg Ser Ser Gly Pro Pro Pro Pro | 140 | 145 | 150 |     |
| Arg Ser Pro Arg Trp Gly Pro Trp Cys Gly Arg Arg Trp Cys Thr Ala |     |     |     |     |
| Thr Arg Ala Gly Ala Ser Ser Pro Ala Cys                         |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

[illegible]

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..480

D) OTHER INFORMATION: / Ceres Seq. ID 1501163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

|             |             |             |             |             |            |     |
|-------------|-------------|-------------|-------------|-------------|------------|-----|
| ctctgcgcct  | accatcgcct  | gaccgacgcg  | ccctcgtttt  | ctctgaaaaac | gaaggctcgc | 60  |
| gtcttcgcct  | ctcgcgcaaaa | aggggaaaaa  | aggagagata  | acacacacac  | acacaaaacc | 120 |
| caatccctgc  | cgccgcgcgat | ggaccgcgtta | ctgcgcggct  | ctcgccgcaca | ctctctccgc | 180 |
| ctcgcctgcg  | cgcagcggcga | gaagcgcgcg  | gtgtcgtact  | gcgcgcacc   | ggaatgtggc | 240 |
| aaactactact | acggcgacgg  | ccatccgatg  | atccgcgcacc | gcctccgat   | gacgcacttg | 300 |
| ctgctggcgc  | ctcagcgcct  | ctcaaacatg  | atgcaggttg  | acccgccaaa  | cccgcccgcc | 360 |
| gacgcgcacc  | ctctgcgcctt | ccacgcgcag  | gactaacatc  | acttctcgct  | ctctgcacg  | 420 |
| cgccgaacac  | acgacgcgta  | gattccgcgt  | ctaacgcctg  | cgaggactgc  |            | 480 |

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..114
```

D) OTHER INFORMATION: / Ceres Seq. ID 1501164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met	Asp	Pro	Ser	Ser	Ala	Gly	Ser	Gly	Gly	Asn	Ser	Leu	Pro	Ser	Val
1			5					10					15		
Gly	Pro	Asp	Gly	Gln	Lys	Arg	Arg	Val	Cys	Tyr	Phe	Tyr	Asp	Pro	Asp
			20				25						30		
Val	Gly	Asn	Tyr	Tyr	Tyr	Gly	Gln	Gly	His	Pro	Met	Lys	Pro	His	Arg
		35					40					45			

Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln  
50 55 60  
Met Gln Val Tyr Arg Pro Asn Pro Ala Asp Arg Asp Leu Cys Arg  
65 70 75 80  
Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu  
85 90 95  
Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu  
100 105 110  
Asp Cys

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

Met Lys Pro His Arg Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr  
1 5 10 15  
Gly Leu Leu Asn Gln Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp  
20 25 30  
Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg  
35 40 45  
Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg  
50 55 60  
Phe Asn Val Gly Glu Asp Cys  
65 70

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1501166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln Met Gln  
1 5 10 15  
Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg Phe His  
20 25 30  
Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu Thr Gln  
35 40 45  
Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu Asp Cys  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -  
(B) LOCATION: 1..520  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501167

atctcaactt	ctctctctct	gcgtccgcga	tgtctctcgt	ttctctctct	ctgtcttgtt	60
tttgttctgt	cgatgtcgaa	aactctctcc	agaccagact	tcgtctgtgt	tcgggttgat	120
ccagatctca	cggtcccact	cgagggaagc	agacggatag	gagccggagg	ccgaggttgc	180
aaataaatgt	cgggagcatg	cagcgcggtg	acgaacgggg	ccggataaac	gctgtgtctg	240
cattgcgcga	stctctcgat	ctgtctgaac	ctgtggccctt	ctctagccctt	tcattggagc	300
cgtagggcgg	cgctcccgat	gtgcgcagct	ccgcgtctggg	ctctagcggta	aaagggggcg	360
gagctgagct	cgatgctctc	cgatgctctc	cgatgctctc	cgatgctctc	cgatgctctc	420
agatagacca	cgcccgccag	gcagagagcc	ggggcggggt	tacagagcta	tccccagcta	480
gtgaacatct	ctcatctctt	cgctattctc	ttctctctct			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..155  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501168

1	Leu	Thr	Phe	Phe	Leu	Ala	Ala	Ser	Ala	Met	Leu	Ser	Leu	Ser	Phe	Ser
				5						10					15	
Leu	Leu	Cys	Phe	Cys	Val	Val	Asp	Val	Glu	Asn	Ser	Phe	Gln	Thr	Lys	
			20					25					30			
Leu	Arg	Leu	Leu	Ser	Ala	Cys	Thr	Ser	Pro	His	Gly	Pro	Arg	Arg	Gly	
		35					40					45				
Arg	Arg	Arg	Asp	Arg	Arg	Arg	Arg	Arg	Leu	Gln	Lys	Met	Val	Gly		
	50					55				60						
Ser	Met	Gln	Ala	Val	Asp	Pro	Ala	Gly	Arg	Ile	Ser	Ala	Leu	Leu	Ala	80
65				70					75							
Leu	Arg	Xaa	Ser	Ser	Pro	Cys	Ser	Ser	Arg	Trp	Pro	Cys	Ser	Ala	Leu	
			85						90				95			
Ser	Leu	Ala	Arg	Val	Ala	Gly	Ala	Ser	Asp	Val	Ala	Ala	Ser	Ala	Leu	
			100					105					110			
Gly	Leu	Ala	Gly	Lys	Gly	Glu	Gly	Gly	Val	Ser	Xaa	Ser	Thr	Gly		
		115					120				125					
Ala	Gly	Arg	Leu	Ala	His	Gly	Arg	His	Thr	Lys	Glu	Asp	Ser	His	Ala	
	130					135					140					
Pro	Asp	Ala	Gly	Gly	Arg	Gly	Gly	Cys	Thr	Ser						
145					150					155						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501169

Met Leu Ser Leu Ser Phe Ser Leu Leu Cys Phe Cys Val Val Asp Val  
1 5 10 15  
Glu Asn Ser Phe Gln Thr Lys Leu Arg Leu Leu Ser Ala Cys Thr Ser

20	25	30
Pro His Gly Pro Arg Arg Gly Arg Arg Asp Arg Arg Arg Arg		
35	40	45
Arg Leu Gln Lys Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly		
50	55	60
Arg Ile Ser Ala Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser		
65	70	75
Arg Trp Pro Cys Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser		
85	90	95
Asp Val Ala Ala Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly		
100	105	110
Gly Val Ser Xaa Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His		
115	120	125
Thr Lys Glu Asp Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys		
130	135	140
Thr Ser		
145		

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly Arg Ile Ser Ala	
1 5 10 15	
Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser Arg Trp Pro Cys	
20 25 30	
Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser Asp Val Ala Ala	
35 40 45	
Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly Val Ser Xaa	
50 55 60	
Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His Thr Lys Glu Asp	
65 70 75 80	
Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys Thr Ser	
85 90	

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1501203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

arctgcagcc agagccaccc acottatcgt catcctcgt cgetcctcat cggcagcgcc	60
tctctctctt cctctctctt cccccaccgt gccgacatgg ctgcgcaaga agagaagacc	120
gctgttttg ttgctgtgc tgccgatgct gcgacagagg agcctacgcc ggcggsgagc	180
agcaacctca gccggtggg gggcgcgca gggcaggacc atcgcgcccc ggcggggctc	240
gcaccaacctc ttgcattct ccaccatgat gaaccttctc aatgacctta gcatcaagga	300
gatggcagag cagatgcgca aggaccggcg gttcaccgag atggcggasa gctgcagaag	360
acgggtgggt ccccgcgca gcaacagcag cagcaggcgc ggcagcagca gcagcagctg	420
gaccgcgaga agtacgtggc gacgatgcag cagctgatgc ag	

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Xaa	Cys	Ser	Gln	Ser	His	Pro	Pro	Tyr	Arg	His	Pro	Arg	Ser	Leu	Leu	
1																
Ile	Ala	Ser	Ala	Ser	Ser	Ser	Ser	Ser	Phe	Phe	Pro	Thr	Ala	Ala	Asp	
Met	Ala	Ala	Gln	Glu	Glu	Lys	Thr	Ala	Val	Val	Val	Ala	Ala	Ala	Ala	
Asp	Val	Ala	Thr	Glu	Glu	Pro	Thr	Pro	Ala	Xaa	Ser	Ser	Asn	Leu	Ser	
Arg	Leu	Gly	Arg	Arg	Ala	Gly	Gln	Asp	His	Arg	Arg	Pro	Ala	Gly	Leu	
65																
Arg	Gln	Pro	Leu	Arg	Glu	Leu	Leu	His	His	Asp	Glu	Pro	Ser	Gln		

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

Xaa	Ala	Ala	Arg	Ala	Thr	His	Leu	Ile	Val	Ile	Leu	Ala	Arg	Ser	Ser	
1																
Ser	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Ser	Ser	Pro	Pro	Leu	Pro	Thr		
Trp	Leu	Arg	Lys	Lys	Arg	Arg	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Pro		
Met	Ser	Arg	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Xaa	Ala	Ala	Thr	Ser	Ala	
Gly	Trp	Gly	Gly	Ala	Gln	Gly	Arg	Thr	Ile	Gly	Ala	Arg	Arg	Gly	Ser	
65																
Ala	Asn	Pro	Phe	Asp	Phe	Ser	Thr	Met	Met	Asn	Leu	Leu	Asn	Asp	Pro	
Ser	Ile	Lys	Glu	Met	Ala	Glu	Gln	Ile	Ala	Lys	Asp	Pro	Ala	Phe	Thr	
Glu	Met	Ala	Xaa	Ser	Cys	Arg	Arg	Arg	Trp	Cys	Pro	Arg	Gly	Ser	Asn	
Ser	Ser	Ser	Arg	Arg	Gly	Ser	Ser	Ser	Ser	Ser	Trp	Thr	Arg	Arg	Ser	
130																
Thr	Trp	Arg	Arg	Cys	Ser	Ser										

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..103  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501206  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:  
Met Ser Arg Gln Arg Ser Leu Arg Arg Arg Xaa Ala Ala Thr Ser Ala  
1      5      10      15  
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser  
20      25      30  
Ala Asn Pro Phe Asp Phe Ser Thr Met Met Asn Leu Leu Asn Asp Pro  
35      40      45  
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr  
50      55      60  
Glu Met Ala Xaa Ser Cys Arg Arg Arg Trp Cys Pro Arg Gly Ser Asn  
65      70      75      80  
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Ser Trp Thr Arg Arg Ser  
85      90      95  
Thr Trp Arg Arg Cys Ser Ser  
100

(2) INFORMATION FOR SEQ ID NO:1798:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 509 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..509  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

aataaaatcgc ggaattccca acgccgcacc ttcaaccgcgc ggctccccag tccaatccaa 60  
cccaaacccca gtccggcgac gggtccgggc agcgcgcgat cggatcgctc cgggttcggc 120  
ttctctgtcga acggcgcgga ttcttgcgcc cgatcggagg gcgtgagctg cggcgactcg 180  
gcgtctgac tctgtcggct ggtttcttct tgggatargg gtgggatgga cggggaagcg 240  
atccgagtg gtggcgggcaa ctggcgccgc gctactctc ccggcgccgc caccgmaccc 300  
gccatcacca tgcaggatcc gaaccagaa cagaaccaga accagaacca gaaccaaagc 360  
cagttctgt tcagcgccaa ctccacggcg ctgcagctgt tcggaagcgc cgcggtcccc 420  
acggttggtc ctgctggtta tataavttac actgggaaac acccaccttc ctgttatgaa 480  
ccaagcaagt acttcaaaaca tcggcgacg

(2) INFORMATION FOR SEQ ID NO:1799:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 169 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..169  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Asn Lys Ser Arg Asn Ser Gln Arg Arg Thr Phe Thr Ala Gly Leu Pro  
1      5      10      15  
Ser Pro Ile Gln Pro Asn Pro Ser Pro Ala Thr Val Pro Gly Ser Ala  
20      25      30  
Arg Ser Asp Arg Arg Gly Phe Gly Phe Ser Ser Asn Gly Ala Asp Ser  
35      40      45  
Cys Pro Arg Ser Glu Gly Xaa Gly Cys Gly Xaa Ser Ala Ser Asp Leu

50	55	60
Leu Arg Ser Ala Ser Ser Trp Xaa Xaa Ser Gly Met Asp Gly Glu Ala		
65	70	75
Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala Tyr Leu Ser Gly Ala		80
	85	90
Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro Asn Gln Asn Gln Asn		95
	100	105
Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu Phe Ser Ala Asn Ser		110
	115	120
Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val Pro Thr Val Gly Pro		125
	130	135
Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro Pro Ser Cys Tyr Glu		140
145	150	155
Pro Ser Lys Tyr Phe Lys His Arg Arg		160
	165	

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

Ile Asn Arg Gly Ile Pro Asn Ala Ala Pro Ser Pro Pro Gly Ser Pro		
1	5	10
Val Gln Ser Asn Pro Thr Pro Val Arg Arg Phe Arg Ala Ala Arg		15
	20	25
Asp Arg Ile Val Ala Gly Ser Ala Ser Arg Arg Thr Ala Arg Ile Pro		30
	35	40
Ala Pro Asp Arg Arg Ala Xaa Ala Ala Ala Xaa Arg Leu Ile Cys		45
	50	55
Cys Gly Arg Leu Leu Leu Gly Xaa Xaa Val Gly Trp Thr Gly Lys Arg		60
65	70	75
Ser Gly Trp Val Ala Ala Thr Trp Arg Pro Pro Thr Ser Pro Ala Pro		80
	85	90
Pro Pro Xaa Pro Pro Ser Pro Cys Arg Ile Arg Thr Arg Thr Arg Thr		95
	100	105
Arg Thr Arg Thr Arg Thr Lys Ala Ser Ser Cys Ser Ala Pro Thr Pro		110
	115	120
Arg Arg Cys Ser Cys Ser Glu Xaa Pro Arg Ser Pro Arg Leu Val Leu		125
	130	135
Leu Val Ile		140
145		

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

Met Asp Gly Glu Ala Ile Arg Met Gly Gly Asn Leu Ala Pro Ala		
1	5	10
		15

Tyr Leu Ser Gly Ala Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro  
20 25 30  
Asn Gln Asn Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu  
35 40 45  
Phe Ser Ala Asn Ser Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val  
50 55 60  
Pro Thr Val Gly Pro Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro  
65 70 75 80  
Pro Ser Cys Tyr Glu Pro Ser Lys Tyr Phe Lys His Arg Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

aacgggaactt	agctgcgag	cgcacaagc	cccacgcgcg	ctcccatcaa	gcggcgctaa	60
aggtttctctc	gcccgcaacg	cgatgccgaa	gaacaaggga	aaggaggcca	agaaccggaa	120
gcggggcgaag	aacgargcgg	acgacgagaa	gcgggagctg	gntgttcaag	gaggacgggc	180
aggagtacgc	gcaggtgacg	cgatgctggg	gcaacggccg	ctcgaggcgc	ccgtcttctc	240
gaacaccgcg	tccgatcttt	gcccagaagg	tctacttggg	catcaataag	caaactcttc	300
ccctcaaaact	gattgtgggt	ccatctctct	ctgtctggaa	aatgttgtaa	ccaaactacc	360
ctatttctctg	tccagtttgg	gcattggaag	ataagttgtg	tacttctatt	ctcaagttgt	420
tgtctttgtga	ttatgaaatg	tttccaataa	tcagcagttt	ttgatgtatg	gtcggtg	

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

Thr	Glu	Leu	Ser	Cys	Arg	Ala	Pro	Lys	Ala	Pro	Pro	Pro	Leu	Pro	Ser
1			5				10						15		
Ser	Gly	Ala	Lys	Gly	Phe	Leu	Ala	Arg	Asn	Ala	Met	Pro	Lys	Asn	Lys
			20				25						30		
Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys	Asn	Xaa	Ala	Asp	Asp
			35				40					45			
Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg	Ala	Gly	Val	Arg	Ala
			50				55					60			
Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg	Gly	Ala	Val	Phe	Leu
65						70				75				80	
Asn	Thr	Arg	Ser	Asp	Leu	Cys	Pro	Glu	Gly	Leu	Leu	Gly	His	Gln	
						85				90				95	

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

Arg	Asn	Leu	Ala	Ala	Glu	Arg	Pro	Lys	Pro	His	Arg	Arg	Ser	His	Gln
1		5						10					15		
Ala	Ala	Leu	Lys	Val	Ser	Ser	Pro	Ala	Thr	Arg	Cys	Arg	Arg	Thr	Arg
		20					25					30			
Glu	Arg	Glu	Ala	Arg	Thr	Gly	Ser	Gly	Ala	Arg	Thr	Xaa	Arg	Thr	Thr
		35					40					45			
Arg	Ser	Gly	Ser	Trp	Xaa	Phe	Lys	Glu	Asp	Gly	Gln	Glu	Tyr	Ala	Gln
	50					55				60					
Val	Thr	Arg	Met	Leu	Gly	Asn	Gly	Arg	Cys	Glu	Ala	Pro	Ser	Ser	
65			70					75							

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

Met	Pro	Lys	Asn	Lys	Gly	Lys	Gly	Gly	Lys	Asn	Arg	Lys	Arg	Gly	Lys
1		5						10					15		
Asn	Xaa	Ala	Asp	Asp	Glu	Lys	Arg	Glu	Leu	Xaa	Val	Gln	Gly	Gly	Arg
		20					25					30			
Ala	Gly	Val	Arg	Ala	Gly	Asp	Ala	Asp	Ala	Gly	Gln	Arg	Pro	Leu	Arg
		35					40					45			
Gly	Ala	Val	Phe	Leu	Asn	Thr	Arg	Ser	Asp	Leu	Cys	Pro	Glu	Gly	Leu
	50				55					60					
Leu	Gly	His	Gln												
65															

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1501268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

acgatccac	tcctcccgc	tcctcccaagg	agtcgaagg	caaagctaag	cttagctcat	60
tgctcaagct	tcgctctctt	tcctctctgcg	agactgcaca	ctgccaccac	gcgcaatg	120
ggcattccac	catttggttg	cggccttgct	cctctactc	ctgtccctt	ccaccctga	180
ggcgacgtcc	tcggcgctgc	ttggcatcag	ctacggctgc	gttggaacaa	acctccctgc	240
agctacatca	gtgcgcgaga	ttgtggcttc	cttggggctc	ggccgcgtcc	gactctacga	300
tgctgacagc	accaccattc	gcgcctctgc	caacacgggc	gtcgagctcg	tcgtcggtc	360
ccctgacgag	tgctctgcc	ctgtctccac	cccgacgggc	cgmgcctcct	gggtccgctc	420
caacatttcc	ccctgcgctc	ccggccacaa	agatcgctt	cctcacagtc	ggcaacgag	

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..159  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501269  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Asp	Pro	Thr	Leu	Pro	Ala	His	Leu	Lys	Glu	Ser	Arg	Cys	Lys	Ala	Lys
1			5					10					15		
Leu	Ser	Ser	Leu	Leu	Lys	Leu	Pro	Ser	Leu	Ser	Leu	Cys	Glu	Thr	Ala
			20				25					30			
His	Cys	His	His	Ala	Gln	Trp	Arg	His	Ser	Thr	Ile	Cys	Cys	Arg	Pro
			35				40					45			
Cys	Ser	Phe	Tyr	Ser	Cys	Ser	Leu	Pro	Pro	Leu	Arg	Arg	Arg	Pro	Arg
			50			55				60					
Arg	Cys	Leu	Ala	Ser	Ala	Thr	Val	Ala	Leu	Ala	Thr	Ser	Leu	Gln	
65					70				75					80	
Leu	His	Gln	Cys	Arg	Arg	Leu	Trp	Leu	Pro	Trp	Ala	Ser	Ala	Ala	Ser
			85				90						95		
Asp	Ser	Thr	Met	Leu	Thr	Ala	Pro	Pro	Phe	Ala	Pro	Ser	Pro	Thr	Arg
			100				105						110		
Ala	Ser	Ser	Ser	Ser	Ala	Ser	Leu	Thr	Ser	Ala	Ser	Pro	Leu	Ser	
			115			120						125			
Pro	Pro	Arg	Arg	Ala	Xaa	Pro	Pro	Gly	Ser	Ala	Pro	Thr	Phe	Pro	Pro
			130			135					140				
Ala	Leu	Pro	Ala	Thr	Lys	Ile	Ala	Phe	Leu	Thr	Val	Gly	Asn	Glu	
145					150				155						

(2) INFORMATION FOR SEQ ID NO:1808:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 121 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..121  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501270  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

Met	Ala	Ala	Phe	His	His	Leu	Leu	Pro	Ala	Leu	Leu	Leu	Leu	Leu	
1			5					10					15		
Leu	Pro	Ser	Thr	Pro	Glu	Ala	Thr	Ser	Ser	Ala	Leu	Leu	Gly	Ile	Ser
			20				25					30			
Tyr	Gly	Arg	Val	Gly	Asn	Asn	Leu	Pro	Ala	Ala	Thr	Ser	Val	Pro	Gln
			35				40					45			
Ile	Val	Ala	Ser	Leu	Gly	Val	Gly	Arg	Val	Arg	Leu	Tyr	Asp	Ala	Asp
			50			55				60					
Ser	Thr	Thr	Ile	Arg	Ala	Phe	Ala	Asn	Thr	Gly	Val	Glu	Leu	Val	Val
65				70				75						80	
Gly	Val	Pro	Asp	Glu	Cys	Leu	Ala	Thr	Val	Ser	Thr	Pro	Thr	Gly	Xaa
			85				90					95			
Ala	Ser	Trp	Val	Arg	Ser	Asn	Ile	Ser	Pro	Cys	Ala	Pro	Gly	His	Lys
			100				105					110			
Asp	Arg	Leu	Pro	His	Ser	Arg	Gln	Arg							
			115			120									

(2) INFORMATION FOR SEQ ID NO:1809:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 422 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..422  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501280

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

aaggagagag	agagagggcag	aggagagagat	tggaggggag	ccccgcccc	aggcaagaga	60
aaccgcggcg	cgcggagaga	gggtgagggt	gagttctcag	aagcccgtag	ggacttggct	120
gctcttgaga	aggactatga	ggaagtccgt	gcagagggtg	ccgatgacga	gggtgacgag	180
ggagacgact	attgagtagc	tggtcaataa	gtagtctctc	ggtggttaat	ggttgggtta	240
ttttgagtat	atactctatg	gttcactacc	attggatact	gctgctgtgt	gtgtttccat	300
tttgactact	gtagtaaatt	gttcgtagcc	ccctattggc	catgattgtt	catatcatcc	360
ttctttggtt	tgcaacgcta	ttcgtccaat	ttcgggtgat	atgctataat	gctattatgt	420

(2) INFORMATION FOR SEQ ID NO:1810:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501281

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

Lys	Glu	Arg	Glu	Arg	Gly	Arg	Gly	Arg	Asp	Trp	Arg	Glu	Ala	Pro	Ala
1			5					10						15	
Gln	Gly	Lys	Arg	Asn	Arg	Gly	Ala	Arg	Arg	Glu	Gly	Glu	Gly	Glu	Phe
			20					25						30	
Ser	Glu	Ala	Arg	Glu	Asp	Leu	Ala	Ala	Leu	Glu	Lys	Asp	Tyr	Glu	Glu
			35					40						45	
Val	Gly	Ala	Glu	Gly	Ala	Asp	Asp	Glu	Gly	Asp	Glu	Gly	Asp	Asp	Tyr
			50					55						60	

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..65  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501282

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

Arg	Arg	Glu	Arg	Glu	Ala	Glu	Gly	Glu	Ile	Gly	Gly	Arg	Pro	Leu	Pro
1				5				10						15	
Lys	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Gly	Glu	Arg	Val	Arg	Val	Ser	Ser
			20					25						30	
Gln	Lys	Pro	Val	Arg	Thr	Trp	Leu	Leu	Arg	Arg	Thr	Met	Arg	Lys	
			35					40						45	
Ser	Val	Gln	Arg	Val	Pro	Met	Thr	Arg	Val	Thr	Arg	Glu	Thr	Thr	Ile
			50					55						60	

Glu  
65

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..570  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501306  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:  
ataaagcacc ctctccttgc ggaattcgg acacggccac cacacatccc ttctctcttt 60  
ttctcctcgg gctcggagcat tcgtgctgct ccgaccccac cgccacaggc tcggcggttc 120  
ggcgatctcg ctacccggcg ggaacatgac tacttcaagg cgcttgctg acaggaagac 180  
cgcaaatgtc cagaagaaca tcaccaggag gggttctgtg cctgaaacca ctgtcaagaa 240  
gggaaatgac taccctgttg gccctctagt gcttgggttc ttcatctttg tcgtcattgg 300  
atcatcgttg ttccagatca tcaggacggc aaccaggcgg ggggtggctt gagagccggc 360  
ccacatctaa tcccacagtat agagagttgc ttgttatata tgcatacagc taggattggg 420  
tagcagctaa aatgtttaac gtgacaagac tgccctgcac tccgttcatt tgggtggcct 480  
tgaatctgga actgaaccaa aaggcagaat catgtacctt atataaagtg ttaaatgggt 540  
(2) INFORMATION FOR SEQ ID NO:1813:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..56  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501307  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:  
Ile Lys His Pro Leu Leu Ala Arg Ile Arg Thr Arg Pro Pro His Ile  
1 5 10 15  
Pro Ser Ser Leu Ser Pro Arg Gly Ser Ser Ile Arg Ala Ala Pro Thr  
20 25 30  
Pro Pro Pro Gln Ala Arg Arg Ser Gly Asp Leu Ala His Arg Arg Glu  
35 40 45  
His Asp Tyr Phe Lys Ala Pro Cys  
50 55  
(2) INFORMATION FOR SEQ ID NO:1814:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..48  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501308  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:  
Lys Ala Pro Ser Pro Cys Ala Asn Ser Asp Thr Ala Thr Thr His Pro  
1 5 10 15  
Phe Leu Ser Phe Ser Ser Arg Leu Glu His Ser Cys Cys Ser Asp Pro  
20 25 30  
Thr Ala Thr Gly Ser Ala Val Arg Arg Ser Arg Ser Pro Ala Gly Thr  
35 40 45  
(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 68 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..68  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501309  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:  
Met Thr Thr Ser Arg Arg Leu Ala Asp Arg Lys Thr Ala Lys Phe Gln  
1          5          10          15  
Lys Asn Ile Thr Arg Arg Gly Ser Val Pro Glu Thr Thr Val Lys Lys  
20          25          30  
Gly Asn Asp Tyr Pro Val Gly Pro Leu Val Leu Gly Phe Phe Ile Phe  
35          40          45  
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser  
50          55          60  
Gly Gly Val Ala  
65

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1036 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..1036  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501310  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:  
aaccacaagag cgaaaaatgga tccgcaccag ttcgccccct cccagcagtc ggcgctgacc 60  
atggaatcgg cggagatcac ggcgcgcgcc gcgcgcgcgc gcgcacccaa cggcgctgac 120  
cgggctatcg tcgaggacga cgacgaggac gacgacgtcc ccgaggtggc cgctgcata 180  
tcgacgatgc tcgaccgcgg gggtagcgtg gagagccacc gcctcttctt ggcgcgcgcg 240  
accgcgctgg agatgctccg cgaccgcggt acgccgttcc ggaggaagag ctgcgccgga 300  
ccctcccggg gtctccgcgc tgggtgggaat acagggccaga rctcgaacgc ctgcctctt 360  
ccactacct cgctccgac ccgtccagca aggtgaaagt tgtgttctgt ccacctggac 420  
ctgtcaaaaat cgcagctatc cggctgatat ataccggaat caaagatgag aacttgtcca 480  
gactgattct gatactgcag ggcacaaataa tgtctacaac cagagaatcc atcaaggagw 540  
tctttcgatt taaagtgcac acattccaga tcacggaatt actggtgac atcactaagc 600  
atgtcctcaa gcccaagcat gaagtgttga ctgcagaggg gaaagctaa cctctgaagg 660  
agtacaatgt ggtggaattc cagttgcctc gcatgctgga gaatgatgct gttgctcgct 720  
attacgggct aggcgaaggga actgttgtta aggttatata cgacagcgag cttaccggga 780  
accatgtgac gtaccgatgc attacctgag gggcccatgt gtttccggtg atgaagtgtc 840  
gtaaagcagtc gttaaaaaaat tacctctaag aggggcaggt gacactgttc tctgtaggct 900  
ttgtaagcac ccaattatgc aggatgaagc tcgctgtaag ctattggtaa aatcatcttg 960  
cgccattgcc gtaccttaag tgcttgggtg taatcttgga aacagtgaga caactaatcc 1020  
tgtagtggag tatctc

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 131 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1501311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

Asn Pro Arg Ala Lys Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln  
1 5 10 15  
Ser Ala Leu Thr Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala  
20 25 30  
Ala Arg Ala Pro Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp  
35 40 45  
Glu Asp Asp Asp Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu  
50 55 60  
Asp Arg Gly Gly Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg  
65 70 75 80  
Thr Ala Leu Glu Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys  
85 90 95  
Ser Ser Pro Gly Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly  
100 105 110  
Gln Xaa Ser Asn Ala Ser Pro Ser Pro Leu Pro Ser Pro Thr Arg  
115 120 125  
Pro Ala Arg  
130

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1501312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln Ser Ala Leu Thr Met  
1 5 10 15  
Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Arg Ala Pro Asn  
20 25 30  
Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Val  
35 40 45  
Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly Ser  
50 55 60  
Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu Met  
65 70 75 80  
Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly Pro  
85 90 95  
Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn Ala  
100 105 110  
Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1501313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro

13  
12  
11  
10  
9  
8  
7  
6  
5  
4  
3  
2  
1

1	5	10	15
Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Asp	20	25	30
Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly	35	40	45
Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu	50	55	60
Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly	65	70	75
Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn	85	90	95
Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg	100	105	110

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

atagagacav	ggaggggag	tgtgtccgagg	tcaataggat	ataactccag	gactcctctc	60
catcagaatc	agagacgagt	cgaagtggagg	ggcagaggcc	acaaaaacaga	gagtaccocaa	120
acgatgatc	tgtgcatctc	cccgcccgct	ccgcaaccat	ctaattcaga	agcagacatc	180
aatggcgagc	hagcgctgca	acggcaacgg	caacggcaac	ggcaacggga	agggcgctcc	240
ggcggtgtg	gtggtaccgg	agatcaagtt	caccaagctc	ttcatcaacg	gcgagttcgt	300
cgacgccgc	tcgggcaaga	catcgatac	cagggaccca	ggtaccaggg	ctacacgctc	360
aaggagccta	tcggcgctcgt	gggcgtcatc	atccccgga	acttccccac	catgatgttc	420
ttctcgaagg	tcagccggg	gctcgccrcg	ggctgcac			

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

Met Ala Ser Xaa Gly Cys Asn Gly Asn Gly Asn Gly Asn Gly Asn Gly	5	10	15
Lys Ala Ala Pro Ala Gly Val Val Val Pro Glu Ile Lys Phe Thr Lys	20	25	30
Leu Phe Ile Asn Gly Glu Phe Val Asp Ala Ala Ser Gly Lys Thr Phe	35	40	45
Asp Thr Arg Asp Pro Gly Thr Arg Ala Thr Arg Ser Arg Ser Leu Ser	50	55	60
Ala Ser Trp Ala Ser Ser Ser Pro Gly Thr Ser Pro Pro	65	70	75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1501324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

gcctcgcgca	ctcgcactta	acctagccgc	cagccctcga	cgaccgacgc	gacgtcgcct	60
tcgccccctgc	tccaaacccct	gcccccttcg	tcgtctcggc	ctcggcgagga	agatccctcca	120
tcgacggcttc	tgctgatgcc	tctgtgtgca	tcgttctgag	gagagcctca	gtggctcggat	180
ccttgatgtg	ttgggccccgc	tcgaggcgat	tgtcaccact	tcacacaggg	gcaaatgtcgc	240
gtcggctctc	cccccttgga	tcctccaccg	ccaatgctcg	atgcctgcat	cgacaaagct	300
ccccctccgaa	gtctcccccct	tctggatcct	tcccctgccc	gtgcttgctt	cctcgtcctg	360
ggatactccg	ccggccccctt	catcgtccag	agaacctggc	atgagacacg	ccaccagagc	420
ttgtttacag	ttcagccccag	ttggccatta	ctttgctagt	gcttcacatg	acaggactgc	480
tagaatttgg	tcaattgata	aaatccagcc	tttgcaata	atggctgggc	atctttctga	540
tgt						

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1501325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Pro	Arg	Ala	Leu	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Pro	Arg	Arg	Pro	Thr	
1			5					10					15			
Arg	Arg	Arg	Leu	Arg	Pro	Cys	Ser	Asn	Pro	Cys	Pro	Leu	Arg	Arg	Ser	
			20					25				30				
Gly	Leu	Gly	Arg	Lys	Ile	Leu	His	Arg	Arg	Ser	Cys	Arg	Cys	Leu	Cys	
			35				40					45				
Cys	His	Arg	Ser	Glu	Glu	Ser	Leu	Ser	Gly	Arg	Ile	Leu	Asp	Val	Leu	
			50				55				60					
Gly	Pro	Val	Glu	Ala	Ile	Val	Thr	Thr	Ser	His	Arg	Gly	Lys	Val	Arg	
			65			70				75				80		
Ser	Val	Leu	Pro	Leu	Trp	Ile	Leu	His	Arg	Gln	Cys	Ser	Met	Pro	Ala	
				85					90				95			
Ser	Thr	Lys	Leu	Pro	Ser	Glu	Val	Ser	Pro	Phe	Arg	Ile	Leu	Pro	Leu	
				100				105					110			
Pro	Val	Leu	Ala	Ser	Ser	Ser	Trp	Asp	Thr	Pro	Pro	Ala	Pro	Ser	Ser	
			115				120					125				
Ser	Arg	Glu	Pro	Gly	Met	Arg	His	Ala	Thr	Arg	Ala	Cys	Leu	Gln	Phe	
				130			135					140				
Ser	Pro	Val	Gly	His	Tyr	Phe	Ala	Ser	Ala	Ser	His	Asp	Arg	Thr	Ala	
				145			150				155				160	
Arg	Ile	Trp	Ser	Ile	Asp	Lys	Ile	Gln	Pro	Leu	Arg	Ile	Met	Ala	Gly	
				165				170					175			
His	Leu	Ser	Asp													
			180													

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1501326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

aatcaccttc	ttcgttttc	ctctctgattc	wccccctgcw	ggctgtctct	gctcccatcc	60
catggagccc	gacgcgcgcc	aaaaccctag	ccccagcccc	gtccccccgc	ccatctccgc	120
ctactaccag	acgcgcgcgc	aacaccacgc	cgctgtaact	agcgactggc	tcgcccacgc	180
cgccgcgcga	gcgcgcgcct	tccccggcgc	cgataccgcc	gatgcmgcmc	cgcccccgctc	240
ccccgggggc	ggcggcgctga	tcgaggagtt	caacttcttg	cgccgcgaagc	ccgaggccgc	300
cgaggcggtg	gcgcgccatca	tggtctctgc	cgcmtcctc	cgctccagca	gggccaccac	360
catgatggag	ctcgagatcg	agctcaagaa	ggcatctgac	aagctcaagt	cctgggatgc	420
tacatccatt	tctctttctg	ctgcttggtga	ttgttctatg	cggtttgtaa	caggagacctc	480
acatctggag	catgagaagt	ttgatgcagc	aaaatcgcg	ctaattgagc	gaggag	

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1501327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Ile	Thr	Phe	Phe	Val	Ser	Ser	Ser	Asp	Xaa	Pro	Pro	Xaa	Gly	Leu	Leu	
1				5					10					15		
Cys	Ser	His	Pro	Met	Glu	Pro	Asp	Ala	Gln	Asn	Pro	Ser	Pro	Ser		
				20				25				30				
Pro	Val	Pro	Pro	Pro	Ile	Ser	Ala	Tyr	Tyr	Gln	Thr	Arg	Ala	Glu	His	
				35				40				45				
His	Ala	Val	Val	Thr	Ser	Asp	Trp	Leu	Ala	His	Ala	Ala	Ala	Ala	Ala	
				50			55				60					
Ala	Ala	Phe	Pro	Gly	Ala	Asp	Thr	Ala	Asp	Xaa	Pro	Pro	Pro	Ser		
				65		70			75					80		
Pro	Gly	Gly	Gly	Gly	Val	Ile	Glu	Glu	Phe	Asn	Phe	Trp	Arg	Arg	Lys	
				85				90				95				
Pro	Glu	Ala	Ala	Glu	Ala	Val	Ala	Ile	Met	Ala	Leu	Ala	Xaa	Val		
				100				105				110				
Ile	Arg	Ser	Ser	Arg	Ala	Thr	Thr	Met	Met	Glu	Leu	Glu	Ile	Glu	Leu	
				115				120				125				
Lys	Lys	Ala	Ser	Asp	Lys	Leu	Lys	Ser	Trp	Asp	Ala	Thr	Ser	Ile	Ser	
				130			135			140						
Leu	Ser	Ala	Ala	Cys	Asp	Leu	Phe	Met	Arg	Phe	Val	Thr	Arg	Thr	Ser	
				145		150			155					160		
His	Leu	Glu	His	Glu	Lys	Phe	Asp	Ala	Ala	Lys	Ser	Arg	Leu	Ile	Glu	
				165				170						175		

Arg Gly

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

Met Glu Pro Asp Ala Ala Gln Asn Pro Ser Pro Ser Pro Val Pro Pro

1	5	10	15
Pro Ile Ser Ala Tyr Tyr Gln Thr Arg Ala Glu His His Ala Val Val	20	25	30
Thr Ser Asp Trp Leu Ala His Ala Ala Ala Ala Ala Phe Pro	35	40	45
Gly Ala Asp Thr Ala Asp Xaa Xaa Pro Pro Pro Ser Pro Gly Gly Gly	50	55	60
Gly Val Ile Glu Glu Phe Asn Phe Trp Arg Arg Lys Pro Glu Ala Ala	65	70	75
Glu Ala Val Ala Ala Ile Met Ala Leu Ala Xaa Val Ile Arg Ser Ser	85	90	95
Arg Ala Thr Thr Met Met Glu Leu Glu Ile Glu Leu Lys Lys Ala Ser	100	105	110
Asp Lys Leu Lys Ser Trp Asp Ala Thr Ser Ile Ser Leu Ser Ala Ala	115	120	125
Cys Asp Leu Phe Met Arg Phe Val Thr Arg Thr Ser His Leu Glu His	130	135	140
Glu Lys Phe Asp Ala Ala Lys Ser Arg Leu Ile Glu Arg Gly	145	150	155

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..492
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

acactgcgtc	tcgccactgt	cgtccaccga	tccgtcatgg	cgactgctgc	gccattgttg	60
ctcttccacg	gtctctctct	cctcctctcc	ctggcgctcg	gcccatggcg	tgaacgtgaa	120
gccccgggag	caccacatcc	tcaacaggca	gagcttcccc	ccggggttcg	tcttcggcac	180
ggcgctcttcg	cgctaccagg	tggaggggaa	cacgcacagg	tacgggcgcg	ggccctgcac	240
ctgggaacac	ttctctaagt	atccaggcac	tactctgat	aacgcgacgc	cggaactgac	300
agtcgacagg	tacaatcgct	acatggatga	tgtggacaat	atgttcctgg	ttagcttcga	360
cgctaccgcg	ttctcgatct	catggctcgc	tattttcccc	agtgaggattg	ggagggttaa	420
caaggatggt	gtggactatt	accacaggct	catcaactac	tgtctggcga	accatattac	480
tcctacgtg	gt					

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

Thr Leu Ala Leu Ala Thr Val Val His Arg Ser Val Met Ala Thr Ala	5	10	15
Ala Pro Leu Leu Leu Phe His Gly Leu Leu Leu Leu Ser Leu Ala	20	25	30
Leu Gly Pro Trp Arg Glu Arg Glu Ala Arg Gly Ala Pro His Pro Gln	35	40	45
Gln Ala Glu Leu Pro Pro Gly Val Arg Leu Arg His Gly Val Phe Gly	50	55	60
Val Pro Gly Gly Gly Glu His Ala Gln Val Arg Ala Arg Ala Leu His			

(2) INFORMATION FOR SEO ID NO:1829:

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(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
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(D) OTHER INFORMATION: / Ceres Seq. ID 1501331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

(2) INFORMATION FOR SEQ ID NO:1830:

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(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
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(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1501339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

(2) INFORMATION FOR SEQ ID NO:1831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..136  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501340  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Val Glu Ser Arg Thr Phe Leu Pro Arg Ser Arg Xaa Gln Ser Ala Thr  
1 5 10 15  
Thr His Thr Pro Pro Thr Asn Thr Met Asp Ala Ala Lys Glu Ala  
20 25 30  
Leu Ile Leu Asp Leu His Ala Val Glu Ala Val Lys Leu Gly Thr Phe  
35 40 45  
Val Leu Lys Ser Gly Ile Thr Ser Pro Ile Tyr Leu Asp Leu Arg Val  
50 55 60  
Leu Val Ser His Pro Arg Leu Leu Ala Ser Val Ala Ser Leu Leu Gly  
65 70 75 80  
Ala Leu Pro Ala Thr Arg Pro Tyr Asp Leu Leu Cys Gly Val Pro Xaa  
85 90 95  
Thr Ala Leu Pro Phe Ala Ala Leu Ser Val Ala Xaa Ser Val Pro  
100 105 110  
Met Leu Leu Ser Arg Tyr Asp Thr Lys Arg Val Glu Gly Ala Phe Arg  
115 120 125  
Xaa Ala Gln Xaa Val Leu Ile Val  
130 135

(2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 135 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..135  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

Arg Val Lys Asn Phe Ser Pro Pro Phe Ala Xaa Thr Val Gly His Tyr  
1 5 10 15  
Thr His Ala Ala His Gln His His Gly Arg Arg Arg Glu Gly Gly Ala  
20 25 30  
Asp Pro Gly Pro Ala Arg Gly Gly Gly Arg Glu Ala Gly His Leu Arg  
35 40 45  
Ala Gln Val Arg Asp His Leu Pro Asp Leu Pro Gly Pro Ala Arg Ala  
50 55 60  
Arg Leu Pro Pro Ala Pro Ala Arg Leu Arg Arg Val Pro Pro Arg Arg  
65 70 75 80  
Ala Pro Gly His Ala Pro Leu Arg Pro Ser Leu Arg Arg Ala Leu Xaa  
85 90 95  
Ser Ala Ala Leu Arg Gly Arg Ala Leu Arg Arg Xaa Leu Arg Ala His  
100 105 110  
Ala Ala Gln Pro Leu Arg His Gln Ala Arg Arg Gly Arg Leu Pro Xaa  
115 120 125  
Arg Pro Xaa Arg Ala His Arg  
130 135

(2) INFORMATION FOR SEQ ID NO:1833:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 112 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1501342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

Met	Asp	Ala	Ala	Ala	Lys	Glu	Ala	Leu	Ile	Leu	Asp	Leu	His	Ala	Val	
1					5			10					15			
Glu	Ala	Val	Lys	Leu	Gly	Thr	Phe	Val	Leu	Lys	Ser	Gly	Ile	Thr	Ser	
			20					25					30			
Pro	Ile	Tyr	Leu	Asp	Leu	Arg	Val	Leu	Val	Ser	His	Pro	Arg	Leu	Leu	
			35					40					45			
Ala	Ser	Val	Ala	Ser	Leu	Leu	Gly	Ala	Leu	Pro	Ala	Thr	Arg	Pro	Tyr	
			50				55					60				
Asp	Leu	Leu	Cys	Gly	Val	Pro	Xaa	Thr	Ala	Leu	Pro	Phe	Ala	Ala	Ala	
			65				70					75			80	
Leu	Ser	Val	Ala	Xaa	Ser	Val	Pro	Met	Leu	Leu	Ser	Arg	Tyr	Asp	Thr	
			85					90						95		
Lys	Arg	Val	Glu	Gly	Ala	Phe	Arg	Xaa	Ala	Gln	Xaa	Val	Leu	Ile	Val	
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:1834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..539

(D) OTHER INFORMATION: / Ceres Seq. ID 1501345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

agcagcccat	ccccagcagc	actgcctcgt	cgtctcgcgt	attggcgttg	gcatacccggt	60
cggcattgtg	cccattacca	tgccgcccgt	gcccgcggcc	gacgatttac	tcattctcga	120
gttcacgcgg	agcaaccgcc	gtatccccc	cgccgtgttc	aactccttca	tcgcctccca	180
atccccacc	tcgccttct	cccgcaacct	acagcgcttc	cgaaaagccc	tagtgcctcg	240
cgccctcgac	gcgcctctct	acaccgtggg	cgctctctgc	tctccagcc	tctcctcca	300
caaggcgcca	aaggtcctcg	ccgaccccga	cgcagccgcg	tgtctccccc	accagattcc	360
ttttacagaa	aatgaagaaa	acgatgaggc	tagggctgcg	gtggccgcgt	tcaagcgctc	420
cctcgacctt	gagtgggcca	acctcccgcm	ctccacgctc	gagctcgtmg	ccggggacgg	480
gtcccaccag	actggtgcmg	ctgcccga	caccatgcgt	acaaagcttc	gcctgttcg	

(2) INFORMATION FOR SEQ ID NO:1835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

Ser	Ser	Pro	Ser	Pro	Ala	Ala	Leu	Pro	Arg	Arg	Leu	Ala	Tyr	Trp	Arg	
1					5			10					15			
Trp	His	His	Arg	Arg	His	Cys	Ala	His	Tyr	His	Ala	Ala	Ala	Ala	Ala	
			20					25					30			
Gly	Arg	Arg	Phe	Thr	His	Ser	Arg	Val	His	Arg	Glu	Gln	Pro	Pro	Tyr	
			35				40						45			

Pro Pro Arg Arg Val Gln Leu Leu His Arg Leu Pro Ile Pro Thr Leu  
50 55 60  
Arg Leu Leu Pro His Leu Thr Ala Pro Pro Lys Ser Pro Ser Ala Pro  
65 70 75 80  
Arg Pro Arg Arg Arg Pro Leu His Arg Gly Arg Leu Leu Leu Leu Gln  
85 90 95  
Pro Pro Pro Pro Gln Gly Ala Lys Gly Pro Arg Arg Pro Arg Arg Ser  
100 105 110  
Arg Leu Leu Pro Pro Pro Asp Ser Phe Tyr Arg Lys  
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1501347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

Ala Ala His Pro Gln Gln His Cys Leu Val Val Ser His Ile Gly Val  
1 5 10 15  
Gly Ile Thr Val Gly Ile Val Pro Ile Thr Met Pro Pro Leu Pro Ala  
20 25 30  
Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile Ala Ser Asn Arg Arg Ile  
35 40 45  
Pro His Ala Val Phe Asn Ser Phe Ile Ala Ser Gln Ser Pro Pro Ser  
50 55 60  
Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg Lys Ala Leu Val Leu Arg  
65 70 75 80  
Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly Ala Ser Cys Ser Ser Ser  
85 90 95  
Leu Leu Leu His Lys Ala Arg Lys Val Leu Ala Asp Pro Asp Ala Ala  
100 105 110  
Ala Cys Phe Pro His Gln Ile Pro Phe Thr Glu Asn Glu Glu Asn Asp  
115 120 125  
Glu Ala Arg Ala Ala Val Ala Asp Leu Lys Arg Leu Leu Asp Leu Glu  
130 135 140  
Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu Leu Xaa Ala Gly Asp Gly  
145 150 155 160  
Ser His Gln Thr Gly Xaa Ala Ala Asp His Thr Met Arg Thr Lys Leu  
165 170 175  
Arg Leu Phe

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

Met Pro Pro Leu Pro Ala Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile  
1 5 10 15  
Ala Ser Asn Arg Arg Ile Pro His Ala Val Phe Asn Ser Phe Ile Ala

20										25										30																																	
Ser	Gln	Ser	Pro	Pro	Ser	Ala	Phe	Ser	Arg	Thr	Ser	Gln	Arg	Leu	Arg					Ser	Gln	Arg	Leu	Arg									Ser	Gln	Arg	Leu	Arg																
Lys	Ala	Leu	Val	Leu	Arg	Ala	Leu	Asp	Ala	Ala	Leu	Tyr	Thr	Val	Gly																																						
Ala	Ser	Cys	Ser	Ser	Ser	Leu	Leu	Leu	His	Lys	Ala	Arg	Lys	Val	Leu																																						
65																																																					
Ala	Asp	Pro	Asp	Ala	Ala	Ala	Cys	Phe	Pro	His	Gln	Ile	Pro	Phe	Thr																																						
Glu	Asn	Glu	Glu	Asn	Asp	Glu	Ala	Arg	Ala	Ala	Val	Ala	Asp	Leu	Lys																																						
Arg	Leu	Leu	Asp	Leu	Glu	Trp	Ala	Asn	Leu	Pro	Xaa	Ser	Thr	Leu	Glu																																						
Leu	Xaa	Ala	Gly	Asp	Gly	Ser	His	Gln	Thr	Gly	Xaa	Ala	Ala	Asp	His																																						
Thr	Met	Arg	Thr	Lys	Leu	Arg	Leu	Phe																																													
145																																																					

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1501364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

agccttccaa	tctctaggag	aaacgtcttg	ccctccactc	caacatcgac	acgactactc	60
gtccgactag	aaacaaactt	ttcaatccat	cggtccgagt	tcagttcaca	cttcacaggc	120
gagcgcgacc	atggataccc	aagcacgtcc	ggttcccccg	gtcaagctcg	gcacccaggg	180
attccgaggtg	tccaagctgg	ggttcgggtg	catggggctg	acggggcgat	acaactcccc	240
gctggacgac	gagggcggca	tcgccgtcat	cgcgcacgct	ttcagccggc	gagtcacott	300
gttcgacacc	tccgacgtat	acggggccctc	caccaacgaa	atccctcccg	gcaaggcgct	360
gaagcagctg	ccgcggggagc	aggtgcaggt	ggccaccaag	ttcgggatam	ggcgtgacga	420
gagcggcacs	ggnaccgtgt	gcggccggcc	ggagtagctt	cgtrcctgct	gcgaggccag	480
cctgcgccgc	ctcgccatcg	actgcacga	c			

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1501365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Ser	Leu	Pro	Ile	Ser	Arg	Arg	Asn	Val	Leu	Pro	Ser	Thr	Pro	Thr	Ser
1															
Thr	Arg	Leu	Leu	Val	Arg	Leu	Glu	Pro	Asn	Phe	Ser	Ile	His	Arg	Ser
Gln	Phe	Ser	Ser	His	Phe	Thr	Gly	Glu	Arg	Asp	His	Gly	Tyr	Pro	Ser
Thr	Ser	Gly	Ser	Pro	Arg	Gln	Ala	Arg	His	Pro	Gly	Ile	Arg	Gly	Val
Gln	Ala	Gly	Val	Arg	Val	His	Gly	Ala	Asp	Gly	Arg	Ile	Gln	Leu	Pro
65															
Ala	Gly	Arg	Gly	Arg	His	Arg	Arg	His	Arg	Ala	Arg	Phe	Gln	Pro	

85 90 95  
Arg Ser His Leu Val Arg His Leu Arg Arg Ile Arg Ala Pro His Gln  
100 105 110  
Arg Asn Pro Pro Arg Gln Gly Ala Glu Ala Ala Ala Gly Ala Gly  
115 120 125  
Ala Gly Gly His Gln Val Arg Asp Xaa Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..127

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

Met Asp Thr Gln Ala Arg Pro Val Pro Arg Val Lys Leu Gly Thr Gln  
1 5 10 15  
Gly Phe Glu Val Ser Lys Leu Gly Phe Gly Cys Met Gly Leu Thr Gly  
20 25 30  
Ala Tyr Asn Ser Pro Leu Asp Asp Glu Ala Gly Ile Ala Val Ile Ala  
35 40 45  
His Ala Phe Ser Arg Gly Val Thr Leu Phe Asp Thr Ser Asp Val Tyr  
50 55 60  
Gly Pro Leu Thr Asn Glu Ile Leu Leu Gly Lys Ala Leu Lys Gln Leu  
65 70 75 80  
Pro Arg Glu Gln Val Gln Val Ala Thr Lys Phe Gly Ile Xaa Arg Asp  
85 90 95  
Glu Ser Gly Xaa Xaa Thr Val Cys Gly Arg Pro Glu Tyr Val Arg Xaa  
100 105 110  
Cys Cys Glu Ala Ser Leu Arg Arg Leu Gly Ile Asp Cys Ile Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..100

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

Met Gly Leu Thr Gly Ala Tyr Asn Ser Pro Leu Asp Asp Glu Ala Gly  
1 5 10 15  
Ile Ala Val Ile Ala His Ala Phe Ser Arg Gly Val Thr Leu Phe Asp  
20 25 30  
Thr Ser Asp Val Tyr Gly Pro Leu Thr Asn Glu Ile Leu Leu Gly Lys  
35 40 45  
Ala Leu Lys Gln Leu Pro Arg Glu Gln Val Gln Val Ala Thr Lys Phe  
50 55 60  
Gly Ile Xaa Arg Asp Glu Ser Gly Xaa Xaa Thr Val Cys Gly Arg Pro  
65 70 75 80  
Glu Tyr Val Arg Xaa Cys Cys Glu Ala Ser Leu Arg Arg Leu Gly Ile  
85 90 95  
Asp Cys Ile Asp  
100

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

atctataaca	gccgccacct	tcccccttat	actcgccgga	ggcaaccagt	actcgtgcc	60
cgactgccac	ccctccctctt	ccttgtgatc	tccgaatacc	catctcagat	tccaagggcc	120
gcgcgcgtgt	atccccgggt	ctccccacc	accatatct	tagtatccgc	gcctcaaatc	180
ctctcgcaaa	cgccccgcgc	taagcagttg	ttgtctgccg	tgatttgagc	cgggcggaag	240
gattgatccc	gggaacgaggt	gtctcagctc	ttgatcttga	tcctgacatc	gggagcgctt	300
ctctggttat	tggtgggagc	gaagaagcca	tgataccttc	cgtgagcgct	tctcctgctc	360
ctcgagcctt	ctcaggctcc	agcctacgct	caaaattacc	gtcaattcca	tccatctcca	420
gtctcaaac	ctccaaatat	gtggtctcct	cgtgaaacc	actctacct	gcaccgctag	480
atggtccgcg	cactgccgag	cttaagtctc	ggagac			

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

Ile	Tyr	Asn	Ser	Arg	His	Leu	Pro	Pro	Tyr	Thr	Arg	Arg	Gln	Pro
1		5							10				15	
Val	Leu	Val	Pro	Arg	Leu	Pro	Pro	Leu	Leu	Phe	Leu	Val	Ile	Ser
			20					25				30		Glu
Tyr	Pro	Ser	Gln	Ile	Pro	Arg	Ala	Ala	Pro	Cys	Asn	Pro	Arg	Leu
		35					40					45		Ser
Pro	Pro	Thr	Ile	Tyr	Leu	Val	Ser	Ala	Pro	Gln	Ile	Pro	Arg	Glu
		50				55					60			Thr
Pro	Arg	Arg	Lys	Gln	Leu	Leu	Ser	Ala	Val	Ile				
		65			70				75					

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

Met	Ile	Pro	Ser	Val	Arg	Leu	Ser	Pro	Gly	Pro	Ala	Ala	Phe	Ser	Gly
1			5						10					15	
Ser	Ser	Leu	Arg	Ser	Lys	Leu	Pro	Ser	Ile	Pro	Ser	Ile	Ser	Ser	Leu
			20					25				30			
Lys	Pro	Ser	Lys	Tyr	Val	Val	Ser	Ser	Leu	Lys	Pro	Leu	Tyr	Leu	Ala
		35				40						45			

Pro Leu Asp Gly Pro Arg Thr Ala Glu Leu Lys Ser Arg Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

aattcttgcaa	agcaggarcc	cggttcggtc	tcgaccttcc	gtctcgctct	cgccccgc	60
accccgcgga	scctagccta	gccttgcccc	cgaccgcgga	ttccccctcg	gccgcgcgc	120
gccgcgaccc	gcaccgcgga	tgatgaactg	cgccggaggg	nangaccocg	tgagggaact	180
cctgatctcc	ggcgccgctg	acgacgaaga	ttagccatc	ttctgcgacg	gaggacttgg	240
gattgagggt	gtcaatggag	atgcttggtg	atttgagcag	tctaatttgg	gcaaaaggag	300
tagagatgaa	ccatgttcat	ctggtctaaa	atccaaagct	tgctgtgaaa	aaatgaggag	360
ggacaagctg	aatgacaggt	tcttggaatt	aarttcgggt	atgaatcccg	aaaacaagc	420
aaagtgggat	aaagccaata	tcttgarcga	mgcagcccg	atggtggcac	aacttagagg	480
tgaggcagaa	aagcttaaa	aatcaaatga	gaagctgcgg	grgaatatc		

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

Met	Met	Asn	Cys	Ala	Gly	Gly	Xaa	Asp	Pro	Val	Glu	Asp	Phe	Leu	Ile
1		5					10				15				
Ser	Gly	Ala	Val	Asp	Asp	Glu	Asp	Leu	Ala	Ile	Phe	Cys	Asp	Gly	Gly
		20					25				30				
Leu	Gly	Ile	Xaa	Gly	Val	Asn	Gly	Asp	Ala	Cys	Gly	Phe	Glu	Gln	Ser
		35					40				45				
Asn	Leu	Gly	Lys	Arg	Ser	Arg	Asp	Glu	Pro	Cys	Ser	Ser	Gly	Leu	Lys
		50					55				60				
Ser	Lys	Ala	Cys	Arg	Glu	Lys	Met	Arg	Arg	Asp	Lys	Leu	Asn	Asp	Arg
		65					70				75				
Phe	Leu	Glu	Leu	Xaa	Ser	Val	Met	Asn	Pro	Gly	Lys	Gln	Ala	Lys	Leu
		85					90				95				
Asp	Lys	Ala	Asn	Ile	Leu	Xaa	Xaa	Ala	Ala	Arg	Met	Val	Ala	Gln	Leu
		100					105								
Arg	Gly	Glu	Ala	Glu	Lys	Leu	Lys	Glu	Ser	Asn	Glu	Lys	Leu	Arg	Xaa
		115					120								
Asn	Leu														
		130													

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501418  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:  
Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile Ser  
1 5 10 15  
Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Leu  
20 25 30  
Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser Asn  
35 40 45  
Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys Ser  
50 55 60  
Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg Phe  
65 70 75 80  
Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu Asp  
85 90 95  
Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu Arg  
100 105 110  
Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa Asn  
115 120 125  
Ile

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1501439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

gaggcgatgc catcgagagac tcggagccgg caaaacccta aggggaaggt tctgcaagg 60  
aggaggagaga tcagagggcgc cagcacatgc tctggaggga gcccttcgcg ctgcgcctccg 120  
tcctctcccc cgccaagcct aaagtattcc catcactcac caagatagtt gggacgctcg 180  
ggcccaattc acactcggtt gagattattc aggaatgcct cactgctgga atgtcagttg 240  
cacgatttga tttctcatgg atggatgctg cgtatcacca ggagaccctt gataatttga 300  
ggaagcggcg acagaagtgt aagaagttgt gccctgtaat gttggatact ctgggtccag 360  
aaattcaggt tcacaattcc actggtgagc caattgagtt gaaagctggg aatcatgtga 420  
tcataactcg agatatttct aaagctctct ctgctgagat cctaccaatt aagttgtgtg 480  
atctggcaaa agctgtgaag aagggkgata ctccttttat gggccaatat ctcttcacag 540  
gaatgtg

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Met Leu Leu Glu Glu Pro Phe Arg Leu Ala Ser Val Leu Ser Pro Ala  
1 5 10 15  
Lys Pro Lys Val Phe Pro Ser Leu Thr Lys Ile Val Gly Thr Leu Gly  
20 25 30  
Pro Asn Ser His Ser Val Glu Ile Ile Gln Glu Cys Leu Thr Ala Gly

35 40 45  
Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His  
50 55 60  
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys  
65 70 75 80  
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His  
85 95  
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile  
100 105 110  
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile  
115 120 125  
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe  
130 135 140  
Met Gly Gln Tyr Leu Phe Thr Gly Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His  
1 5 10 15  
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys  
20 25 30  
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His  
35 40 45  
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile  
50 55 60  
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile  
65 70 75 80  
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe  
85 90 95  
Met Gly Gln Tyr Leu Phe Thr Gly Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

Met Asp Ala Ala Tyr His Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala  
1 5 10 15  
Ala Gln Asn Val Lys Lys Leu Cys Pro Val Met Leu Asp Thr Leu Gly  
20 25 30  
Pro Glu Ile Gln Val His Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys  
35 40 45  
Ala Gly Asn His Val Ile Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser  
50 55 60

Ala Glu Ile Leu Pro Ile Lys Phe Gly Asp Leu Ala Lys Ala Val Lys  
65 70 75 80  
Lys Xaa Asp Thr Leu Phe Met Gly Gln Tyr Leu Phe Thr Gly Ser  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

tcgcatacgg	gaagcttgcc	ttctaatcc	tgagctaaca	ataatcttga	caaaggaaga	60
agggcacaca	gttcaacgca	acgaatatgt	ttatgctggt	ggccttgttg	aatatgttaa	120
atggttgaa	actgacaaga	aacccttgca	tgacccgatt	gcgttcagaa	aggagttgga	180
tggtataaca	gtggatgtct	cccttcaatg	gtcctctgat	tctactctgt	atacagtgtc	240
aggatacgc	aacagtatcc	gcactattga	tggtgggtact	catattgatg	gtctaaaggg	300
ttcattgacg	agaacccatt	ataaccttgc	aaagaagctg	aagmtattaa	ggataaggat	360
attaccttga	gtggggagca	tgtaagagaa	ggaatgacat	gcatacttc	agtgaaggtc	420
cctagtccag	agtttgagg	tcaaacaaag	acaaggttgg	gaaatccaga	agtcaggaga	480
atagttgacg	agtctgttca	agaaactta	acagagtact	tagagcttca	tccagatggt	540
ctggattcaa	tc					

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Arg Ile Arg Glu Leu Ala Phe Leu Asn Pro Glu Leu Thr Ile Ile Leu	
1 5 10 15	
Thr Lys Glu Glu Gly His Thr Val Gln Arg Asn Glu Tyr Cys Tyr Ala	
20 25 30	
Gly Gly Leu Val Glu Tyr Val Lys Trp Leu Asn Thr Asp Lys Lys Pro	
35 40 45	
Leu His Asp Pro Ile Ala Phe Arg Lys Glu Leu Asp Gly Ile Thr Val	
50 55 60	
Asp Val Ser Leu Gln Trp Ser Ser Asp Ser Tyr Ser Asp Thr Val Leu	
65 70 75 80	
Gly Tyr Ala Asn Ser Ile Arg Thr Ile Asp Gly Gly Thr His Ile Asp	
85 90 95	
Gly Leu Lys Ala Ser Leu Thr Arg Thr Ile Asn Asn Leu Ala Lys Lys	
100 105 110	
Ser Lys Xaa Leu Arg Ile Arg Ile Leu Pro	
115 120	

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -  
(B) LOCATION: 1..515  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501485

actaccacgag	ttaactttac	actctgcgac	ccatccgggt	caactggctca	ctgcacaacgc	60
ggcccaataca	cgcgcgcgcg	acccgcgatg	atggcgcgctg	cggcgatctc	cgcgctcgcgc	120
ggccacccctg	tcgtttctctc	cccccgcttc	aggcaacccgc	tcacgctctcc	ttctcgaagc	180
gggtaccccaa	tcgcgcgcgc	cgcctcgggc	gttcggccgcg	gcccgggtgcg	ggtgcgccccc	240
ggtgcacacc	ccgctgttgtc	cgccgcgcgcg	gggaagatgtg	ccaaacacgcg	tcctaagatg	300
gaggggtaag	cagcgatgata	gtctggagac	gggaataatga	atctgaatgta	ggcgctcgcgc	360
atggcgatga	ttttttccaa	gccataatgt	aggaccccgtg	aacctattcaa	tcggaaatcata	420
ttctctactgt	gttggcctacg	tatttatttg	gtctcc			480

(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1501486

Tyr	Pro	Ser	Ser	Leu	His	Thr	Arg	Ala	Pro	Ile	Arg	Val	Thr	Gly	Ser
1			5					10					15		
Leu	Thr	Pro	Arg	Pro	Asn	His	Ala	Arg	Ala	Thr	Arg	Asp	Asp	Gly	Gly
			20					25					30		
Gly	Gly	Asp	Leu	Arg	Leu	Gln	Arg	Pro	Pro	Arg	Arg	Leu	Leu	Pro	Pro
		35					40					45			
Leu	Gln	Ala	Ala	Ala	His	Ala	Pro	Phe	Ser	Gln	Arg	Ser	Pro	Asn	Arg
		50				55					60				
Arg	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Arg	Arg	Gly	Arg	Gly	Arg	Arg	Arg
65					70					75				80	
Val	Gln	Pro	Arg	Cys	Val	Gly	Arg	Arg	Gly	Glu	Gly	Cys	Gln	Thr	Gly
			85						90					95	

(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501487

Met	Met	Ala	Ala	Ala	Ala	Ile	Ser	Gly	Ser	Ser	Gly	His	Leu	Val	Val
1			5					10					15		
Ser	Ser	Pro	Arg	Phe	Arg	Gln	Pro	Leu	Thr	Leu	Pro	Ser	Arg	Ser	Gly
			20					25					30		
Arg	Pro	Ile	Ala	Ala	Ala	Pro	Ala	Val	Ala	Arg	Gly	Val	Ala		
		35					40				45				
Val	Ala	Ala	Val	Ser	Ser	Pro	Ala	Val	Ser	Ala	Val	Ala	Gly	Lys	Asp
		50					55				60				
Ala	Lys	Gln	Ala	Pro	Lys	Asp	Phe	Leu	His	Ile	Asn	Asp	Phe	Asp	Lys

65 70 75 80  
Asp Thr Ile Met Asn Ile Leu Asn Arg Ala Ile Glu Val Lys Ala Ala  
85 90 95  
Ile Lys Ser Gly Asp Arg Ser Phe Gln Pro Phe Asn Gly Lys Ser Met  
100 105 110  
Ala Met Ile Phe Ala Lys Pro Ser Met Arg Thr Arg Val Ser Phe Glu  
115 120 125  
Ala Gly Phe Phe Leu Leu Gly Gly His Ala Ile Tyr Leu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

Met Ala Ala Ala Ala Ile Ser Gly Ser Ser Gly His Leu Val Val Ser  
1 5 10 15  
Ser Pro Arg Phe Arg Gln Pro Leu Thr Leu Pro Ser Arg Ser Gly Arg  
20 25 30  
Pro Ile Ala Ala Ala Ala Ser Ala Val Ala Arg Gly Gly Val Ala Val  
35 40 45  
Ala Ala Val Ser Ser Pro Ala Val Ser Ala Val Ala Gly Lys Asp Ala  
50 55 60  
Lys Gln Ala Pro Lys Asp Phe Leu His Ile Asn Asp Phe Asp Lys Asp  
65 70 75 80  
Thr Ile Met Asn Ile Leu Asn Arg Ala Ile Glu Val Lys Ala Ala Ile  
85 90 95  
Lys Ser Gly Asp Arg Ser Phe Gln Pro Phe Asn Gly Lys Ser Met Ala  
100 105 110  
Met Ile Phe Ala Lys Pro Ser Met Arg Thr Arg Val Ser Phe Glu Ala  
115 120 125  
Gly Phe Phe Leu Leu Gly Gly His Ala Ile Tyr Leu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..577
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

aacctctctg	ctctctctcc	cacgggtccg	ccatttcgtc	ccccgcgtac	caactcaaac	60
ccctctcgct	ctcaaaccct	aaccttagcc	ctagcccgct	cccgccggac	cgacgatgcc	120
gaagaggctg	gcggggcgcc	ggacgaagag	gagttccgcg	ccgaggtgga	ggagcgcttc	180
atcaacgagg	agtacaagat	ctggaagaag	aacacaccct	tcctctacga	cctcgtatcc	240
acccacgcgc	tcgaatggcc	ctcccttacc	gtgcagtggc	tccccagacc	caccgagccg	300
ccggggaagg	accactccgt	ccagaagatg	atccttgga	cgcacacctc	tgacacagag	360
cccaactacc	tcatgtctcg	gcaggtccag	ctgcccctcg	acgacgcgga	ggccgacgcc	420
cgcgactacg	acgatgacca	cgcgcacatc	gggtggtttg	ggccmgsctc	gggsaargtg	480
caaatgtgtc	agcagataaa	tcattgatga	gaggtcaatc	gagctcgcta	tatgccccaa	540
aattcattta	taattgctac	taagacagtt	agcgcaag			

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..192

SEQUENCE DESCRIPTION: SEQ ID NO:1859:

1 5 10 15

20 25 30

Arg Ser Arg Arg Thr Asp Asp Ala Glu Glu Val Gly Gly Ala Ala Asp  
35 40 45

Glu Glu Glu Phe Arg Ala Glu Val Glu Glu Arg Leu Ile Asn Glu Glu  
50 55 60

Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp Leu Val Ile  
65 70 75 80

Thr His Ala Leu Glu Trp Pro Ser Leu Thr Val Gln Trp Leu Pro Asp  
                95                    80                    65

Arg Thr Glu Pro Pro Gly Lys Asp His Ser Val Gln Lys Met Ile Leu  
100 105 110

Gly Thr His Thr Ser Asp Asn Glu Pro Asn Tyr Leu Met Leu Ala Gln

Val Gln Leu Pro Leu Asp Asp Ala Glu Ala Asp Ala Arg Xaa Tyr Asp

Asp Asp His Ala Asp Ile Gly Gly Phe Gly Xaa Xaa Ser Xaa Xaa Val

Gln Ile Val Gln Gln Ile Asn His Asp Gly Glu Val Asn Arg Ala Arg

Tyr Met Pro Gln Asn Ser Phe Ile Ile Ala Thr Lys Thr Val Ser Ala

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

FEATURE:

(B) LOC

SEQUENCE DESCRIPTION:

Ser Ser Ser His Gly Phe Ala Ile Ser Ser Phe

5 10

Gln Leu Lys Pro Pro Pro Leu Ser Asn Pro Asn Pro Ser Pro Ser Pro  
20 25 30

Leu Pro Ala Asp Arg Arg Cys Arg Arg Gly Arg Arg Gly Gly Gly Arg  
35 40 45

Arg Gly Val Pro Arg Arg Gly Gly Gly Ala Pro His Gln Arg Gly Val  
50 55 60

Gln Asp Leu Glu Glu Glu His Thr Leu Pro Leu Arg Pro Arg His His  
65 70 75 80

Pro Arg Ala Arg Met Ala Leu Pro Tyr Arg Ala Val Ala Pro Arg Pro

85 90 95  
His Arg Ala Ala Gly Glu Gly Pro Leu Arg Pro Glu Asp Asp Pro Trp  
100 105 110  
His Ala His Leu

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

aaaaaactct	ctgtctctct	aggttttttg	attttagccg	ccgccgctgc	tcacttcaca	60
tcctctcgaga	agagcgctgc	tcctcgccga	tcgatacgat	ggcgcgtctc	tcgcacctcc	120
acaccgcgga	cgccctcaag	tcctctgagg	ctcacctcgc	cgcaaaaacc	tatgtgtctg	180
gtgactccat	tactaaggat	gacattaagg	tcttcgcgcg	ggtgccgctg	aaagcctggcg	240
ctgagtttcc	taaatgcccc	cgctggtacg	agaccgtctc	tgccggtctg	gcctcaagat	300
tcctcggttaa	ggctgtttgt	gtaaatctgc	ctgcgggata	agctcctcgt	gcagctgctc	360
ctgcgggtga	ggctgaggat	gatgatgacc	ttgatctttt	tggtgatgaa	actgaggagg	420
acaagaaggc	agctgatgag	cgctgcgcgc	ctgccaaagg	ctcttctaaa	aagaaagaaa	480
gtggtaaatc	ctccgtctct	atggatgtca	aaccatggga	cgatgagact	gatatgaaga	540
agctggaggga	ggctgtccgc	agtgtccaga	tggagggtct	gacttgggga	gcatacaaac	600
ttgtgcctgt	tggatacggc	atacaagaag	tgactatcat	gttgacaatt	gtgcagcgtc	660
ttgtgtccat	cgacactcta	attgaggacc	accttacgca	agagcccatc	aatgatgacg	720
tcacagagttg	gcacatttgt	gctttcaaca	agatctagag	ttcagtttct	gagatggggc	780
aacggcagcgc	gctcagctcg	tcaagtttgt	gctgggatgc	cagtttatcc	cttctagtct	840
attacagaaa	tggtgttcgc	agctgagctc	attataaaca	tcttggtctg	agttttattgt	900
tgagtggtgc	cagttttttt	caatatatcat	ttatcttaaa	aacagcggtg	ctgatgtttt	960
tttgtct						

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Lys	Thr	Leu	Cys	Leu	Ser	Arg	Phe	Phe	Asp	Phe	Ser	Arg	Arg	Arg	Cys
1			5						10						15
Ser	Ser	His	Ile	Pro	Arg	Glu	Asp	Ala	Cys	Ser	Ser	Pro	Ile	Asp	Thr
			20					25					30		
Met	Ala	Val	Phe	Ser	Asp	Leu	His	Thr	Ala	Asp	Gly	Leu	Lys	Ser	Leu
			35				40					45			
Glu	Ala	His	Leu	Ala	Gly	Lys	Thr	Tyr	Val	Ser	Gly	Asp	Ser	Ile	Thr
			50			55					60				
Lys	Asp	Asp	Ile	Lys	Val	Phe	Ala	Ala	Val	Pro	Ser	Lys	Pro	Gly	Ala
			65			70				75					80
Glu	Phe	Pro	Asn	Ala	Ala	Arg	Trp	Tyr	Glu	Thr	Val	Ser	Ala	Ala	Val
			85					90					95		
Ala	Ser	Arg	Phe	Pro	Gly	Lys	Ala	Val	Gly	Val	Asn	Leu	Pro	Ala	Gly
			100				105					110			
Ser	Arg	Pro	Ala	Ala	Ala	Ala	Pro	Ala	Asp	Glu	Ala	Glu	Asp	Asp	Asp

	115		120		125	
Asp	Leu	Asp	Leu	Phe	Gly	Asp
130						Glu
Asp	Glu	Arg	Ala	Ala	Ala	Ala
145						Lys
Gly	Lys	Ser	Ser	Val	Leu	Met
						Asp
Asp	Met	Lys	Lys	Leu	Glu	Glu
						Ala
Leu	Thr	Trp	Gly	Ala	Ser	Lys
						Leu
Lys	Met	Thr	Ile	Met	Leu	Thr
210						Ile
Thr	Leu	Ile	Glu	Asp	His	Leu
225						Thr
Gln	Ser	Cys	Asp	Ile	Val	Ala
						Phe
						Asn
						Lys
						Ile

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1501517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

Met	Ala	Val	Phe	Ser	Asp	Leu	His	Thr	Ala	Asp	Gly	Leu	Lys	Ser	Leu
1															
Glu	Ala	His	Leu	Ala	Gly	Lys	Thr	Tyr	Val	Ser	Gly	Asp	Ser	Ile	Thr
Lys	Asp	Asp	Ile	Lys	Val	Phe	Ala	Ala	Val	Pro	Ser	Lys	Pro	Gly	Ala
Glu	Phe	Pro	Asn	Ala	Ala	Arg	Trp	Tyr	Glu	Thr	Val	Ser	Ala	Ala	Val
Ala	Ser	Arg	Phe	Pro	Gly	Lys	Ala	Val	Gly	Val	Asn	Leu	Pro	Ala	Gly
65															
Ser	Ala	Pro	Ala	Ala	Ala	Ala	Pro	Ala	Asp	Glu	Ala	Glu	Asp	Asp	Asp
Asp	Leu	Asp	Leu	Phe	Gly	Asp	Glu	Thr	Glu	Glu	Asp	Lys	Lys	Ala	Ala
Asp	Glu	Arg	Ala	Ala	Ala	Ala	Lys	Ala	Ser	Ser	Lys	Lys	Lys	Glu	Ser
Gly	Lys	Ser	Ser	Val	Leu	Met	Asp	Val	Lys	Pro	Trp	Asp	Asp	Glu	Thr
Asp	Met	Lys	Lys	Leu	Glu	Glu	Ala	Val	Arg	Ser	Val	Gln	Met	Glu	Gly
145															
Leu	Thr	Trp	Gly	Ala	Ser	Lys	Leu	Val	Pro	Val	Gly	Tyr	Gly	Ile	Lys
Lys	Met	Thr	Ile	Met	Leu	Thr	Ile	Val	Asp	Asp	Leu	Val	Ser	Ile	Asp
Thr	Leu	Ile	Glu	Asp	His	Leu	Thr	Gln	Glu	Pro	Ile	Asn	Glu	Tyr	Val
Gln	Ser	Cys	Asp	Ile	Val	Ala	Phe	Asn	Lys	Ile					
210															

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..584  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

agctgacaac	cagacgcgc	agggtttcag	gcttccacga	atctcccgc	cgccctcaat	60
tcccctcgag	gccgcgcct	cctccctcgc	cttcggctct	cggttagtta	accatccagg	120
ttctgtcaag	atgtctgata	gccatgagac	tgacaggaaac	attgagattt	gaaaaattaa	180
gaaactgatc	aaggcattgg	aatcagccag	aggcaatggc	acaagcatga	tctctctaat	240
catgcccaca	cgatgacagg	ttgctcgagt	ggctaagatg	ttaggtgatg	aatatgggtac	300
tgcttcgaac	atcaagagta	gagttaatcg	tcaatctgtg	ttggctgccca	tcacctcagc	360
tcagacagag	ttgaagctct	acaacaaagt	gctctctaac	ggattgggtc	tgtacactgg	420
aactattgtt	actgaagacg	gaaaggaaag	gaaagttaac	attgattttg	agccattcaa	480
gcctatcaat	gtgtcaactc	acctttgtga	caacaagttc	cacactgagg	ctttaaatga	540
gctcttgtaa	tctgatgaca	agtttgggtt	cattgttatg	gatg		

(2) INFORMATION FOR SEQ ID NO:1865:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 194 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..194  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

Ala	Asp	Asn	Gln	Thr	Arg	Gln	Gly	Phe	Arg	Leu	Pro	Arg	Ile	Ser	Pro	
1				5				10					15			
Pro	Pro	Ser	Ile	Pro	Leu	Gly	Ala	Ala	Ser	Ser	Pro	Arg	Phe	Gly		
			20					25				30				
Pro	Arg	Leu	Val	Asn	His	Pro	Gly	Ser	Val	Lys	Met	Ser	Asp	Ser	His	
			35					40				45				
Glu	Thr	Asp	Arg	Asn	Ile	Glu	Ile	Trp	Lys	Ile	Lys	Lys	Leu	Ile	Lys	
			50					55				60				
Ala	Leu	Glu	Ser	Ala	Arg	Gly	Asn	Gly	Thr	Ser	Met	Ile	Ser	Leu	Ile	
			65					70				75			80	
Met	Pro	Pro	Arg	Asp	Gln	Val	Ala	Arg	Val	Ala	Lys	Met	Leu	Gly	Asp	
				85				90				95				
Glu	Tyr	Gly	Thr	Ala	Ser	Asn	Ile	Lys	Ser	Arg	Val	Asn	Arg	Gln	Ser	
			100					105				110				
Val	Leu	Ala	Ala	Ile	Thr	Ser	Ala	Gln	Gln	Arg	Leu	Lys	Leu	Tyr	Asn	
			115					120				125				
Lys	Val	Pro	Pro	Asn	Gly	Leu	Val	Leu	Tyr	Thr	Gly	Thr	Ile	Val	Thr	
			130					135				140				
Glu	Asp	Gly	Lys	Glu	Lys	Lys	Val	Thr	Ile	Asp	Phe	Glu	Pro	Phe	Lys	
			145					150				155			160	
Pro	Ile	Asn	Val	Ser	Leu	Tyr	Leu	Cys	Asp	Asn	Lys	Phe	His	Thr	Glu	
				165					170				175			
Ala	Leu	Asn	Glu	Leu	Leu	Glu	Ser	Asp	Asp	Lys	Phe	Gly	Phe	Ile	Val	
			180					185					190			
Met	Asp															

(2) INFORMATION FOR SEQ ID NO:1866:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..151  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

Met	Ser	Asp	Ser	His	Glu	Thr	Asp	Arg	Asn	Ile	Glu	Ile	Trp	Lys	Ile
1				5					10					15	
Lys	Lys	Leu	Ile	Lys	Ala	Leu	Glu	Ser	25	Ala	Arg	Gly	Asn	Gly	Thr
		20											30		Ser
Met	Ile	Ser	Leu	Ile	Met	Pro	Pro	Arg	Asp	Gln	Val	Ala	Arg	Val	Ala
		35				40						45			
Lys	Met	Leu	Gly	Asp	Glu	Tyr	Gly	Thr	Ala	Ser	Asn	Ile	Lys	Ser	Arg
	50					55					60				
Val	Asn	Arg	Gln	Ser	Val	Leu	Ala	Ala	Ile	Thr	Ser	Ala	Gln	Gln	Arg
	65				70					75				80	
Leu	Lys	Leu	Tyr	Asn	Lys	Val	Pro	Pro	Asn	Gly	Leu	Val	Leu	Tyr	Thr
				85					90					95	
Gly	Thr	Ile	Val	Thr	Glu	Asp	Gly	Lys	105	Glu	Lys	Lys	Val	Thr	Ile
			100										110		Asp
Phe	Glu	Pro	Phe	Lys	Pro	Ile	Asn	Val	Ser	Leu	Tyr	Leu	Cys	Asp	Asn
		115				120							125		
Lys	Phe	His	Thr	Glu	Ala	Leu	Asn	Glu	Leu	Leu	Glu	Ser	Asp	Asp	Lys
	130					135						140			
Phe	Gly	Phe	Ile	Val	Met	Asp									
	145				150										

(2) INFORMATION FOR SEQ ID NO:1867:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1501546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

Met	Ile	Ser	Leu	Ile	Met	Pro	Pro	Arg	Asp	Gln	Val	Ala	Arg	Val	Ala
1				5					10					15	
Lys	Met	Leu	Gly	Asp	Glu	Tyr	Gly	Thr	Ala	Ser	Asn	Ile	Lys	Ser	Arg
		20					25					30			
Val	Asn	Arg	Gln	Ser	Val	Leu	Ala	Ala	Ile	Thr	Ser	Ala	Gln	Gln	Arg
		35				40						45			
Leu	Lys	Leu	Tyr	Asn	Lys	Val	Pro	Pro	Asn	Gly	Leu	Val	Leu	Tyr	Thr
	50				55					60					
Gly	Thr	Ile	Val	Thr	Glu	Asp	Gly	Lys	Glu	Lys	Lys	Val	Thr	Ile	Asp
	65				70				75					80	
Phe	Glu	Pro	Phe	Lys	Pro	Ile	Asn	Val	Ser	Leu	Tyr	Leu	Cys	Asp	Asn
			85					90					95		
Lys	Phe	His	Thr	Glu	Ala	Leu	Asn	Glu	Leu	Leu	Glu	Ser	Asp	Asp	Lys
		100					105						110		
Phe	Gly	Phe	Ile	Val	Met	Asp									
		115													

(2) INFORMATION FOR SEQ ID NO:1868:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1030 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1501547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

aaagaagaacc	gtatgcacaga	gcgcgcgcctc	caagaagacct	ttccaggccgc	ccagctctcc	60
cgctctctctc	ctgtcttaacc	cgctcgtctct	cgcgcgcgcag	ggccgcaccg	cgcgctctcc	120
cacgctcacc	aactttgtgca	gggaagaacct	cccacacgcgc	tactttaacct	accacagaacg	180
gggatccacc	catcgccggc	cggaagtgggg	agccatccgc	gcgcgactgc	cacgtgmagt	240
ttacatgctc	caggcagcagg	aggctcactgc	tgccagagatg	gagcgacacct	tcattgccaat	300
caaacctcgt	ggtgtccaaa	gagcgctgat	ttcttgtagat	atgagccgat	ttgagagaaa	360
aggcttaaat	ctgtttgcca	tcaaacgtgat	tgttccatctc	aaagaattttg	ctgagagaacg	420
ctaccatgat	ctcaaggaaa	ggcctttctt	cggtgggttg	tgtgattttt	tcagctctgg	480
ccctgtgtctt	gcaattgtgt	gaagaaggaga	gggtgtctatc	aagtatggga	gaaaactaat	540
ttgtgccaca	gaccocacaga	aaactgaacc	aggaaccatc	aggggtgatc	ttgcacatgt	600
tgttggaaga	aacatcaatg	atggaagtga	tggtccagg	acagccagg	atgagatcgc	660
tttatggttt	gacccaacgt	ctgtgctctc	ctgtccacgc	actggggag	tgtgggatcta	720
tgggttgtaat	taacgacaga	gtcaactcgt	ttttttttct	tccttttgatc	tcggttttica	780
caaatgtcc	gcagacacct	gtcaataaag	tcgctacgct	cacttctgag		840
ttgtgattgt	cctcttcaggt	gtagtgaagg	atggaaaagg	agggaaata		900
ccgtgaataa	tagagcgtgc	actgagtagt	cgcgagtgtc	aaatcaaat	atataatccc	960
gtcaactgg	tcattgtaatc	caagatggtg	atgcagatgt	ttctttggat	ctattttctc	1020
gcatatggcc						

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1501548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

1	Lys	Gly	Thr	Leu	Ala	Met	Ser	Ala	Ala	Ser	Lys	Lys	Leu	Phe	Gln	Ala
2	Ala	Arg	Ser	Leu	Val	Leu	Ser	Ala	Ser	Asn	Arg	Ser	Val	Leu	Ala	Ala
3	Glu	Gly	Arg	Thr	Ala	Ala	Leu	Ala	Thr	Leu	Thr	Asn	Phe	Gly	Arg	Lys
4	Thr	Leu	Pro	Thr	Ala	Tyr	Leu	Ser	Tyr	His	Lys	Gln	Gly	Ser	His	His
5	Ala	Ala	Ser	Gly	Trp	Gly	Ala	Ile	Ala	Ala	Val	Pro	Ala	Xaa	Val	80
6	Tyr	Met	Leu	Gln	Asp	Gln	Glu	Ala	His	Ala	Ala	Glu	Met	Glu	Arg	Thr
7	Phe	Ile	Ala	Ile	Lys	Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile	Ser	Glu
8	Ile	Met	Ser	Arg	Phe	Glu	Arg	Lys	Gly	Gly	Lys	Lys	Val	Ala	Ile	Lys
9	Leu	Ile	Val	Pro	Ser	Phe	Glu	Phe	Ala	Glu	Lys	His	Thr	His	Asp	Leu
10	Lys	Gln	Arg	Pro	Phe	Phe	Ser	Gly	Leu	Cys	Asp	Phe	Ile	Ser	Ser	Gly
11	Pro	Val	Leu	Ala	Met	Val	Trp	Glu	Gly	Glu	Gly	Val	Leu	Lys	Tyr	Gly
12	Arg	Lys	Leu	Ile	Gly	Ala	Thr	Asp	Pro	Gln	Lys	Ser	Glu	Pro	Gly	Thr
13	Ile	Arg	Gly	Asp	Leu	Ala	Ile	Val	Val	Gly	Arg	Asn	Ile	Ile	His	Gly

(2) INFORMATION FOR SEQ ID NO:1870:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1501549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

Met	Ser	Ala	Ala	Ser	Lys	Lys	Leu	Phe	Gln	Ala	Ala	Arg	Ser	Leu	Val
1				5					10					15	
Leu	Ser	Ala	Ser	Asn	Arg	Ser	Val	Leu	Ala	Ala	Glu	Gly	Arg	Thr	Ala
			20					25					30		
Ala	Leu	Ala	Thr	Leu	Thr	Asn	Phe	Gly	Arg	Lys	Thr	Leu	Pro	Thr	Ala
		35					40					45			
Tyr	Leu	Ser	Tyr	His	Lys	Gln	Gly	Ser	His	His	Ala	Ala	Ser	Gly	Trp
	50					55					60				
Gly	Ala	Ile	Ala	Ala	Ala	Val	Pro	Ala	Xaa	Val	Tyr	Met	Leu	Gln	Asp
65					70					75					80
Gln	Glu	Ala	His	Ala	Ala	Glu	Met	Glu	Arg	Thr	Phe	Ile	Ala	Ile	Lys
			85						90					95	
Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile	Ser	Glu	Ile	Met	Ser	Arg	Phe
			100					105					110		
Glu	Arg	Lys	Gly	Tyr	Lys	Leu	Val	Ala	Ile	Lys	Leu	Ile	Val	Pro	Ser
		115					120					125			
Lys	Glu	Phe	Ala	Glu	Lys	His	Tyr	His	Asp	Leu	Lys	Glu	Arg	Pro	Phe
		130				135					140				
Phe	Ser	Gly	Leu	Cys	Asp	Phe	Leu	Ser	Ser	Gly	Pro	Val	Leu	Ala	Met
145					150					155					160
Val	Trp	Glu	Gly	Glu	Gly	Val	Ile	Lys	Tyr	Gly	Arg	Lys	Leu	Ile	Gly
			165						170					175	
Ala	Thr	Asp	Pro	Gln	Lys	Ser	Glu	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Leu
			180					185					190		
Ala	Ile	Val	Val	Gly	Arg	Asn	Ile	Ile	His	Gly	Ser	Asp	Gly	Pro	Glu
		195					200					205			
Thr	Ala	Lys	Asp	Glu	Ile	Ala	Leu	Trp	Phe	Glu	Pro	Lys	Glu	Leu	Val
	210					215					220				
Ser	Tyr	Thr	Ser	Asn	Ala	Glu	Lys	Trp	Ile	Tyr	Gly	Val	Asn		
225				230						235					

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1501550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

Met Leu Gln Asp Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr Phe  
1 5 10 15  
Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu Ile  
20 25 30  
Met Ser Arg Phe Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys Leu  
35 40 45  
Ile Val Pro Ser Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu Lys  
50 55 60  
Glu Arg Pro Phe Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly Pro  
65 70 75 80  
Val Leu Ala Met Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly Arg  
85 90 95  
Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr Ile  
100 105 110  
Arg Gly Asp Leu Ala Ile Val Val Gly Arg Asn Ile Ile His Gly Ser  
115 120 125  
Asp Gly Pro Glu Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu Pro  
130 135 140  
Lys Glu Leu Val Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr Gly  
145 150 155 160  
Val Asn

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

attggcgac	aaatcagcaa	caggcgcggc	gaacaaatgg	ggcgctgtga	gtccggaggc	60
ctctttagtt	taggggctct	ggcccargtc	gacctgtgtt	tttttttcca	atagcggatt	120
arcaccaacag	agaacctttc	acggccctgc	tagagagagt	ttaacaatca	aaatagaaaa	180
cagaaacaaa	attcatcaga	gtgagagttc	atcttcttct	ccaagctgat	ttctgtttgt	240
tagctactca	cgtaacacaga	aaatctcgcg	ttcagctctc	ctccagctctc	tccgcctccc	300
gcttactctt	ctgactctgt	cctctttcgt	ttctttcttg	tggcgacagg	ctggcggtcg	360
gggtgctgcg	ccgctctcac	cttcaccgcc	gacgagcatt	cacaagtagt	ggtctcttca	420
wggtggcgcg	gtagagggtga	cgaaaaagcc	ttgacaatga	gcagcatagg	cacaggttat	480
gatctgtctg	tcaccacctt	ctctcccgat	ggccggtctc	tccaggtcga	gtatgccacc	540
aargctgtcg	acaaacagcg	gac				

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Thr Phe Ser  
1 5 10 15  
Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Xaa Ala Val Asp  
20 25 30  
Asn Ser Gly

35

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

aggggcaaaag	aggaaaatttc	tttgggctgg	gtctaataaa	ccctaattggg	ctgcggcctc	60
gtagataaac	cagcactact	catccgtcgc	cccacggaa	tttcggcggc	gcsgcggtct	120
ctgtatctca	accaagcgct	gtctccgctc	cggtcacccg	tcactccacg	caaacatgtc	180
gaggaggaag	accagggagc	ccaaggagga	gaacgtcacc	cttggaccga	ctgtccgtga	240
aggagagtat	gtcttttgtg	tcgtctacat	ctttgcaccc	ttcaatgaca	ccttcattca	300
tatcactgat	ttgtctggga	gggaaactct	ggttcggatc	accggtggca	tgaaggtgaa	360
ggctgacgct	gaagagtcgt	caacctacgc	tgtatgctt	gctgctcaag	acgtcgacaa	420
caagaccaa	gagcttgcca	ttactgcact	gcacattaag	cttcgtgcc	ccggaggcaa	480
gatgaaaatc	ggacgcattg	aggacgct	ctgtgcctc	agggcgcttg	ctcgttctgt	540

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

Met	Gly	Cys	Gly	Leu	Val	Asp	Lys	Pro	Ala	Leu	Leu	Ile	Arg	Arg	Pro
1		5						10						15	
Thr	Glu	Val	Ser	Ala	Ala	Xaa	Arg	Ala	Arg	Asp	Leu	Asn	Gln	Gly	Val
		20					25					30			
Ser	Pro	Leu	Arg	Ser	Pro	Val	Thr	Pro	Arg	Lys	His	Val	Glu	Glu	
		35					40				45				
Asp	Gln	Gly	Ala	Gln	Gly	Gly	Glu	Arg	His	Pro	Trp	Thr	His	Cys	Pro
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met	Ser	Arg	Arg	Lys	Thr	Arg	Glu	Pro	Lys	Glu	Glu	Asn	Val	Thr	Leu
1				5				10					15		
Gly	Pro	Thr	Val	Arg	Glu	Gly	Glu	Tyr	Val	Phe	Xaa	Val	Ala	His	Ile
		20					25					30			

Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly  
35 40 45  
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp  
50 55 60  
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Gln Asp Val  
65 70 75 80  
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu  
85 90 95  
Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr Pro Gly Pro Gly Ala Gln  
100 105 110  
Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly Met Lys Ile Gly Arg Ile  
115 120 125  
Glu Asp  
130

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

Met Lys Val Lys Ala Asp Arg Asp Glu Ser Pro Tyr Ala Ala Met  
1 5 10 15  
Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr  
20 25 30  
Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr  
35 40 45  
Pro Gly Pro Gly Ala Gln Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly  
50 55 60  
Met Lys Ile Gly Arg Ile Glu Asp  
65 70

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

gtcatcaatc aaataactcag acaacccatgg ggcaccacgca ggcgcasacg gcaaggacga 60  
caccgaggag ctgctttgcag cccaccggca gctgtrgtgc catgccctgg gctacgtcaa 120  
gtccatggcg ctaaatggcg cccctggacct gcgcaccccc gacaccatcg accgctgcgg 180  
cgggagcgcc accctggggcg agctgctcgc cgccagcgag atccccggcg ccaaccacga 240  
ctacctccgg cggttcctatgc gaacgctgac agccatgcgc atcttcggcg ccagccacga 300  
ccccgcgaag gccgacgacg cgcccgccat ctccctaccag ctgaccgccg cgtcccgct 360  
gctcgtcagc agcagcagca gcgtcgacga cgccggccgg cctcgaagga gaacactact 420  
accgccagca tctctcccaa catcgccac ctgggtccgcc ccaacaccat ctccctgctg 480  
ttcagcatgg gcgag

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..165  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501572  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:  
Val Ile Asn Gln Ile Leu Arg Gln Pro Trp Gly Thr Ser Arg Arg Xaa  
1 5 10 15  
Arg Gln Gly Arg His Arg Gly Ala Ala Cys Ser Pro Pro Ala Ala Xaa  
20 25 30  
Val Pro Cys Pro Gly Leu Arg Gln Val His Gly Ala Gln Val Arg Pro  
35 40 45  
Gly Pro Ala His Pro Arg His His Arg Pro Leu Arg Arg Glu Arg His  
50 55 60  
Pro Gly Arg Ala Ala Arg Arg Gln Arg Asp Pro Gly Val Gln Pro Arg  
65 70 75 80  
Leu Pro Pro Ala Gly His Ala His Ala Asp Ser His Ala His Leu Arg  
85 90 95  
Gly Gln Pro Arg Pro Arg Gln Gly Arg Arg Gly Arg His Leu Leu  
100 105 110  
Pro Ala Asp Pro Gly Val Pro Ala Ala Arg Gln Gln Gln Gln Arg  
115 120 125  
Arg Arg Arg Arg Ala Ser Lys Glu Asn Thr Thr Thr Pro Ser Ile  
130 135 140  
Leu Pro Asn Ile Ala His Leu Val Arg Pro Asn Thr Ile Ser Leu Leu  
145 150 155 160  
Phe Ser Met Gly Glu  
165  
(2) INFORMATION FOR SEQ ID NO:1880:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 164 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..164  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501573  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:  
Ser Ser Ile Lys Tyr Ser Asp Asn His Gly Ala Pro Ala Gly Ala Xaa  
1 5 10 15  
Gly Lys Asp Asp Thr Glu Glu Leu Leu Ala Ala His Arg Gln Leu Xaa  
20 25 30  
Cys His Ala Leu Gly Tyr Val Lys Ser Met Ala Leu Lys Cys Ala Leu  
35 40 45  
Asp Leu Arg Ile Pro Asp Thr Ile Asp Arg Cys Gly Gly Ser Ala Thr  
50 55 60  
Leu Gly Glu Leu Leu Ala Ala Ser Glu Ile Pro Ala Ser Asn His Asp  
65 70 75 80  
Tyr Leu Arg Arg Val Met Arg Thr Leu Thr Ala Met Arg Ile Phe Ala  
85 90 95  
Ala Ser His Asp Pro Ala Lys Ala Asp Asp Ala Ala Ala Ile Ser Tyr  
100 105 110  
Gln Leu Thr Pro Ala Ser Arg Leu Leu Val Ser Ser Ser Ser Val  
115 120 125  
Asp Asp Ala Ala Gly Pro Arg Arg Arg Thr Leu Leu Pro Arg Ala Ser  
130 135 140  
Ser Pro Thr Ser Pro Thr Trp Ser Ala Pro Thr Pro Ser Pro Cys Cys

145  
Ser Ala Trp Ala

150

155

160

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

Met Ala Leu Lys Cys Ala Leu Asp Leu Arg Ile Pro Asp Thr Ile Asp  
1 5 10 15  
Arg Cys Gly Gly Ser Ala Thr Leu Gly Glu Leu Leu Ala Ala Ser Glu  
20 25 30  
Ile Pro Ala Ser Asn His Asp Tyr Leu Arg Arg Val Met Arg Thr Leu  
35 40 45  
Thr Ala Met Arg Ile Phe Ala Ala Ser His Asp Pro Ala Lys Ala Asp  
50 55 60  
Asp Ala Ala Ala Ile Ser Tyr Gln Leu Thr Pro Ala Ser Arg Leu Leu  
65 70 75 80  
Val Ser Ser Ser Ser Ser Val Asp Asp Ala Gly Pro Arg Arg Arg  
85 90 95  
Thr Leu Leu Pro Arg Ala Ser Ser Pro Thr Ser Pro Thr Trp Ser Ala  
100 105 110  
Pro Thr Pro Ser Pro Cys Cys Ser Ala Trp Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

atcttaacag ccaggaagct ggcgtcttgc ttgtccttgt tcttttccca cccggctacc 60  
cccgctgctcg ccgcccgttt ccccggtggt tcagagctcg agtcggctag ctaggccgcc 120  
tggtctaatt ccttgcttcc tataagtaca ggttcattgt gtgctgtgct cccagctcca 180  
tcaactgacac aagagagcac gctactactc atcactcgcc aactgcgaga gatcagggag 240  
gcggcacact ccatccactg accgctcatg gcgaaggctc acctctacgt cgccgcggcc 300  
tgccgcgctg tcctcgcgct cgccgccccg gccctcgccg gcgaccccga catgctgcag 360  
gacgtctgcc cggtctgacta cgcttccccg gtgaagctga acgggttcgc gtgcaaggcg 420  
aacctttcgg cggacgactt ctctctcgac gggctgagga accccggcaa caccacaac 480  
ccggcgggct ccgtggtgac

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1501583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

```
Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu
1          5          10          15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20          25          30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35          40          45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50          55          60
Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1501584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

```
Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1          5          10          15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe
20          25          30
Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val
35          40          45
Val
```

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

```
agtggacagg tggcatcttc tgcgtcgca acacctcgcc gcccaaacgt aacgtcccca 60
acaaactcct ctccctccccc ttccacagcag aagtaaccag gccggccatg gacatgcagt 120
tcttccccga caggcgcaact tgcgcctgcg gasegctggc acggcatgta ctttcacggc 180
gaggaagacg gggtaggagt caccctgcgc cggcgccgtg ggaagctgaa cgaggcgtag 240
gtrgtgcacc acctcgagcg caacggcgct aactacgtcc tcttccacag cgccgcctac 300
ggcggttacc tcgccatcgt aagcatggaa gcgactccgg cgccgtcttc gggccaaggt 360
caagggccccc gcgcgaactgt cctgcgcgtc cagcgccctt acgacgcccc agggcagaa 420
gacgtctcgt ggcagttccc ctctgcgacg acgggtccga cgatgtcgtc atgcgcaatc 480
gcgtgtacgg cactggcac aactaaggcg acgag
```

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

Ser	Gly	Gln	Val	Ala	Ser	Ser	Ala	Leu	Ala	Thr	Pro	Arg	Arg	Pro	Asn
1			5					10						15	
Val	Thr	Val	Pro	Thr	Asn	Ser	Ser	Pro	Ser	Gln	Gln	Lys	Tyr		
			20				25					30			
Gln	Arg	Arg	Pro	Trp	Thr	Cys	Ser	Ser	Pro	Thr	Gly	Ala	Leu	Ala	
		35					40				45				
Pro	Ala	Xaa	Arg	Trp	His	Gly	Met	Tyr	Leu	His	Ala	Glu	Glu	Asp	Gly
		50				55					60				
Val	Arg	Ile	Thr	Leu	Arg	Arg	Arg	Gly	Thr	Leu	Asn	Glu	Ala	Trp	
65				70					75					80	
Xaa	Val	His	His	Glu	Arg	Asn	Gly	Val	Asn	Tyr	Val	Leu	Leu	His	
			85					90					95		
Ser	Ala	Ala	Tyr	Gly	Arg	Tyr	Leu	Ala	Ile	Val	Ser	Met	Glu	Ala	Thr
			100				105					110			
Pro	Ala	Pro	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Ala	Arg	Arg	Thr	Cys	Leu
		115				120						125			
Ala	Val	Gln	Arg	Leu	Tyr	Asp	Ala	Pro	Gly	Gln	Asn	Asp	Val	Leu	Trp
		130				135					140				
Gln	Phe	Arg	Phe	Ala	Thr	Thr	Gly	Pro	Thr	Met	Ser	Ser	Cys	Ala	Ile
145				150						155					160
Ala	Cys	Thr	Ala	Pro	Gly	Thr	Thr	Thr	Ala	Thr					
			165												

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

Trp	Thr	Gly	Gly	Ile	Phe	Cys	Ala	Arg	Asn	Thr	Ser	Ala	Pro	Lys	Arg
1				5					10					15	
Asn	Arg	Pro	Asn	Lys	Leu	Leu	Ser	Leu	Pro	Phe	Pro	Ala	Glu	Val	Pro
			20					25					30		
Ala	Pro	Ala	Met	Asp	Met	Gln	Phe	Phe	Pro	Asp	Arg	Arg	Thr	Cys	Ala
		35				40					45				
Cys	Gly	Xaa	Leu	Ala	Arg	His	Val	Pro	Ser	Arg	Arg	Gly	Arg	Arg	Gly
		50				55					60				
Glu	Asp	His	Pro	Ala	Pro	Ala	Pro	Trp	Asp	Ala	Glu	Arg	Gly	Val	Gly
65				70					75					80	
Xaa	Ala	Pro	Pro	Arg	Ala	Gln	Arg	Arg	Gln	Leu	Arg	Pro	Pro	Pro	Gln
			85					90						95	
Arg	Arg	Leu	Arg	Pro	Leu	Pro	Arg	His	Arg	Lys	His	Gly	Ser	Asp	Ser
			100				105					110			
Gly	Ala	Val	Phe	Gly	Pro	Arg	Ser	Arg	Arg	Pro	Pro	His	Leu	Pro	Arg
		115				120						125			
Arg	Pro	Ala	Pro	Leu	Arg	Arg	Pro	Arg	Ala	Glu	Arg	Arg	Pro	Val	Ala
		130				135					140				
Val	Pro	Leu	Arg	Asp	Asp	Gly	Ser	Asp	Asp	Val	Val	Met	Arg	Asn	Arg
145				150						155					160
Val	Tyr	Gly	Thr	Trp	His	Asn	Tyr	Gly	Asp	Glu					
			165						170						

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Met	Asp	Met	Gln	Phe	Phe	Pro	Asp	Arg	Arg	Thr	Cys	Ala	Cys	Gly	Xaa
1			5							10				15	
Leu	Ala	Arg	His	Val	Pro	Ser	Arg	Arg	Gly	Arg	Arg	Gly	Glu	Asp	His
			20						25				30		
Pro	Ala	Pro	Ala	Pro	Trp	Asp	Ala	Glu	Arg	Gly	Val	Gly	Xaa	Ala	Pro
			35					40					45		
Pro	Arg	Ala	Gln	Arg	Arg	Gln	Leu	Arg	Pro	Pro	Gln	Arg	Arg	Leu	
			50				55				60				
Arg	Pro	Leu	Pro	Arg	His	Arg	Lys	His	Gly	Ser	Asp	Ser	Gly	Ala	Val
			65				70			75				80	
Phe	Gly	Pro	Arg	Ser	Arg	Arg	Pro	Pro	His	Leu	Pro	Arg	Arg	Pro	Ala
			85					90					95		
Pro	Leu	Arg	Arg	Pro	Arg	Ala	Glu	Arg	Arg	Pro	Val	Ala	Val	Pro	Leu
			100				105						110		
Arg	Asp	Asp	Gly	Ser	Asp	Asp	Val	Val	Met	Arg	Asn	Arg	Val	Tyr	Gly
			115				120					125			
Thr	Trp	His	Asn	Tyr	Gly	Asp	Glu								
			130				135								

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

atcacaaagca	atcgatcaag	ctagcatggc	gggtgaaggtg	tgggtgttcg	ccgtggcact	60
gatgatgtgc	gctgggtgtag	ggcttggagc	tgacgacgac	ggcggcagac	cttattagcc	120
gctgtcgtct	garctcgccc	aactaccgcg	gcgccctggc	aaaggccatc	ctcttcttcg	180
argggcagcg	gtcggggcg	ctgccggcaa	accagagagt	cagggtggcg	ggggactcgg	240
cgctcaccca	cgggccaacc	gaaacagtga	acttgacggg	tggctactac	gacgccggag	300
acaacgtcaa	gttcggtttc	ccgatggcgt	tcagcgctac	cttcctgarc	tggagcrccg	360
tcgagtaccg	cbacgaggtg	gcggcgccgg	gtcagctccg	cmacctcccg	tccgccatcc	420
agtkggggcg	cgacttcctt	ctccgtdecc	ac			

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:  
Ser Gln Ala Ile Asp Gln Ala Ser Met Ala Val Lys Val Trp Val Phe  
1 5 10 15  
Ala Val Ala Leu Met Met Cys Ala Gly Val Gly Leu Gly Ala Asp Asp  
20 25 30  
Asp Gly Gly Xaa Pro Tyr  
35

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..30  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:  
Met Ala Val Lys Val Trp Val Phe Ala Val Ala Leu Met Met Cys Ala  
1 5 10 15  
Gly Val Gly Leu Gly Ala Asp Asp Asp Gly Gly Xaa Pro Tyr  
20 25 30

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..43  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:  
Met Ala Phe Ser Val Thr Leu Leu Xaa Trp Ser Xaa Val Glu Tyr Arg  
1 5 10 15  
Xaa Glu Val Ala Ala Ala Gly Gln Leu Arg Xaa Leu Arg Ser Ala Ile  
20 25 30  
Gln Xaa Gly Ala Asp Phe Leu Leu Arg Xaa His  
35 40

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..501  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

aaactgctgg	aatatactta	caccgggaag	aaggcgaaag	ccgtcgcgct	ctcgggcrgcg	60
gcggcgccgg	cgccagcggc	gatgctgtcg	ttcgagcagc	aggtgtgtgg	ggatctgggtg	120
gaagatccga	acggaggtct	ggtggtgctc	tctctgggtc	tcctctctcg	ttccctagcc	180
gctaccctcc	tcctccatct	ccaccagacc	cccggcaacg	cggttgagg	aggatgtctc	240
ctcgtctctc	ccgccaccga	taccctcaag	gccgggatcc	ggcgccgcct	ccaagacaag	300
ctgcaggttc	acgacgtgcc	ccctgacctc	gccgcgcasa	ggcgccnmm	cccttacgcc	360
tctgggtgc	ttcttctctc	ttcccccg	cmctcgcmcg	cgacctctc	amctcccgcm	420
ttctccctc	ccgcgtccaa	gcctactctc	ttcttctccg	cccacmgtc	camcgatacc	480

tctctcgatg ctttcacgtg c

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1501625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Lys Leu Leu Glu Tyr Thr Tyr Thr Gly Lys Lys Ala Lys Ala Val Ala  
1 5 10 15  
Leu Ser Xaa Ala Ala Ala Ala Ala Ala Ala Met Leu Ala Phe Glu  
20 25 30  
Gln Gln Val Leu Ala Asp Leu Val Glu Asp Pro Asn Gly Gly Leu Val  
35 40 45  
Val Leu Ser Ser Gly Leu Pro Leu Ala Ser Leu Ala Ala Thr Leu Leu  
50 55 60  
Leu His Leu His Gln Thr Pro Gly Asn Ala Ala Gly Gly Gly Cys Leu  
65 70 75 80  
Leu Val Leu Ser Ala Thr Asp Thr Leu Lys Ala Arg Ile Arg Arg Arg  
85 90 95  
Leu Gln Asp Lys Leu Gln Val His Asp Val Pro Pro Asp Leu Ala Ala  
100 105 110  
Xaa Ser Ala Xaa Xaa Leu Tyr Ala Ser Gly Leu Leu Ser Ser Ser Leu  
115 120 125  
Pro Ala Xaa Ser Xaa Pro Thr Ser Ser Xaa Pro Xaa Ser Ser Pro Pro  
130 135 140  
Ala Ser Lys Pro Tyr Ser Ser Ser Pro Pro His Xaa Ser Xaa Asp Thr  
145 150 155 160  
Ser Ser Asp Ala Phe Ile Cys  
165

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

Thr Ala Gly Ile Tyr Leu His Arg Glu Gly Glu Gly Arg Arg Ala  
1 5 10 15  
Leu Gly Xaa Gly Gly Gly Gly Ser Gly Asp Ala Cys Val Arg Ala  
20 25 30  
Ala Gly Val Gly Gly Ser Gly Gly Arg Ser Glu Arg Arg Ser Gly Gly  
35 40 45  
Ala Leu Leu Gly Ser Pro Ser Arg Phe Pro Ser Arg Tyr Pro Pro Pro  
50 55 60  
Pro Ser Pro Pro Asp Pro Arg Gln Arg Gly Trp Arg Arg Met Ser Pro  
65 70 75 80  
Arg Pro Leu Arg His Arg Tyr Pro Gln Gly Pro Asp Pro Ala Pro Pro  
85 90 95  
Pro Arg Gln Ala Ala Gly Ser Arg Arg Ala Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1501627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

Met	Leu	Ala	Phe	Glu	Gln	Gln	Val	Leu	Ala	Asp	Leu	Val	Glu	Asp	Pro
1				5				10					15		
Asn	Gly	Gly	Leu	Val	Val	Leu	Ser	Ser	Gly	Leu	Pro	Leu	Ala	Ser	Leu
			20				25						30		
Ala	Ala	Thr	Leu	Leu	Leu	His	Leu	Gln	Thr	Pro	Gly	Asn	Ala	Ala	
			35				40					45			
Gly	Gly	Gly	Cys	Leu	Leu	Val	Leu	Ser	Ala	Thr	Asp	Thr	Leu	Lys	Ala
			50				55					60			
Arg	Ile	Arg	Arg	Arg	Leu	Gln	Asp	Lys	Leu	Gln	Val	His	Asp	Val	Pro
					70					75				80	
Pro	Asp	Leu	Ala	Ala	Xaa	Ser	Ala	Xaa	Xaa	Leu	Tyr	Ala	Ser	Gly	Leu
					85					90				95	
Leu	Ser	Ser	Ser	Leu	Pro	Ala	Xaa	Ser	Xaa	Pro	Thr	Ser	Ser	Xaa	Pro
					100					105				110	
Xaa	Ser	Ser	Pro	Pro	Ala	Ser	Lys	Pro	Tyr	Ser	Ser	Ser	Pro	Pro	His
					115					120				125	
Xaa	Ser	Xaa	Asp	Thr	Ser	Ser	Asp	Ala	Phe	Ile	Cys				
					130					135				140	

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427

(D) OTHER INFORMATION: / Ceres Seq. ID 1501632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

aaactctgct	gcattctctt	ccactctcca	gtctccacta	gcactcagtcg	ccgctgccta	60
tcctcgagca	ccatttccat	caacagcatc	cgctcttggc	aagctagcga	casaaactcat	120
ggcactccgc	gcgcttgaca	acacgatgcc	cgcmgcccgc	gaggagcgcg	ccaagaagct	180
ggctaaggtg	ggcgctcccg	cmgcmgcccgc	caaggcccgcm	gctcccccg	ggagtggcgg	240
caagaagaag	aaggggaacg	acagagaactc	ggcgccaag	gccacggcg	cgcgcgcgga	300
gcaggcmgtg	gagtacatct	cgctggagga	gctggaggcg	gcggccaacc	ctaaggccaa	360
ggccgcgggg	ctggctcgcg	gccttgactc	caaggactgg	gtcaggacct	gcraggcgct	420
caacgac						

(2) INFORMATION FOR SEQ ID NO:1898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

Asn Ser Ala Ala Ser Ser Ser Thr Leu Gln Ser Pro Leu Ala Ser Val  
1 5 10 15  
Ala Ala Ala Tyr Pro Arg Ala Pro Phe Pro Ser Thr Ala Ser Ala Ser  
20 25 30  
Gly Lys Leu Ala Thr Xaa Leu Met Ala Leu Arg Ala Leu Asp Asn Thr  
35 40 45  
Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly  
50 55 60  
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly  
65 70 75 80  
Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala  
85 90 95  
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu  
100 105 110  
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu  
115 120 125  
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

Met Ala Leu Arg Ala Leu Asp Asn Thr Met Pro Xaa Ala Val Glu Glu  
1 5 10 15  
Arg Pro Lys Lys Val Ala Lys Val Gly Val Pro Xaa Xaa Ala Ala Lys  
20 25 30  
Ala Xaa Ala Ser Pro Gly Ser Gly Gly Lys Lys Lys Lys Gly Asn Asp  
35 40 45  
Glu Asn Ser Ala Pro Arg Ala Thr Ala Ala Ala Ala Glu Gln Xaa Val  
50 55 60  
Glu Tyr Ile Ser Ser Glu Glu Leu Glu Ala Ala Asn Pro Lys Ala  
65 70 75 80  
Lys Ala Ala Gly Leu Val Ala Gly Leu Asp Ser Lys Asp Trp Val Arg  
85 90 95  
Thr Cys Xaa Ala Leu Asn Asp  
100

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly  
1 5 10 15  
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly  
20 25 30

Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala  
35 40 45  
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu  
50 55 60  
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu  
65 70 75 80  
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp  
85 90

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..541
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

ccggaacgcc	cgccccgtcc	gtccctctccc	catccacatc	catcccggtg	gctccctactg	60
ctctctcgatt	tgatcacccga	ttagggggagg	cggtttacca	gtgagcacgc	gcgagaratat	120
ggataggagg	aaagggaagc	tagcggsttc	gctctcgccg	ggagatggcg	cargcggtkg	180
aggagtggtta	ccggcagatg	cccatcatca	cgcgcctccta	cctcamcgcc	gctgtcgctca	240
ccaccgtcgg	ctgcamcctc	gaaatcattt	cgccgtatca	cctgtacctt	aaaccgaagc	300
tcgtgtgtgca	gcactacgag	atttrcgccc	tcgtcaccaa	sttsctcttan	yttccgcaaa	360
gatggatttg	gattttctat	tccacatgtw	ctttcttgca	cgatactgca	agctttctgga	420
ggaaaactca	tttagaggaa	gaactgctga	ctttttttac	atgcwcttgt	ttgggtctac	480
tgtctctaact	ggcattgggt	ctgatcgagg	ggatgatacc	ttacatttct	gagacatttg	540

c

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Met	Ala	Xaa	Ala	Xaa	Glu	Glu	Trp	Tyr	Arg	Gln	Met	Pro	Ile	Ile	Thr
1				5				10					15		
Arg	Ser	Tyr	Leu	Xaa	Ala	Ala	Val	Val	Thr	Thr	Val	Gly	Cys	Xaa	Leu
			20					25				30			
Glu	Ile	Ile	Ser	Pro	Tyr	His	Leu	Tyr	Leu	Asn	Pro	Lys	Leu	Val	Val
			35					40				45			
Gln	His	Tyr	Glu	Ile	Xaa	Arg	Leu	Val	Thr	Xaa	Xaa	Leu	Xaa	Xaa	Pro
			50				55				60				
Gln	Arg	Trp	Ile	Trp	Ile	Phe	Tyr	Ser	Thr	Cys	Xaa	Phe	Leu	His	Asp
			65				70				75			80	
Thr	Ala	Ser	Phe	Trp	Arg	Lys	Thr	His	Leu	Glu	Glu	Glu	Leu	Leu	Thr
				85				90				95			
Phe	Phe	Thr	Cys	Xaa	Cys	Leu	Val	Leu	Leu	Ser					
				100				105							

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..96  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501641  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:  
Met Pro Ile Ile Thr Arg Ser Tyr Leu Xaa Ala Ala Val Val Thr Thr  
1 5 10 15  
Val Gly Cys Xaa Leu Glu Ile Ile Ser Pro Tyr His Leu Tyr Leu Asn  
20 25 30  
Pro Lys Leu Val Val Gln His Tyr Glu Ile Xaa Arg Leu Val Thr Xaa  
35 40 45  
Xaa Leu Xaa Xaa Pro Gln Arg Trp Ile Trp Ile Phe Tyr Ser Thr Cys  
50 55 60  
Xaa Phe Leu His Asp Thr Ala Ser Phe Trp Arg Lys Thr His Leu Glu  
65 70 75 80  
Glu Glu Leu Leu Thr Phe Phe Thr Cys Xaa Cys Leu Val Leu Leu Ser  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1904:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..56  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501642  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:  
Met Asp Leu Asp Phe Leu Phe His Met Xaa Phe Leu Ala Arg Tyr Cys  
1 5 10 15  
Lys Leu Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe  
20 25 30  
Tyr Met Xaa Leu Phe Gly Ala Thr Val Leu Thr Gly Ile Gly Ser Asp  
35 40 45  
Arg Arg Asp Asp Thr Leu His Phe  
50 55

(2) INFORMATION FOR SEQ ID NO:1905:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1144 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1144  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501643  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:  
tttacaggca cagctaaagc aagagtcact gctaaggcaa caggagcaac aacaattagc 60  
tgaacaatcc cagctgaggc aacaagagca agaaaaacta gccaaagagc aaacccgtat 120  
tgctctctct gaggcctgaaa agcaacagtt ggaagaccata attactatgt tgacaaagaa 180  
agctacagag gacgcttctg agtttgctgc acgcaaggca ttttcaatgc aagataggga 240  
aaaaacttgaa cagcagttgc atgacatggc ttgtgatgt gagaggctag aggggagtcg 300  
tcaaaaaact ctaatggaga ttgattctca atcgtcagaa atagagaaac tgtttgagga 360  
gaactcagcc ttatctgctt cttatcaaga agccattgat gttactgtac aatgggaaaa 420  
ccagaaaatt tcaggttaga gactgtctga agcaaaatga agagctccgt tctcacttgg 480

agaaactaag	acttgaacaa	gttagcctgt	tgaagtaag	caatatcgct	acccaatcag	540
atggggcaaac	tgaaaacagt	atctcaaacc	caccacaaat	ggctatcgag	aatatttctc	600
taaarggwtc	agctttataaa	agwacagwgc	agatctgagg	ggttgctggc	agagataatg	660
aaacttttcag	ctgagcttag	gaaagcagtc	catgcacaga	ataaccttgc	acgctttatac	720
agacctgtat	taagagacat	tgagagcaat	ctgatgaaaa	tgaacaaga	aacttatgcg	780
acgactccagt	gatacatgtt	gacatgttgt	gaaactcagt	cctctggcat	ggccgcatgg	840
gctccacgtt	actgattttc	gtcgtggatg	tatttatctc	atgccatctt	caagatgctg	900
gtgcaaaagca	gttcttttcg	tgGCCaccat	ttataagtag	agttcagtcg	agatcgttgt	960
actgttatca	tactcatgta	tacccgattc	ccagactggt	tcactctgta	aattggaagc	1020
gatgtttgga	tgccatgtta	tcaagtggat	cataaacatc	caaacacagc	cttaaaatag	1080
atcgtttcga	cattattatt	tctctgctgt	caatccaggc	tctaacaact	tctcggctctt	1140
gttt						

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1501644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

Leu	Gln	Ala	Gln	Leu	Lys	Gln	Glu	Ser	Leu	Leu	Arg	Gln	Gln	Glu	Gln
1			5						10					15	
Gln	Gln	Leu	Ala	Glu	Gln	Ser	Gln	Leu	Arg	Gln	Gln	Glu	Gln	Glu	Lys
			20					25						30	
Leu	Ala	Lys	Glu	Gln	Thr	Arg	Ile	Ala	Ser	Leu	Glu	Ala	Glu	Lys	Gln
			35					40						45	
Gln	Leu	Glu	Asp	Gln	Ile	Thr	Met	Leu	Thr	Lys	Lys	Ala	Thr	Glu	Asp
			50					55						60	
Ala	Ser	Glu	Phe	Ala	Ala	Arg	Lys	Ala	Phe	Ser	Met	Gln	Asp	Arg	Glu
			65					70						75	
Lys	Leu	Glu	Gln	Gln	Leu	His	Asp	Met	Ala	Leu	Met	Ile	Glu	Arg	Leu
			85					90						95	
Glu	Gly	Ser	Arg	Gln	Lys	Leu	Leu	Met	Glu	Ile	Asp	Ser	Gln	Ser	Ser
			100					105						110	
Glu	Ile	Glu	Lys	Leu	Phe	Glu	Glu	Asn	Ser	Ala	Leu	Ser	Ala	Ser	Tyr
			115					120						125	
Gln	Glu	Ala	Ile	Asp	Val	Thr	Val	Gln	Trp	Glu	Asn	Gln	Lys	Ile	Ser
			130					135						140	

Gly  
145

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1501645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

Met	Leu	Thr	Lys	Lys	Ala	Thr	Glu	Asp	Ala	Ser	Glu	Phe	Ala	Ala	Arg
1				5					10					15	
Lys	Ala	Phe	Ser	Ser	Gln	Asp	Arg	Glu	Lys	Leu	Glu	Gln	Gln	Leu	His
				20				25						30	
Asp	Met	Ala	Leu	Met	Ile	Glu	Arg	Leu	Glu	Gly	Ser	Arg	Gln	Lys	Leu

35 40 45  
Leu Met Glu Ile Asp Ser Gln Ser Ser Glu Ile Glu Lys Leu Phe Glu  
50 55 60  
Glu Asn Ser Ala Leu Ser Ala Ser Tyr Gln Glu Ala Ile Asp Val Thr  
65 70 75 80  
Val Gln Trp Glu Asn Gln Lys Ile Ser Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Met Leu Leu Tyr Asn Gly Lys Thr Arg Lys Phe Gln Val Arg Asp Cys  
1 5 10 15  
Leu Lys Gln Asn Glu Glu Leu Arg Ser His Leu Glu Lys Leu Arg Leu  
20 25 30  
Glu Gln Val Ser Leu Leu Lys Val Ser Asn Ile Ala Thr Gln Ser Asp  
35 40 45  
Gly Gln Thr Glu Asn Ser Ile Ser Asn Pro Pro Gln Met Val Ile Glu  
50 55 60  
Asn Ile Ser Leu Xaa Xaa Ser Ala Tyr Lys Xaa Thr Xaa Gln Ile  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

ttttttcgcc tataattact cttccccggt cgccctcgcg aggtcgaaacc cccaaggcga 60  
ggcgacgaaa cctcgcgcaag tcccacaactc gaacctcagt caggcgcggt gagggagggga 120  
gagttcgagg accgagggcgg cgctcgggcga gatgaagctt aacgtcaaga cctcaagggg 180  
caccaaactc gagatcgagg cgagcccgga tgcgtcggtt gctgacgtga agaggatcat 240  
tgagaccact cagggtcaga gtacctaccg ggcggaccag caaatgctta tataccaagg 300  
gaaaattctc aaggatgaga ccactttgga aagcaacgga gttctganga acagcttctc 360  
tgttataaat tgttccaagg ctaaggcatc gtcgagtggg gcttctacca ctactgtctg 420  
aaaagctctt gcaactctgg cccaactctg tgcctctgtg cccctgtgtg catcagttgc 480  
aagaacacca acacaggctc ctgttgccac agctgaaacg gcacctccaa gtgcccaacc 540  
tcaggctgct cagctgtctac ggttgctgct actgatgatg ctgatgtgta cagtcag

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu  
1 5 10 15  
Ala Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr  
20 25 30  
Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr  
35 40 45  
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val  
50 55 60  
Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser  
65 70 75 80  
Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala Pro Ala Thr Leu  
85 90 95  
Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser Val Ala Arg Thr  
100 105 110  
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Ser Ala  
115 120 125  
Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu Met Met Leu  
130 135 140  
Met Cys Thr Val  
145

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1501691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

Met Leu Ile Tyr Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu  
1 5 10 15  
Ser Asn Gly Val Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys  
20 25 30  
Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala  
35 40 45  
Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser  
50 55 60  
Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala  
65 70 75 80  
Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu  
85 90 95  
Leu Met Met Leu Met Cys Thr Val  
100

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1501692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

Met Leu Ser Lys Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr

1 5 10 15  
Ala Ala Lys Ala Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro  
20 25 30  
Pro Ala Ala Ser Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr  
35 40 45  
Ala Glu Thr Ala Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu  
50 55 60  
Arg Leu Leu Leu Met Met Leu Met Cys Thr Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

ccgctcgatc ggcgcccat caatcaatca atcaattctc gacctcacta ctgcgatctct 60  
cgctctcatca gtgtgactgt gtgagtgctc gagcacggta gcacgcgcga tggacgctct 120  
gtctgtgact accttctctg tccccgtggt ggcgtctctc ctgcgttccg ggctcgggtc 180  
cgcggcacgc ctgcgcggcg ccttctctgt gttcgggtgac tccctcgtgg acaacggcaa 240  
caacaactac ctgatgacga cggcgcgcgc cg

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

Ala Arg Ser Arg Pro His Gln Ser Ile Asn Gln Phe Ser Thr Ser Leu  
1 5 10 15  
Leu Asp Leu Ser Ser His Gln Cys Asp Cys Val Ser Val Arg Ala Arg  
20 25 30

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

Met Asp Ala Leu Leu Val Thr Thr Phe Leu Val Pro Val Val Ala Leu  
1 5 10 15  
Leu Leu Gly Ser Gly Ser Gly Ser Ala Ala Pro Leu Xaa Arg Ala Phe  
20 25 30  
Phe Val Phe Gly Asp Ser Leu Val Asp Asn Gly Asn Asn Asn Tyr Leu

35 40 45  
Met Thr Thr Ala Arg Ala  
50

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 562 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..562
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:

gagcagccga	tctcttttcc	tctctctcgc	agtctcgccct	cgcccaaccc	agtcctctgc	60
gcgcgtcttc	tctctgtcaa	ggaccgccag	ggaaggacct	gctgtttcaa	agtattgtgc	120
gagacacct	cacgctgagc	tctgccgaca	tgaagtttt	cgggataatc	ccagactctc	180
aattgagaga	acgttcttaa	ggatggatga	gatgatgaga	gacaggaggg	cagggaggga	240
attattctgg	tacggtgtaa	tgacaattgg	aaagcatata	gaaaggctat	caacatgagt	300
ctatttctac	ccctctgtca	gaagccagct	tatcaggggg	cagtaaatga	tggatgtacc	360
gcgtgtgtgg	ttctcattag	agacaaccga	atcattgtgg	gaaatgctgg	tgattctcgt	420
tggttactct	caaggaataa	tcaggcgatt	gatctatcca	ccgattttaa	accaaacctt	480
ccagacgaaa	gacaaagat	agaagctgca	rgacatgtgg	taacttttag	cgagagagga	540
aatgtgcctc	gtattgtgta	tg				

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501711

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:

Thr	Thr	Ala	Phe	Ser	Phe	Leu	Ser	Leu	Ala	Val	Ser	Pro	Arg	Pro	Thr
1				5						10				15	
Gln	Ser	Leu	Ala	Arg	Ala	Leu	Ser	Pro	Ala	Arg	Thr	Ala	Arg	Glu	Gly
		20						25					30		
Pro	Ala	Val	Ser	Lys	Tyr	Cys	Ala	Arg	His	Leu	His	Ala	Glu	Leu	Arg
		35				40						45			
Arg	His	Glu	Ser	Phe	Arg	Asp	Asn	Leu	Gln	Thr	Ala	Ile	Glu	Arg	Thr
		50				55					60				
Phe	Leu	Arg	Met	Asp	Glu	Met	Met	Arg	Asp	Arg	Arg	Ala	Gly	Arg	Glu
		65				70				75				80	
Leu	Ser	Gly	Tyr	Gly	Val	Met	Thr	Ile	Gly	Lys	His	Ile	Glu	Arg	Leu
				85				90					95		
Ser	Thr														

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

Met	Ser	Leu	Phe	Leu	Pro	Phe	Cys	Gln	Lys	Pro	Ala	Tyr	Gln	Gly	Pro
1				5				10						15	
Val	Met	Asp	Gly	Cys	Thr	Ala	Cys	Val	Val	Leu	Ile	Arg	Asp	Asn	Arg
			20					25					30		
Ile	Ile	Val	Gly	Asn	Ala	Gly	Asp	Ser	Arg	Cys	Val	Leu	Ser	Arg	Asn
			35				40					45			
Asn	Gln	Ala	Ile	Asp	Leu	Ser	Thr	Asp	Phe	Lys	Pro	Asn	Leu	Pro	Asp
			50			55					60				
Glu	Arg	Gln	Arg	Ile	Glu	Ala	Ala	Xaa	His	Val	Val	Thr	Phe	Ser	Glu
			65		70				75						80
Arg	Gly	Asn	Val	His	Arg	Ile	Asp	Asp							

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

Met	Asp	Gly	Cys	Thr	Ala	Cys	Val	Val	Ile	Arg	Asp	Asn	Arg	Ile
1			5					10					15	
Ile	Val	Gly	Asn	Ala	Gly	Asp	Ser	Arg	Cys	Val	Leu	Ser	Arg	Asn
			20					25				30		
Gln	Ala	Ile	Asp	Leu	Ser	Thr	Asp	Phe	Lys	Pro	Asn	Leu	Pro	Asp
			35			40					45			
Arg	Gln	Arg	Ile	Glu	Ala	Ala	Xaa	His	Val	Val	Thr	Phe	Ser	Glu
			50			55				60				
Gly	Asn	Val	His	Arg	Ile	Asp	Asp							

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1501718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

aaggcagcaa	ggccactaac	actagttatc	acatccacca	taacgacccat	ggctaccacc	60
tcagctttgc	tagctcttgt	ctgtttagcc	agcctccttg	caggcacggt	gttcagtgtat	120
gatatacgta	ccatccatat	acccttggtg	gatcgggttc	aagccttgga	ggccgaatac	180
aaccgcacat	atgcgacccc	agaggaattc	cagcaacgct	tcattggtcta	tagcgagaat	240
ttcaagtcca	tcgagaccat	gaaccagcct	gggagctcat	atgagctcgg	tgagaaccca	300
ttcgctgacc	tcaccgagga	ggagttcaag	gacacgtatc	ttatgaagct	tgacaacgtg	360
gcctcgtccc	ctgaggccat	ggcactgacc	gtcgatacca	tgaatagagc	aggcacatct	420
ggcggcagca	acaccaacga	ggctcccaat	agtgtggact	ggaggaccaa	gggagcagtg	480
acgcgggtca	agagccagca	acattgtg				

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..169  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501719  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

Lys	Ala	Ala	Arg	Pro	Leu	Thr	Leu	Val	Ile	Thr	Thr	Thr	Thr
1													
Met	Ala	Thr	Thr	Ser	Ala	Leu	Leu	Ala	Leu	Val	Leu	Ala	Ser
Leu	Ala	Gly	Thr	Val	Phe	Ser	Asp	Asp	Ile	Val	Pro	Ile	His
Leu	Leu	Asp	Arg	Phe	Gln	Ala	Trp	Gln	Ala	Glu	Tyr	Asn	Arg
Ala	Thr	Pro	Glu	Glu	Phe	Gln	Gln	Arg	Phe	Met	Val	Tyr	Ser
Val	Lys	Phe	Ile	Glu	Thr	Met	Asn	Gln	Pro	Gly	Ser	Ser	Tyr
Gly	Glu	Asn	Arg	Phe	Ala	Asp	Leu	Thr	Glu	Glu	Glu	Phe	Lys
Tyr	Leu	Met	Lys	Leu	Asp	Asn	Val	Ala	Ser	Ser	Pro	Glu	Ala
Leu	Thr	Val	Asp	Thr	Met	Asn	Arg	Ala	Gly	Thr	Ser	Gly	Ser
Thr	Asn	Glu	Ala	Pro	Asn	Ser	Val	Asp	Trp	Arg	Thr	Lys	Gly
Thr	Pro	Val	Lys	Ser	Gln	Gln	His	Cys					

- (2) INFORMATION FOR SEQ ID NO:1922:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501720  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

Met	Ala	Thr	Thr	Ser	Ala	Leu	Leu	Ala	Leu	Val	Leu	Leu	Ala	Ser	Leu
1															
Leu	Ala	Gly	Thr	Val	Phe	Ser	Asp	Asp	Ile	Val	Pro	Ile	His	Ile	Pro
Leu	Leu	Asp	Arg	Phe	Gln	Ala	Trp	Gln	Ala	Glu	Tyr	Asn	Arg	Thr	Tyr
Ala	Thr	Pro	Glu	Glu	Phe	Gln	Gln	Arg	Phe	Met	Val	Tyr	Ser	Glu	Asn
Val	Lys	Phe	Ile	Glu	Thr	Met	Asn	Gln	Pro	Gly	Ser	Ser	Tyr	Glu	Leu
Gly	Glu	Asn	Arg	Phe	Ala	Asp	Leu	Thr	Glu	Glu	Glu	Phe	Lys	Asp	Thr
Tyr	Leu	Met	Lys	Leu	Asp	Asn	Val	Ala	Ser	Ser	Pro	Glu	Ala	Met	Ala
Leu	Thr	Val	Asp	Thr	Met	Asn	Arg	Ala	Gly	Thr	Ser	Gly	Gly	Ser	Asn
Thr	Asn	Glu	Ala	Pro	Asn	Ser	Val	Asp	Trp	Arg	Thr	Lys	Gly	Ala	Val
Thr	Pro	Val	Lys	Ser	Gln	Gln	His	Cys							

145

150

(2) INFORMATION FOR SEQ ID NO:1923:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

Met	Val	Tyr	Ser	Glu	Asn	Val	Lys	Phe	Ile	Glu	Thr	Met	Asn	Gln	Pro	
1				5					10					15		
Gly	Ser	Ser	Tyr	Glu	Leu	Gly	Glu	Asn	Arg	Phe	Ala	Asp	Leu	Thr	Glu	
				20				25					30			
Glu	Glu	Phe	Lys	Asp	Thr	Tyr	Leu	Met	Lys	Leu	Asp	Asn	Val	Ala	Ser	
				35				40					45			
Ser	Pro	Glu	Ala	Met	Ala	Leu	Thr	Val	Asp	Thr	Met	Asn	Arg	Ala	Gly	
				50				55				60				
Thr	Ser	Gly	Gly	Ser	Asn	Thr	Asn	Glu	Ala	Pro	Asn	Ser	Val	Asp	Trp	
65				70				75					80			
Arg	Thr	Lys	Gly	Ala	Val	Thr	Pro	Val	Lys	Ser	Gln	Gln	His	Cys		
				85				90					95			

(2) INFORMATION FOR SEQ ID NO:1924:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 911 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..911

(D) OTHER INFORMATION: / Ceres Seq. ID 1501722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

gagcgccgaca	tatggggcccc	gcttgagaag	taagggccac	atgtcggtgg	gaactctccc	60
ggagtcggca	actaatcgac	cccgtagcgc	ggctccaccc	gaagcgcaag	aggaagaggt	120
ggccatacgc	aacaagcaaa	gcatancccc	aaatcccaaa	tccccaatcc	ccaatccca	180
aaccctaggt	tatctcggcg	cggcagcgan	tggcgggcgc	gggacctgag	aagggggaat	240
cgcgcctccc	gcgggaggtg	aaccgggtgc	tctacgtcgc	gaacctgcgc	ttaacatct	300
cgagcgagga	gatgtacgac	atcttcggca	agtcaggcgc	gatccggcag	atccgtcttg	360
gcaacgccaa	ggacacgcgc	gggaccgctt	acgttgtcta	csaggacatc	tacgacgcga	420
agaaacgcgt	cgaccacctc	tmcggcttca	acgtcgccaa	ccgctacctt	atcgtgctct	480
actaccagcc	cgccaagats	tcacaagaag	cggatatcam	gaagaaggag	gacgagatcc	540
accaggtctc	aggagaagta	cggaaatcgg	tccaagacgc	ccggcccggg	ctccagcgac	600
tgagcggcca	gggtattgcc	tctgcagcct	cttgtatgat	gaagagcaat	caaaaggaa	660
aaattggttg	cgctgtgctg	tgttatcatcc	agcgtcgcta	attactctgt	tgttattcag	720
gctccataac	aattgaatag	atattgtgct	gtctaacgcg	cagcgataat	gtttagtttc	780
taccaaaaac	aagaggaatg	agtagtgtac	accctcaccc	tgtggctatg	cttgaattgt	840
tgatctatat	tctgttgtga	gactgagagt	agcatgggta	ggctgtgtaa	tttgtgtctc	900
tattattggt	t					

(2) INFORMATION FOR SEQ ID NO:1925:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 244 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1501723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

Thr	Pro	Thr	Tyr	Gly	Pro	Arg	Leu	Arg	Ser	Lys	Gly	His	Met	Ser	Val
1				5				10						15	
Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala	Pro	Ala	Pro
			20					25					30		
Pro	Glu	Ala	Gln	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys	Gln	Ser	Ile	
			35				40					45			
Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr	Leu	Gly	Tyr
			50				55					60			
Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu	Gly	Glu	Cys
			65				70				75			80	
Ala	Pro	Pro	Ala	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala	Glu	Pro	Ala	
			85					90					95		
Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg	Gln	Val	Arg
			100					105					110		
Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His	Ala	Arg	Asp
			115				120						125		
Arg	Leu	Arg	Cys	Leu	Xaa	Gly	His	Leu	Arg	Arg	Gln	Glu	Arg	Arg	Arg
			130				135					140			
Pro	Pro	Xaa	Arg	Leu	Gln	Arg	Arg	Gln	Pro	Leu	Pro	Tyr	Arg	Ala	Leu
			145				150				155			160	
Leu	Pro	Ala	Arg	Gln	Asp	Xaa	Gln	Glu	Xaa	Gly	Tyr	Xaa	Glu	Glu	Gly
			165					170					175		
Gly	Arg	Asp	Pro	Pro	Gly	Ser	Arg	Arg	Ser	Thr	Glu	Ser	Gly	Pro	Arg
			180					185					190		
Arg	Pro	Ala	Arg	Ala	Pro	Ala	Thr	Glu	Arg	Pro	Gly	Tyr	Cys	Leu	Cys
			195				200					205			
Ser	Leu	Leu	Tyr	Asp	Glu	Gln	Ser	Lys	Gly	Thr	Asn	Trp	Leu	Arg	
			210				215				220				
Cys	Ala	Val	Leu	His	Pro	Ala	Ser	Leu	Ile	Thr	Leu	Leu	Leu	Phe	Arg
			225				230				235				240
Leu	His	Asn	Asn												

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1501724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met	Ser	Val	Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala
1							5				10			15	
Pro	Ala	Pro	Pro	Glu	Ala	Gln	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys	
							20						25	30	
Gln	Ser	Ile	Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr
			35				40						45		
Leu	Gly	Tyr	Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu
			50				55					60			
Gly	Glu	Cys	Ala	Pro	Pro	Ala	Gly	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala
			65				70				75			80	
Glu	Pro	Ala	Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg
				85				90					95		
Gln	Val	Arg	Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His

Ala	Arg	Asp	Arg	Leu	Arg	Cys	Leu	Xaa	Gly	His	Leu	Arg	Arg	Gln	Glu
Arg	Arg	Arg	Arg	Pro	Pro	Xaa	Arg	Leu	Gln	Arg	Arg	Gln	Pro	Leu	Pro
Arg	Ala	Leu	Leu	Pro	Ala	Arg	Gln	Asp	Xaa	Gln	Glu	Xaa	Gly	Tyr	Xaa
Glu	Glu	Gly	Gly	Arg	Asp	Pro	Pro	Gly	Ser	Arg	Arg	Ser	Thr	Glu	Ser
Gly	Pro	Arg	Arg	Pro	Ala	Arg	Ala	Pro	Ala	Thr	Glu	Arg	Pro	Gly	Tyr
Cys	Leu	Cys	Ser	Leu	Leu	Tyr	Asp	Glu	Glu	Gln	Ser	Lys	Gly	Thr	Asn
Trp	Leu	Arg	Cys	Ala	Val	Leu	His	Pro	Ala	Ser	Leu	Ile	Thr	Leu	Leu
Leu	Phe	Arg	Leu	His	Asn	Asn									

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(ix) FEATURE:
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(B) LOCATION: 1..129

SEQUENCE DESCRIPTION:

Tyr Asp Ile Phe Gly Lys Tyr Gly Ala Ile Ar

[illegible]

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 916 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..916

SEQUENCE DESCRIPTION: SEQ ID

catgtca tgacgatact gcaggctcca attgtcagct ga

atccatgtca tgaagttacat gaaggtccca attgtcagct gaacctgtgtc tgaattcttgt  
ccagctatag ctcatTTTTgt tctacttgtc gacatagact caagcttTgct tattagtacg

tccaagaacg acgtacatgg ctctcagctgc tgcggctagc gctgttaagg aggccttggt 180  
cgctcgtcgc gtgtgcacatg tgcctgctgct ccactcttcg gcgggacatc agcgcgccaa 240  
gtgcgcgcct ccaccgcatt gccattacac ggggcagcag ccaccgcctt cgcgggtgct 300  
agcgtcgttg tactcgcgcg cgcaccacc accagtagca gcgcccctgc cgtcgcgcct 360  
gcgcgcgcga cgcgcagtag aagcgcccat gcgcgcgcg ccgcgcgcac caacgcgcac 420  
acctgcgcga acgcccammc cgtcgcgcgt gcgcgmaccg gtcaataact gcagctacat 480  
gtactgcgcg atgcaatgta gcccggtctg ccaagccaaa ccamgacgcc ggcacgcga 540  
agtgcgaagg cgacctgcgc accaaactac aacgggtgct acgacagctg caccagccat 600  
gtctgcgcgc gcgactcctg cgcgcgcagt ggcctgcgct tcggccactg cccctgcgac 660  
aacgcacaag cgaccagctg ctgcacaatcc tgcgcgaacg ttctgtaccg cgaggagcag 720  
tagctgcgga attactacga caggcgtgtg gactactgca tgatcgactg ccaggacacc 780  
tgctacaaga actgcactca ggcgcgctag agagctcttg attggtcttg tcactcagt 840  
tagctgcaat gttctgtat gttcatgacg ttctacgat tgatcaata aaacaagggtg 900  
atgagcattg agctcc

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met Ala Ser Ala Ala Ala Ser Ala Val Lys Glu Ala Leu Val Val  
1 5 10 15  
Val Ala Val Cys Ile Val Leu Leu Leu His Ser Ser Ala Gly His Gln  
20 25 30  
Pro Pro Lys Ser Pro Pro Pro Pro His Cys His Tyr Thr Gly Gln Gln  
35 40 45  
Pro Pro Pro Ser Pro Val Pro Ala Ser Leu Tyr Ser Pro Pro Pro Pro  
50 55 60  
Pro Pro Val Pro Ala Pro Met Pro Ser Pro Pro Pro Pro Pro Pro  
65 70 75 80  
Val Gln Ala Pro Met Pro Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro  
85 90 95  
Ala Pro Thr Pro Xaa Pro Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys  
100 105 110  
Ser Tyr Met Tyr Cys Ala Met Gln Cys Ser Pro Val Cys Gln Ala Lys  
115 120 125  
Pro Xaa Arg Arg His Arg Gln Val Arg Lys Arg Pro Arg His Gln Thr  
130 135 140  
Thr Thr Gly Ala Thr Thr Ala Ala Pro Ala Met Ser Ala Pro Ala Thr  
145 150 155 160  
Pro Ala Pro Ala Val Ala Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr  
165 170 175  
Pro Thr Arg Pro Ala Ala Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala  
180 185 190  
Arg Ser Ser Ala Ala Gly Ile Thr Thr Thr Gly Leu Thr Ser Thr Ala  
195 200 205

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Pro Ser Pro Ser Pro Pro Pro Pro Val Gln Ala Pro Met Pro  
1 5 10 15  
Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro Xaa Pro  
20 25 30  
Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr Cys Ala  
35 40 45  
Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg His Arg  
50 55 60  
Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala Thr Thr  
65 70 75 80  
Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala Val Ala  
85 90 95  
Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro Ala Ala  
100 105 110  
Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala Ala Gly  
115 120 125  
Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

Met Pro Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro  
1 5 10 15  
Xaa Pro Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr  
20 25 30  
Cys Ala Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg  
35 40 45  
His Arg Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala  
50 55 60  
Thr Thr Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala  
65 70 75 80  
Val Ala Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro  
85 90 95  
Ala Ala Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala  
100 105 110  
Ala Gly Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

attctgttcg	gttccttcg	aaaacacaac	aggaaaacac	acgcacaaaa	ctgccgtttc	60
cgaatggcca	cgcccggtgct	ccgccgccca	ttcctcgccg	cgctcctccc	cgccgcggga	120
ggggcgctcg	ggacctctct	ttggttccgt	ccccggagac	gtaggtcctc	tccttccgtg	180
cgccggtgtg	cttcgcgactc	ccccaaagccc	gtcgctctca	cctcctcccc	cacggcggtg	240
gacagccccg	acgaggaacc	accggtccta	ccgctcctcc	aggagcttgc	ggattgtctg	300
attcttccac	ccaagctcct	cgctcagctc	ccgagcgacc	ttcgtctcga	cctcaatgac	360
gctgcgtttg	atctctccaa	cgggccagtt	ctcgacgagt	gtggccaaga	agtgggtgat	420
cgctcctga	acctggcaaa	agcatgggag	ttagctgata	cgtaacatc	aatagcatt	480
gccaagcagc	tgc					

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1501738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

Ile	Leu	Phe	Gly	Ser	Phe	Arg	Lys	His	Asn	Arg	Lys	Thr	His	Ala	Gln
1				5					10					15	
Asn	Cys	Arg	Phe	Arg	Met	Ala	Thr	Ala	Val	Leu	Arg	Arg	Pro	Phe	Leu
				20					25					30	
Ala	Ala	Leu	Leu	Pro	Ala	Ala	Gly	Gly	Ala	Ser	Gly	Thr	Ser	Ser	Trp
				35					40					45	
Phe	Arg	Pro	Arg	Arg	Arg	Arg	Ser	Pro	Ser	Val	Arg	Ala	Val	Ser	
				50					55					60	
Ser	Asp	Ser	Pro	Lys	Pro	Val	Ala	Ser	Thr	Ser	Ser	Pro	Thr	Gly	Gly
				65					70					75	
Asp	Ser	Pro	Asp	Glu	Glu	Pro	Pro	Val	Leu	Pro	Leu	Leu	Gln	Glu	Leu
				85					90					95	
Ala	Asp	Cys	Leu	Ile	Leu	Pro	Pro	Lys	Leu	Leu	Ala	Gln	Leu	Pro	Ser
				100					105					110	
Asp	Leu	Arg	Leu	Asp	Leu	Asn	Asp	Ala	Ala	Phe	Asp	Leu	Ser	Asn	Gly
				115					120					125	
Pro	Val	Leu	Asp	Glu	Cys	Gly	Gln	Glu	Val	Gly	Asp	Leu	Leu	Leu	Asn
				130					135					140	
Leu	Ala	Lys	Ala	Trp	Glu	Leu	Ala	Asp	Thr	Ser	Thr	Ser	Asn	Ser	Ile
				145					150					155	
Ala	Lys	Gln	Leu												160

(2) INFORMATION FOR SEQ ID NO:1934:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1501739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

Phe	Cys	Ser	Val	Pro	Ser	Glu	Asn	Thr	Thr	Gly	Lys	His	Thr	His	Lys
1				5					10					15	
Thr	Ala	Val	Ser	Glu	Trp	Pro	Arg	Pro	Cys	Ser	Ala	Ala	His	Ser	Ser
				20					25					30	

Pro Arg Ser Ser Pro Pro Pro Glu Gly Arg Pro Gly Pro Pro Leu Gly  
35 40 45  
Ser Val Pro Gly Asp Val Gly Pro Leu Leu Pro Cys Ala Arg Cys Leu  
50 55 60  
Pro Thr Pro Pro Ser Pro Ser Pro Pro Pro Pro Pro Ala Val  
65 70 75 80  
Thr Ala Pro Thr Arg Asn His Arg Ser Tyr Arg Ser Ser Arg Ser Leu  
85 90 95  
Arg Ile Ala

(2) INFORMATION FOR SEQ ID NO:1935:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..143  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

Met Ala Thr Ala Val Leu Arg Arg Pro Phe Leu Ala Ala Leu Leu Pro  
1 5 10 15  
Ala Ala Gly Gly Ala Ser Gly Thr Ser Ser Trp Phe Arg Pro Arg Arg  
20 25 30  
Arg Arg Ser Ser Pro Ser Val Arg Ala Val Ser Ser Asp Ser Pro Lys  
35 40 45  
Pro Val Ala Ser Thr Ser Ser Pro Thr Gly Gly Asp Ser Pro Asp Glu  
50 55 60  
Glu Pro Pro Val Leu Pro Leu Leu Gln Glu Leu Ala Asp Cys Leu Ile  
65 70 75 80  
Leu Pro Pro Lys Leu Leu Ala Gln Leu Pro Ser Asp Leu Arg Leu Asp  
85 90 95  
Leu Asn Asp Ala Ala Phe Asp Leu Ser Asn Gly Pro Val Leu Asp Glu  
100 105 110  
Cys Gly Gln Glu Val Gly Asp Leu Leu Asn Leu Ala Lys Ala Trp  
115 120 125  
Glu Leu Ala Asp Thr Ser Thr Ser Asn Ser Ile Ala Lys Gln Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:1936:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 363 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..363  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

acaaacttcc cctgtcacga gactacgaga ccacgccttc cgtgggatca atcgcgtagg 60  
gttttcggaga tgttcggcgg cgcgccgaag aagagcgaca acaccggta ctacgagatc 120  
ctggggggttt ccaagcgacg gtcacaggat gacctcaaga aggcctaccg caaggccgcg 180  
atcaagaacc accccgacaa gggcggcgac cccgagaagt tcaaggagct atgtatgctg 240  
tatgcatgtg gtgaagcaag tgctcgtcgg tgtgtagtgt tcgctcttct gatccattgt 300  
ctgtgctctg tactgtagt atcagcgatca aataaaagaa atgcctgtcc ttgtttagaa 360  
ttg

(2) INFORMATION FOR SEQ ID NO:1937:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..105
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1501742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Thr Asn Phe Pro Cys His Glu Ser Thr Arg Pro Arg Leu Pro Trp Asp  
1 5 10 15  
Gln Ser Ala Arg Val Ser Glu Met Phe Gly Arg Ala Pro Lys Lys Ser  
20 25 30  
Asp Asn Thr Arg Tyr Tyr Glu Ile Leu Gly Val Ser Lys Asp Ala Ser  
35 40 45  
Gln Asp Asp Leu Lys Lys Ala Tyr Arg Lys Ala Ala Ile Lys Asn His  
50 55 60  
Pro Asp Lys Gly Gly Asp Pro Glu Lys Phe Lys Glu Leu Cys Met Leu  
65 70 75 80  
Tyr Ala Cys Gly Glu Ala Ser Ala Arg Arg Cys Val Val Phe Ala Leu  
85 90 95  
Leu Ile His Cys Leu Cys Ser Val Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:1938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

Gln Thr Ser Pro Val Thr Arg Val Arg Asp His Ala Phe Arg Gly Ile  
1 5 10 15  
Asn Arg Leu Gly Phe Arg Arg Cys Ser Ala Ala Arg Arg Arg Ala  
20 25 30  
Thr Thr Pro Gly Thr Thr Arg Ser Trp Gly Phe Pro Arg Thr Arg His  
35 40 45  
Arg Met Thr Ser Arg Arg Pro Thr Ala Arg Pro Pro Ser Arg Thr Thr  
50 55 60  
Pro Thr Arg Ala Ala Thr Pro Arg Ser Ser Arg Ser Tyr Val Cys Cys  
65 70 75 80  
Met His Val Val Lys Gln Val Leu Val Gly Val  
85 90

(2) INFORMATION FOR SEQ ID NO:1939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

Met Phe Gly Arg Ala Pro Lys Lys Ser Asp Asn Thr Arg Tyr Tyr Glu

1	5	10	15
Ile Leu Gly Val Ser Lys Asp Ala Ser Gln Asp Asp Leu Lys Lys Ala	20	25	30
Tyr Arg Lys Ala Ala Ile Lys Asn His Pro Asp Lys Gly Asp Pro	35	40	45
Glu Lys Phe Lys Glu Leu Cys Met Leu Tyr Ala Cys Gly Glu Ala Ser	50	55	60
Ala Arg Arg Cys Val Val Phe Ala Leu Leu Ile His Cys Leu Cys Ser	65	70	75
Val Leu			80

(2) INFORMATION FOR SEQ ID NO:1940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..483
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940:

ctcggttttac ccgacccgcg cgcagccgcg aacgccgaga agacgcgaga kgaaggaggag	60
agggtgagcca ccgaagcgga gacgtgagta gtcgaccaac cccgtcggtc cggcgactcc	120
ggctgcggcg cggcgtgcta gatcgctacc gaccatgggt gtggaggaga tcgccgagggg	180
ggtgaaaac ctcacggtta ccggagatgc ggcggcttta ggcggagagg ggcagaggag	240
ggcgcgcgcg ggcacagcaa ccgcctccag gtgtccaaca ccaagaagcc cctcttcttc	300
tacgtcaacc tcgcacaag taatgtcaac agcacgacga tgtagaagcta tccgtctctg	360
ggatggccat agcaacagtt gtgacgtgg cagaaattct gaagaacaat ggatttgccg	420
ttgaaaagaa aattaggacc tctactgttg aaataaacga cgaatcaaga gggcgctccat	480
tcc	

(2) INFORMATION FOR SEQ ID NO:1941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941:

Arg Phe Thr Arg Thr Arg Arg Ser Pro Gln Arg Arg Glu Asp Ala Arg	1	5	10	15
Xaa Arg Glu Glu Val Ser His Arg Ser Gly Asp Val Ser Ser Arg Pro	20	25	30	
Thr Pro Ser Val Arg Arg Leu Arg Leu Arg Arg Gly Val Leu Asp Arg	35	40	45	
Tyr Arg Pro Trp Trp Trp Arg Arg Ser Pro Arg Gly	50	55	60	

(2) INFORMATION FOR SEQ ID NO:1942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

Met	Val	Val	Glu	Glu	Ile	Ala	Glu	Gly	Val	Lys	Asn	Leu	Thr	Val	Thr	
1			5					10					15			
Gly	Asp	Ala	Ala	Ala	Ser	Gly	Gly	Gly	Gln	Arg	Arg	Gly	Gly	Gly		
			20				25					30				
Gly	Thr	Ala	Thr	Ala	Ser	Arg	Cys	Pro	Thr	Pro	Arg	Ser	Pro	Ser	Ser	
			35				40					45				
Ser	Thr	Ser	Thr	Ser	Pro	Arg	Val	Tyr	Ala	Thr	Ala	Arg	Arg	Cys	Arg	
			50			55					60					
Ala	Ile	Arg	Ser	Trp	Asp	Gly	His	Ser	Asn	Ser	Cys	Asp	Arg	Gly	Arg	
65				70					75					80		
Asn	Ser	Glu	Glu	Gln	Trp	Ile	Cys	Arg								
				85												

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1501758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

Met	Arg	Arg	Leu	Gln	Ala	Glu	Arg	Gly	Arg	Gly	Gly	Ala	Ala	Ala	Ala	
1			5					10					15			
Gln	Gln	Pro	His	Pro	Gly	Val	Gln	His	Gln	Glu	Ala	Pro	Leu	Leu	Leu	
			20				25					30				
Arg	Gln	Pro	Arg	Gln	Glu	Tyr	Met	Gln	His	Asp	Asp	Val	Glu	Leu		
			35			40				45						
Ser	Ala	Leu	Gly	Met	Ala	Ile	Ala	Thr	Val	Val	Thr	Val	Ala	Glu	Ile	
			50			55				60						
Leu	Lys	Asn	Asn	Gly	Phe	Ala	Val	Glu	Lys	Lys	Ile	Arg	Thr	Ser	Thr	
65				70					75					80		
Val	Glu	Ile	Asn	Asp	Glu	Ser	Arg	Gly	Arg	Pro	Phe					
				85				90								

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1501763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

aagattgggt	ccaacaccag	cgcgcgcat	gtcgaagcga	ggcargggag	gttcgcgggg	60
gaacaagtgc	cgcattgcgc	tgggtctgcc	agtggccgcg	acggtgaact	gcgcggacaa	120
caccggcgcc	aagaacctct	acatcatctc	cgtaaggggc	atcaaaggcc	gcctcaatcg	180
cctcccgctc	gcctgcgttg	gcgacatggt	catggccacc	gtcaaagaag	ggaagcccca	240
cctcaggaag	aaggtgatgc	cgcgcgtcat	cgtccgccag	cgcaagccgt	ggcgccgcga	300
ggacggggtc	tacatgtact	tcgaagataa	tgtcggagtg	atttgtgaat	ccaagggtga	360
gatgaaaggt	tccgctatca	ctggacctat	cggcaaggag	tgtgctgac	tttgccctag	420
gattgctagc	gcagcaaacg	ccattgtttg	agagcttggt	ggaatatggt	cagactctta	480
tatgatcatc	ttattatcag	ttgctagact	gcaattgggc	ttatgtttgt	tcactcaatt	540
ttgtagtaaa	cagaatttgg	tataccaagg	ggatct			

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

Arg Leu Gly Pro Thr Pro Ala Ala Met Ser Lys Arg Gly Xaa Gly  
1 5 10 15  
Gly Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala  
20 25 30  
Ala Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile  
35 40 45  
Ile Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala  
50 55 60  
Cys Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp  
65 70 75 80  
Leu Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro  
85 90 95  
Trp Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly  
100 105 110  
Val Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly  
115 120 125  
Pro Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala  
130 135 140  
Ala Asn Ala Ile Val  
145

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

Met Ser Lys Arg Gly Xaa Gly Gly Ser Ala Gly Asn Lys Phe Arg Met  
1 5 10 15  
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr  
20 25 30  
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg  
35 40 45  
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr  
50 55 60  
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val  
65 70 75 80  
Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met  
85 90 95  
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met  
100 105 110  
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu  
115 120 125  
Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val

130 135 140  
(2) INFORMATION FOR SEQ ID NO:1947:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501766  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:  
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn  
1 5 10 15  
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly  
20 25 30  
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala  
35 40 45  
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala  
50 55 60  
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr  
65 70 75 80  
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu  
85 90 95  
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp  
100 105 110  
Leu Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:1948:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 554 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..554  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501771  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:  
attatctctat caagtggtgtg tgccttttatt ttatgtgctg gagctgcact agtgcttttat 60  
ttcaagcttc gaaaccacat ccattttaat gaagcgctcac ttgtgccaac aaaacctaca 120  
ggctcgtgtt ctgcaatggt tgggaacagg ctagaaagca gacctatttc ggcataccaca 180  
tccttcagct caagtttggt ggcataataa ggatctgccca aaacattttaa cctggttgag 240  
atggagagag ctacactagg atttgatgag tccagaatta ttggtgaggg tggttttggg 300  
cgtgtctatg aaggatttct tgaggatgga gaacgggttg ctatcaaggt tttaaagcgg 360  
gacgatcaac aaggtaaccg ggaagttttg gctgargtcg agatgcttag ccgattgcac 420  
cataggaact tggttaaact gataggtata tgcacagagg ggcatagccg atgtttgggt 480  
tatgagcttg ttccgaatgg cagtgtggga atctcacttg catggatcag ataaaggagg 540  
ctgctcagtt tgat

(2) INFORMATION FOR SEQ ID NO:1949:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1501772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Ile	Ile	Leu	Ser	Ser	Val	Cys	Ala	Phe	Ile	Leu	Cys	Ala	Gly	Ala	Ala	
1					5				10				15			
Leu	Val	Leu	Tyr	Phe	Lys	Leu	Arg	Asn	His	Ile	His	Leu	Thr	Glu	Ala	
			20				25					30				
Ser	Leu	Val	Pro	Thr	Lys	Pro	Thr	Gly	Pro	Val	Ser	Ala	Met	Val	Gly	
		35				40					45					
Asn	Arg	Leu	Glu	Ser	Arg	Pro	Ile	Ser	Ala	Ser	Pro	Ser	Phe	Ser	Ser	
	50				55					60						
Ser	Leu	Val	Ala	Tyr	Lys	Gly	Ser	Ala	Lys	Thr	Phe	Asn	Leu	Val	Glu	
	65				70					75				80		
Met	Glu	Arg	Ala	Thr	Leu	Gly	Phe	Asp	Glu	Ser	Arg	Ile	Ile	Gly	Glu	
			85					90						95		
Gly	Gly	Phe	Gly	Arg	Val	Tyr	Glu	Gly	Ile	Leu	Glu	Asp	Gly	Glu	Arg	
		100					105						110			
Val	Ala	Ile	Lys	Val	Leu	Lys	Arg	Asp	Asp	Gln	Gln	Gly	Thr	Arg	Glu	
	115					120						125				
Phe	Leu	Ala	Xaa	Val	Glu	Met	Leu	Ser	Arg	Leu	His	His	Arg	Asn	Leu	
	130				135					140						
Val	Lys	Leu	Ile	Gly	Ile	Cys	Thr	Glu	Gly	His	Ser	Arg	Cys	Leu	Val	
	145				150					155				160		
Tyr	Glu	Leu	Val	Pro	Asn	Gly	Ser	Val	Gly	Ile	Ser	Leu	Ala	Trp	Ile	
			165					170						175		
Arg																

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

Met	Val	Gly	Asn	Arg	Leu	Glu	Ser	Arg	Pro	Ile	Ser	Ala	Ser	Pro	Ser	
1			5					10					15			
Phe	Ser	Ser	Ser	Leu	Val	Ala	Tyr	Lys	Gly	Ser	Ala	Lys	Thr	Phe	Asn	
			20					25				30				
Leu	Val	Glu	Met	Glu	Arg	Ala	Thr	Leu	Gly	Phe	Asp	Glu	Ser	Arg	Ile	
		35				40					45					
Ile	Gly	Glu	Gly	Gly	Phe	Gly	Arg	Val	Tyr	Glu	Gly	Ile	Leu	Glu	Asp	
	50				55					60						
Gly	Glu	Arg	Val	Ala	Ile	Lys	Val	Leu	Lys	Arg	Asp	Asp	Gln	Gln	Gly	
	65				70					75				80		
Thr	Arg	Glu	Phe	Leu	Ala	Xaa	Val	Glu	Met	Leu	Ser	Arg	Leu	His	His	
		85				90						95				
Arg	Asn	Leu	Val	Lys	Leu	Ile	Gly	Ile	Cys	Thr	Glu	Gly	His	Ser	Arg	
	100					105						110				
Cys	Leu	Val	Tyr	Glu	Leu	Val	Pro	Asn	Gly	Ser	Val	Gly	Ile	Ser	Leu	
	115					120						125				
Ala	Trp	Ile	Arg													
	130															

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..97  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501774  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:  
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu  
1          5          10          15  
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg  
          20          25          30  
Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly Thr Arg Glu  
          35          40          45  
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu  
50          55          60  
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val  
65          70          75          80  
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile  
          85          90          95  
Arg

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1501786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:

aaaaaacctcg	caagcgaccc	cagtaatggc	gaccaaggcg	ctatccgtct	cctcgctcac	60
ctccacggccc	tttgcctcct	tttccttgcc	gcggccccgc	aggccttcac	cttcgctccc	120
cctcctccgcg	cttctcgccc	ctcgccccgc	cgctctccact	ctctccgcgc	ccgctccccc	180
cgacgaggac	ggcgctgaca	ccgtggagca	gtcctctcac	ccamgccccg	ctgagacetc	240
agccccccgc	ggatccccgc	gcgggatcga	mcgcctcatg	aagctccagc	gcmgcccga	300
cgggagmcgc	tgccccgggg	ccggaggagg	tggttccctt	acctggacgc	gttcggcccc	360
gcggccgngn	ggcggggast	gtccagcggg	gaggtcatag	aggtgctgga	gccgcacatc	420

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1501787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:

Lys	Asn	Leu	Ala	Ser	Asp	Pro	Ser	Asn	Gly	Asp	Gln	Gly	Ala	Ile	Arg
1		5						10					15		
Leu	Leu	Ala	His	Leu	His	Gly	Leu	Cys	Leu	Leu	Phe	Leu	Ala	Ala	Ala
		20						25					30		
Pro	Gln	Ala	Phe	Thr	Phe	Ala	Ser	Pro	Pro	Pro	Pro	Ser	Arg	Pro	Ser
		35						40					45		
Pro	Pro	Arg	Leu	His	Ser	Leu	Arg	Arg	Arg	Ser	Arg	Arg	Arg	Gly	Arg
		50						55					60		

Arg Arg His Arg Gly Ala Ala Pro Pro Pro Xaa Pro Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

Lys Thr Ser Gln Ala Thr Pro Val Met Ala Thr Lys Ala Leu Ser Val  
1 5 10 15  
Ser Ser Leu Thr Ser Thr Ala Phe Ala Ser Phe Ser Leu Pro Arg Pro  
20 25 30  
Arg Arg Pro Ser Pro Ser Pro Pro Leu Leu Arg Leu Gly Pro Arg  
35 40 45  
Pro Arg Ala Ser Thr Leu Ser Ala Ala Ala Pro Gly Asp Glu Asp Gly  
50 55 60  
Val Asp Thr Val Glu Gln Leu Leu His Pro Xaa Pro Pro Glu Thr Ser  
65 70 75 80  
Ala Pro Ala Gly Ser Arg Gly Arg Ile Xaa Arg Leu Met Lys Leu Gln  
85 90 95  
Arg Xaa Ala Asp Gly Xaa Pro Cys Pro Gly Ala Gly Gly Gly Ser  
100 105 110  
Leu Thr Trp Thr Arg Ser Gly Pro Arg Pro Xaa Gly Ala Xaa Cys Pro  
115 120 125  
Ala Gly Arg Ser  
130

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Met Ala Thr Lys Ala Leu Ser Val Ser Ser Leu Thr Ser Thr Ala Phe  
1 5 10 15  
Ala Ser Phe Ser Leu Pro Arg Pro Arg Arg Pro Ser Pro Ser Pro Pro  
20 25 30  
Leu Leu Arg Leu Leu Gly Pro Arg Pro Arg Ala Ser Thr Leu Ser Ala  
35 40 45  
Ala Ala Pro Gly Asp Glu Asp Gly Val Asp Thr Val Glu Gln Leu Leu  
50 55 60  
His Pro Xaa Pro Pro Glu Thr Ser Ala Pro Ala Gly Ser Arg Gly Arg  
65 70 75 80  
Ile Xaa Arg Leu Met Lys Leu Gln Arg Xaa Ala Asp Gly Xaa Pro Cys  
85 90 95  
Pro Gly Ala Gly Gly Gly Ser Leu Thr Trp Thr Arg Ser Gly Pro  
100 105 110  
Arg Pro Xaa Gly Ala Xaa Cys Pro Ala Gly Arg Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:1956:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 493 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..493  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501794

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

aacctaaacc	tcgtctcggc	tcgcctccgc	cagtcagccc	ccctcaacccc	ggcggccaaa	60
agtcgacgca	ccgaagcggc	ggccatggcg	gactaaagcg	gctgtcagag	agccgggacc	120
tgacgcggat	cgagccatcg	gcgcgcactc	ccacatcccg	gggctagggc	tggactcctc	180
catggaggcg	cgcgacgect	cggaggccat	ggtcggggcag	ctgcccgccg	gccgssacgcg	240
gngctcata	ctccagctca	tcgcgcagg	caagatcgcc	ggccgcgcgc	ttctctcgcg	300
gggccagccc	ggtaccggca	agaccgcgct	cgccatggcg	atcgcccaagt	cgctcggcgc	360
ggagacgccc	ttcgctccg	tcgcagcctc	ggagctcttc	tcgctcgamc	tcctcaagam	420
ggaggcgctc	acgcaggect	tcgcgcgcgc	catcggggtgc	gcatacagga	ggagacggaa	480
atcatcgagg	gcg					

- (2) INFORMATION FOR SEQ ID NO:1957:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..54  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501795

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:

Pro	Lys	Pro	Arg	Leu	Ala	Ser	Pro	Pro	Val	Ser	Pro	Leu	Asn	Pro
1			5					10				15		
Gly	Gly	Gln	Lys	Ser	Thr	His	Arg	Ser	Gly	Gly	His	Gly	Gly	Lys
			20					25				30		
Arg	Leu	Ser	Glu	Ser	Arg	Asp	Leu	Thr	Arg	Ile	Glu	Pro	Ser	Ala
			35				40					45		
Thr	Pro	Thr	Ser	Gly	Gly									
			50											

- (2) INFORMATION FOR SEQ ID NO:1958:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501796

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:

Met	Glu	Ala	Arg	Asp	Ala	Ser	Glu	Gly	Met	Val	Gly	Gln	Leu	Pro	Ala
1				5				10				15			
Arg	Xaa	Xaa	Arg	Xaa	Leu	Ile	Leu	Gln	Leu	Ile	Arg	Gln	Gly	Lys	Ile
			20					25				30			
Ala	Gly	Arg	Ala	Val	Leu	Leu	Ala	Gly	Gln	Pro	Gly	Thr	Gly	Lys	Thr
			35				40					45			
Ala	Leu	Ala	Met	Gly	Ile	Ala	Lys	Ser	Leu	Gly	Ala	Glu	Thr	Pro	Phe
			50				55			60					
Ala	Ser	Val	Ala	Ala	Ser	Glu	Leu	Phe	Ser	Leu	Xaa	Leu	Ser	Lys	Xaa

65                      70                      75                      80  
Glu Ala Leu Thr Gln Ala Phe Arg Arg Ala Ile Gly Cys Ala Ser Arg  
                         85                      90                      95  
Arg Arg Arg Lys Ser Ser Arg Ala  
                         100

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

Met Val Gly Gln Leu Pro Ala Arg Xaa Xaa Arg Xaa Leu Ile Leu Gln  
1                      5                      10                      15  
Leu Ile Arg Gln Gly Lys Ile Ala Gly Arg Ala Val Leu Leu Ala Gly  
                         20                      25                      30  
Gln Pro Gly Thr Gly Lys Thr Ala Leu Ala Met Gly Ile Ala Lys Ser  
                         35                      40                      45  
Leu Gly Ala Glu Thr Pro Phe Ala Ser Val Ala Ala Ser Glu Leu Phe  
50                      55                      60  
Ser Leu Xaa Leu Ser Lys Xaa Glu Ala Leu Thr Gln Ala Phe Arg Arg  
65                      70                      75                      80  
Ala Ile Gly Cys Ala Ser Arg Arg Arg Arg Lys Ser Ser Arg Ala  
                         85                      90                      95

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

atcccaaaaga gcacgcagcg casactgaag caccacttcc tgcactcaact gctagctgct 60  
cacacgcgtgc tagtaacagt ccatacaccag tcaccaccaa tggctcccaa ggtgcgctc 120  
ttccttgccc tcggccttct cttegctgcc gccgcgaatg gctgcgaacc ctactgtccc 180  
ggcccgatcg tcccaacgcc gccagtcgtg ccgacgcgtg cgtgcacag ccacggggcg 240  
tgcccgatcg acgcgtctcaa aatcatgtgt gcgccaacgt gctaggccct gtcaaggtcg 300  
gcctgcccca gcacgagcaa tgctgccac ttctggagg gctggtggac ctcgacgcg 360  
cactgtgcct ctgcaccgsc atcaaggcca acggcgtcga tttctacatc aacgggcatg 420  
accactgcct ggaacacatc agcagcagag acagcccaat c

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

Ile Pro Lys Ser Thr Gln Arg Xaa Leu Lys His His Phe Leu His Ser  
1 5 10 15  
Leu Leu Ala Ala His Thr Val Leu Val Thr Val His His Gln Ser Pro  
20 25 30  
Pro Met Ala Pro Lys Val Ala Leu Phe Leu Ala Leu Gly Leu Leu Phe  
35 40 45  
Ala Ala Ala Ala Asn Gly Cys Glu Pro Tyr Cys Pro Gly Pro Val Val  
50 55 60  
Pro Thr Pro Pro Val Val Pro Thr Pro Ser Ser His Ser His Gly Arg  
65 70 75 80  
Cys Pro Ile Asp Ala Leu Lys Ile Met Cys Ala Pro Thr Cys  
85 90

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

Pro Lys Glu His Ala Ala Xaa Thr Glu Ala Pro Leu Pro Ala Leu Thr  
1 5 10 15  
Ala Ser Cys Ser His Arg Ala Ser Asn Ser Pro Ser Pro Val Thr Thr  
20 25 30  
Asn Gly Ser Gln Gly Cys Ala Leu Pro Cys Pro Arg Pro Ser Leu Arg  
35 40 45  
Cys Arg Arg Glu Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro  
50 55 60  
Asn Ala Ala Ser Arg Ala Asp Ala Val Val Ala Gln Pro Arg Ala Leu  
65 70 75 80  
Pro Asp Arg Arg Ala Gln Asn His Val Cys Ala Asn Val Leu Gly Leu  
85 90 95  
Val Lys Val Gly Leu Pro Gln His Glu Gln Cys Cys Pro Leu Leu Glu  
100 105 110  
Gly Leu Val Asp Leu Asp Ala Ala Leu Cys Leu Cys Thr Xaa Ile Lys  
115 120 125  
Ala Asn Gly Val Asp Phe Tyr Ile Asn Gly His Asp His Cys Leu Glu  
130 135 140  
His Ile Ser Ser Arg Asp Ser Pro Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Gln  
1 5 10 15  
Ser Cys Arg Arg Arg Arg Arg Thr Ala Thr Gly Ala Ala Arg Ser Thr  
20 25 30  
Arg Ser Lys Ser Cys Val Arg Gln Arg Ala Arg Pro Arg Gln Gly Arg

	35		40		45				
Pro	Ala	Pro	Ala	Arg	Ala	Met	Leu	Pro	Thr
	50				55			Ser	Gly
Pro	Arg	Arg	Arg	Thr	Val	Pro	Leu	His	Xaa
	65				70			His	Gln
Arg	Phe	Leu	His	Gln	Arg	Ala			
			85						80

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

agacaacacc	agaccgacga	ggtgtgaact	gtaatttcag	atttcagagc	gcgcaagaac	60
ctctttgacc	accgccgcgc	ccgccgcgaa	scaagccaaa	ctgagtaagc	agctatggag	120
ggatccgcgc	ccgctccgct	ccgcacgcgc	atctgcatca	tccggagcgc	tcccgctgcg	180
cacacggcag	ccattctacgc	ggccgcgcgc	gagctcaagc	ctgtddctctt	cgaggcgctgg	240
atggccaacg	acatccgcgc	gggcgggcag	ctcaccacca	ccaccgcagct	cgagaacttc	300
ccgggcttcc	ccaacggcat	catggcgccc	gacctcatgg	acaactgcgc	cgcgcgatcc	360
ctgcgctttg	gcaccacaat	cctctccgag	accgtcaccg	ccgtcgactt	ttcggcctgc	420
ccattccgag	ttagtgcaga	ctccac				

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

Met	Glu	Gly	Ser	Ala	Ala	Ala	Pro	Leu	Arg	Thr	Arg	Ile	Cys	Ile	Ile
1				5					10				15		
Gly	Ser	Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala
			20					25				30			
Glu	Leu	Lys	Pro	Xaa	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala
			35					40			45				
Ala	Gly	Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly
	50				55				60						
Phe	Pro	Asn	Gly	Ile	Met	Gly	Ala	Asp	Leu	Met	Asp	Asn	Cys	Arg	Ala
	65				70				75				80		
Gln	Ser	Leu	Arg	Phe	Gly	Thr	Asn	Ile	Leu	Ser	Glu	Thr	Val	Thr	Ala
			85						90				95		
Val	Asp	Phe	Ser	Ala	Cys	Pro	Phe	Arg	Val	Ser	Ala	Asp	Ser		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:1966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..68  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

Met	Ala	Asn	Asp	Ile	Ala	Ala	Gly	Gly	Gln	Leu	Thr	Thr	Thr	Asp
1		5						10					15	
Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	Asn	Gly	Ile	Met	Gly	Ala	Asp
		20						25				30		Leu
Met	Asp	Asn	Cys	Arg	Ala	Gln	Ser	Leu	Arg	Phe	Gly	Thr	Asn	Ile
		35				40						45		Leu
Ser	Glu	Thr	Val	Thr	Ala	Val	Asp	Phe	Ser	Ala	Cys	Pro	Phe	Arg
	50					55					60			Val
Ser	Ala	Asp	Ser											
65														

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..758

(D) OTHER INFORMATION: / Ceres Seq. ID 1501813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

aaattcccaa	ccgcgcgacg	gcaacaccag	cggtcggatc	ggggggagaaa	cggaaggggca	60
acagacagagc	cggaattcca	ccgacaaatc	caagatttctg	agcacagaca	caggcgaaac	120
tcgatggcgg	aggggtccaa	gccggacgtg	ccgctgttcc	agctcctcag	cgactttctc	180
cagcaggtgg	agtcaatgag	caatcaggaa	gaagtagagc	tgccgcgtca	gattgaagca	240
ttaggattag	aagtcaactaa	ggtaccagag	cagcccgcta	atmaatctag	cgagctagaa	300
matagctgca	gagttggaca	aaagtgtcat	cgcggcttga	ataaatgtcg	acaaagatga	360
tatcatctgc	catggcctca	gatccagagg	tgaagtctct	cttgagcagc	acacttgata	420
tctggatgcc	ggtcataaca	gcgtctgccca	atgagaggcg	ggggtttgtt	gggacgagca	480
gcgaagcgag	ccagaaaagag	caggagaatt	ccaagaaata	gctggatat	ggcgtgttaa	540
tagtttctgt	ttgtgggtct	gtaccgacct	tatctatgtt	catccaacct	agtgtttcca	600
tgccaaaaag	tttgtggcgt	aataaacaat	aaaaacccat	gtccttcatt	cggattagta	660
atagtgatg	atagatctaa	attactatct	tggtcgcccc	ttagttcatt	tttgaactaa	720
aacgcgaata	atagaaaaaga	acggaggggag	tatgattt			

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1501814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

Lys	Phe	Pro	Thr	Ala	Ala	Arg	Gln	His	Gln	Arg	Ser	Asp	Arg	Gly	Arg
1				5					10					15	
Asn	Gly	Arg	Ala	Thr	Ala	Glu	Arg	Glu	Phe	His	Arg	Gln	Ile	Gln	Asp
		20						25				30			
Phe	Glu	His	Arg	His	Arg	Arg	Asn	Ser	Met	Ala	Glu	Gly	Ser	Lys	Pro
		35				40						45			
Asp	Val	Pro	Leu	Phe	Gln	Leu	Leu	Ser	Asp	Leu	Gln	Gln	Val	Glu	
	50				55					60					
Ser	Met	Ser	Asn	Gln	Glu	Glu	Val	Glu	Leu	Arg	Ala	Lys	Ile	Glu	Ala
65				70					75					80	

Leu Gly Leu Glu Val Thr Lys Val Pro Glu Gln Pro Ala Asn Xaa Leu  
85 90 95  
Ser Glu Leu Glu Xaa Ser Cys Arg Val Gly Gln Ser Cys His Arg Gly  
100 105 110  
Leu Asn Lys Cys Arg Gln Arg  
115

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Pro Asn Arg Arg Thr Ala Thr Pro Ala Val Gly Ser Gly Glu Lys  
1 5 10 15  
Arg Lys Gly Asn Ser Arg Ala Arg Ile Pro Pro Thr Asn Pro Arg Phe  
20 25 30  
Arg Ala Gln Thr Gln Ala Lys Leu Asp Gly Gly Val Gln Ala Gly  
35 40 45  
Arg Ala Ala Val Pro Ala Pro Gln Arg Ser Ser Pro Ala Gly Gly Val  
50 55 60  
Asn Glu Gln Ser Gly Arg Ser Arg Ala Ala Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ala Glu Gly Ser Lys Pro Asp Val Pro Leu Phe Gln Leu Leu Ser  
1 5 10 15  
Asp Leu Leu Gln Gln Val Glu Ser Met Ser Asn Gln Glu Val Glu  
20 25 30  
Leu Arg Ala Lys Ile Glu Ala Leu Gly Leu Glu Val Thr Lys Val Pro  
35 40 45  
Glu Gln Pro Ala Asn Xaa Leu Ser Glu Leu Glu Xaa Ser Cys Arg Val  
50 55 60  
Gly Gln Ser Cys His Arg Gly Leu Asn Lys Cys Arg Gln Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

aaaacgcaca	ggagataaact	agcgagcgag	agcgtngaga	tcgaggagaa	gaaggcaagc	60
aggcagagaa	agagagagag	agatggatga	ggagtacgac	gtgatcgtgt	tggggacggg	120
gctcaaggag	tgcatcatca	ggggcctcct	ctccgtcgat	ggcctcaagg	tccttcacat	180
ggacaggaat	gactactacg	gaggagaatc	ttcgtccctg	aatctaacca	agctctggaa	240
taggttcaag	ggcaacgaca	ggcctccccg	gcacctggcg	gtcacaaaga	gtacaacgct	300
gacatggtgc	ccaagttcat	gatggcaaac	ggcgcgctgg	tccgcgtcct	gatccgcacc	360
agcgtgacca	agtatctcaa	cttcaaggct	gttgacggga	gctttgtgta	caacaatggc	420
aagatccaca	aagttccggc	aaccgacgtg	gaggccctca	agtgcgaacct	gatgggcctg	480
ttcgagaagc	ggcgcccgcc	gaagttcttc	atatacgtdc	aggactacga	ggaggacgac	540
cccaagtccc	acgagggcct	ggacctcaac	aaggtcacca	ccagggaagt	catctccaaa	600

tacggat

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

Met	Val	Pro	Lys	Phe	Met	Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu
1			5						10				15		
Ile	Arg	Thr	Ser	Val	Thr	Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly
			20						25				30		
Ser	Phe	Val	Tyr	Asn	Asn	Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp
			35						40				45		
Val	Glu	Ala	Leu	Lys	Ser	Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg
			50						55				60		
Ala	Arg	Lys	Phe	Phe	Ile	Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro
			65						70				75		
Lys	Ser	His	Glu	Gly	Leu	Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val
			85						90				95		
Ile	Ser	Lys	Tyr	Gly											
			100												

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Met	Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu	Ile	Arg	Thr	Ser	Val
1			5											15	
Thr	Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly	Ser	Phe	Val	Tyr	Asn
			20											30	
Asn	Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp	Val	Glu	Ala	Leu	Lys
			35											45	
Ser	Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg	Ala	Arg	Lys	Phe	Phe
			50											60	
Ile	Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro	Lys	Ser	His	Glu	Gly
			65											80	
Leu	Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val	Ile	Ser	Lys	Tyr	Gly

85

90

95

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met Ala Asn Gly Ala Leu Val Arg Val Leu Ile Arg Thr Ser Val Thr  
1 5 10 15  
Lys Tyr Leu Asn Phe Lys Ala Val Asp Gly Ser Phe Val Tyr Asn Asn  
20 25 30  
Gly Lys Ile His Lys Val Pro Ala Thr Asp Val Glu Ala Leu Lys Ser  
35 40 45  
Asn Leu Met Gly Leu Phe Glu Lys Arg Arg Ala Arg Lys Phe Phe Ile  
50 55 60  
Tyr Xaa Gln Asp Tyr Glu Glu Asp Asp Pro Lys Ser His Glu Gly Leu  
65 70 75 80  
Asp Leu Asn Lys Val Thr Thr Arg Glu Val Ile Ser Lys Tyr Gly  
85 90 95

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..526

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

tctgttcccc ttctcctcct ggcgaccccc tcttctcctc ccgcgctcaa accccagcac 60  
aaaaagcaac cgcccgccgc ctctctcgctc ctctcccgaa tcagccgtcg cggtgcctaa 120  
tcggcgccgac cccccctccg atccgcgggt gccgcgcga gaggcgccgc tcggggcctc 180  
ccccgatgta tagcaacttc aaggagcagg cgatcgagta cgtaacagcg gcagtcagg 240  
aggacaatgc cggsaactac gtcaaggcgt tccctctcta catgaacgcg ctcgagtact 300  
tcaaaaccca cctcaagtac gagaagaacc ccaagatcaa ggaggccatc accgccagt 360  
tcaccgagta cctccgcmmgc gccgaggaga tccgggcggt cctcgatgag ggcggcgcar 420  
ggcctggggc caacggtggc gacgcagctg tmgccacgcg ccccaagacc caagggcagg 480  
gatkgggacg gargcaacgg argggatgac tccgagcagt ccaagc

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168

- (D) OTHER INFORMATION: / Ceres Seq. ID 1501829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Cys Ser Pro Phe Pro Pro Ala His Pro Val Phe Ser Ser Pro Arg Gln

1	5	10	15
Thr Pro Ala	Gln Lys Ala	Thr Ala Arg	Leu Leu Ala
	20	25	30
Asn Gln Pro	Ser Arg Cys	Leu Ile Arg	Pro Pro Ile
	35	40	45
Gly Cys Pro	Pro Gln Arg	Arg Ala Ser	Gly Pro Pro
	50	55	60
Asn Phe Lys	Glu Gln Ala	Ile Glu Tyr	Val Lys Gln
	65	70	75
Asp Asn Ala	Xaa Asn Tyr	Val Lys Ala	Phe Pro Leu
	85	90	95
Leu Glu Tyr	Phe Lys Thr	His Leu Lys	Tyr Glu Lys
	100	105	110
Lys Glu Ala	Ile Thr Ala	Lys Phe Thr	Glu Tyr Leu
	115	120	125
Glu Ile Arg	Ala Val Leu	Asp Glu Gly	Gly Ala Asn
	130	135	140
Gly Gly Asp	Ala Ala Xaa	Ala Thr Arg	Pro Lys Thr
	145	150	155
Xaa Gly Arg	Xaa Gln Arg	Xaa Gly	
	165		

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Tyr Ser	Asn Phe Lys	Glu Gln Ala	Ile Glu Tyr	Val Lys Gln	Ala
1	5	10	15		
Val Gln Glu	Asp Asn Ala	Xaa Asn Tyr	Val Lys Ala	Phe Pro Leu	Tyr
	20	25	30		
Met Asn Ala	Leu Glu Tyr	Phe Lys Thr	His Leu Lys	Tyr Glu Lys	Asn
	35	40	45		
Pro Lys Ile	Lys Glu Ala	Ile Thr Ala	Lys Phe Thr	Glu Tyr Leu	Arg
	50	55	60		
Xaa Ala Glu	Glu Ile Arg	Ala Val Leu	Asp Glu Gly	Gly Ala Xaa	Pro
	65	70	75		
Gly Ala Asn	Gly Gly Asp	Ala Ala Xaa	Ala Thr Arg	Pro Lys Thr	Gln
	85	90	95		
Gly Gln Gly	Xaa Gly Arg	Xaa Gln Arg	Xaa Gly		
	100	105			

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1501850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

atatttttta tatggagatt atttctggwt tatataaaag gacacaagt gggacgaata  
gcagaagact tccttcgtc tgcttcccag agaccagcc atggcgatct cccagatctc

acgcatattc ctggccatcc ttctcctcggm cgccgccttc gccgcgcgcc cagctgcgct 180  
tgcgagacggc gacgacgttg tgccctctac cgaatccacg ttccgagaagg aggtcggaaa 240  
ggaccgcggc gccctcgtcg agttctacgc cccctgggtg ggctcactgca agaagcttgc 300  
tctcgagtat gaaagacttg gtgcaagttt taagaaagct aaatctgtct tgattgcyya 360  
ggttgattgt ratgagcaca agartttgtg cagcaagtat ggagtttccg ggatccaac 420  
aatccaatgg ttcccgaaag gatccttgga gcccacaaag tatgaaggac aacgcactgc 480  
agaagccctt gctgaatttc tcaatactga aggaggcaca aatgtaaagc tggc

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

Phe Phe Tyr Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val 15  
1 5 10  
Gly Thr Asn Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln 30  
20 25 30  
Pro Trp Arg Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser 45  
35 40  
Trp Xaa Pro Pro Ser Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr 60  
50 55 60  
Thr Trp Trp Pro Leu Pro Asn Pro Arg Ser Arg Arg Arg Ser Glu Arg 75  
65 70 80  
Thr Ala Ala Pro Ser Ser Ser Ser Thr Pro Gly Val Val Thr Ala 95  
85 90  
Arg Ser Leu Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys 110  
100 105 110  
Leu Asn Leu Ser 115

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1501852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val Gly Thr Asn 15  
1 5 10  
Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln Pro Trp Arg 30  
20 25 30  
Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser Trp Xaa Pro 45  
35 40 45  
Pro Ser Pro Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr Thr Trp Trp 60  
50 55 60  
Pro Leu Pro Asn Pro Arg Ser Arg Arg Arg Ser Glu Arg Thr Ala Ala 75  
65 70 80  
Pro Ser Ser Ser Ser Thr Pro Pro Gly Val Val Thr Ala Arg Ser Leu 95  
85 90 95  
Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys Leu Asn Leu 110  
100 105 110

Ser

(2) INFORMATION FOR SEQ ID NO:1981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1501853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

Met	Ala	Ile	Ser	Gln	Ile	Ser	Arg	Ile	Phe	Leu	Ala	Ile	Leu	Leu	Leu
1				5				10					15		
Xaa	Ala	Ala	Phe	Ala	Ala	Pro	Ala	Ala	Leu	Ala	Asp	Gly	Asp	Asp	
		20					25				30				
Val	Val	Ala	Leu	Thr	Glu	Ser	Thr	Phe	Glu	Lys	Glu	Val	Gly	Lys	Asp
		35				40					45				
Arg	Gly	Ala	Leu	Val	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys
	50				55				60						
Lys	Leu	Ala	Pro	Glu	Tyr	Glu	Arg	Leu	Gly	Ala	Ser	Phe	Lys	Lys	Ala
	65			70				75						80	
Lys	Ser	Val	Leu	Ile	Xaa	Lys	Val	Asp	Cys	Xaa	Glu	His	Lys	Xaa	Leu
		85						90					95		
Cys	Ser	Lys	Tyr	Gly	Val	Ser	Gly	Tyr	Pro	Thr	Ile	Gln	Trp	Phe	Pro
	100						105					110			
Lys	Gly	Ser	Leu	Glu	Pro	Lys	Lys	Tyr	Glu	Gly	Gln	Arg	Thr	Ala	Glu
	115					120					125				
Ala	Leu	Ala	Glu	Phe	Leu	Asn	Thr	Glu	Gly	Gly	Thr	Asn	Val	Lys	Leu
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..569

(D) OTHER INFORMATION: / Ceres Seq. ID 1501862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

acagcctctc	cgctctcgct	cctcgcgccg	ccgcccgcgt	tcctctctgta	caggtaaagg	60
gaggaaagagg	gcgaaatggt	gaagcacaac	aacgtcatcc	ccaacgggca	cttcaagaag	120
cactggcaga	actatgtcaa	gacatggttc	aaccagccgc	cccgcgaagca	gaggcgccgc	180
atcgctcgct	aaaagaaggc	tgtgaagata	ttccccgcgc	cgactgctgg	tcctctacgc	240
cccattgttc	aatgccagac	tttaaagtac	aacatgaagt	caagggtctg	gagaggcttt	300
acccttgagg	agctgaaggc	tgggctcacc	ggcgagyggg	ggcgcgcgcg	ggactacctg	360
tcgcgctg	cgacaaagat	aaagaggatg	gaagagaagg	cccacgatag	arcggtcaaa	420
gcacaaaaga	aacccacacc	catccccatc	aactggatct	tcgataggac	cattctctgt	480
attctacctt	agtgtttatc	tttttcgatc	ttgtttgtg	tatctatgct	gttattgtaa	540
gctaattcca	tggaacttga	tacgtcgt				

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..101  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501863  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1983:

Ser	Leu	Ser	Ala	Ser	Ala	Pro	Arg	Ala	Ala	Ala	Ser	Pro	Pro	Val
1			5					10					15	
Gln	Val	Arg	Arg	Gly	Arg	Gly	Arg	Asn	Gly	Glu	Ala	Gln	Gln	His
			20					25					30	
Pro	Gln	Arg	Ala	Leu	Gln	Glu	Ala	Leu	Ala	Glu	Leu	Cys	Gln	Asp
			35					40					45	
Val	Gln	Pro	Ala	Arg	Pro	Gln	Ala	Glu	Ala	Pro	His	Arg	Ser	Ser
			50					55				60		Lys
Glu	Gly	Cys	Glu	Asp	Ile	Pro	Pro	Pro	Asp	Cys	Trp	Ser	Ser	Thr
					70						75			80
His	Cys	Ser	Met	Pro	Asp	Phe	Lys	Val	Gln	His	Glu	Val	Lys	Gly
					85				90					95
Glu	Arg	Leu	Tyr	Pro										

(2) INFORMATION FOR SEQ ID NO:1984:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 138 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..138  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1501864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:

Met	Val	Lys	His	Asn	Asn	Val	Ile	Pro	Asn	Gly	His	Phe	Lys	Lys	His
1				5					10					15	
Trp	Gln	Asn	Tyr	Val	Lys	Thr	Trp	Phe	Asn	Gln	Pro	Ala	Arg	Lys	Gln
				20				25					30		
Arg	Arg	Arg	Ile	Ala	Arg	Gln	Lys	Lys	Ala	Val	Lys	Ile	Phe	Pro	Arg
				35				40					45		
Pro	Thr	Ala	Gly	Pro	Leu	Arg	Pro	Ile	Val	Gln	Cys	Gln	Thr	Leu	Lys
				50				55				60			
Tyr	Asn	Met	Lys	Ser	Arg	Ala	Gly	Arg	Gly	Phe	Thr	Leu	Glu	Glu	Leu
				70						75				80	
Lys	Ala	Gly	Leu	Thr	Gly	Glu	Gly	Arg	Arg	Ala	Arg	Asp	Tyr	Leu	Cys
				85					90					95	
Ala	Leu	Pro	His	Lys	Ile	Lys	Arg	Met	Glu	Glu	Lys	Ala	His	Asp	Arg
				100				105					110		
Xaa	Val	Lys	Ala	Gln	Lys	Lys	Pro	Thr	Pro	Ile	Pro	Ile	Asn	Trp	Ile
				115				120					125		
Phe	Asp	Arg	Thr	Ile	Pro	Val	Ile	Leu	Pro						

(2) INFORMATION FOR SEQ ID NO:1985:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 72 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Lys Ala  
1 5 10 15  
Gly Leu Thr Gly Glu Gly Arg Arg Ala Arg Asp Tyr Leu Cys Ala Leu  
20 25 30  
Pro His Lys Ile Lys Arg Met Glu Glu Lys Ala His Asp Arg Xaa Val  
35 40 45  
Lys Ala Gln Lys Lys Pro Thr Pro Ile Pro Ile Asn Trp Ile Phe Asp  
50 55 60  
Arg Thr Ile Pro Val Ile Leu Pro  
65 70

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1501872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctggggcag cgtgcgcacg 60  
trgggtacct agctcgctct gctagcctac catggctgat caccaccggg gcgcgacggg 120  
argtgcgggg ggctacggcg acctccagcg cggggggcgg atgcacggcg aggcgcagca 180  
gcagcagaag caggcgccca tgatgacggc gctcaaggcc gcgacggcg cgacctcctt 240  
gaaccactgc cggcgcgcgcg gcatactggcc cttaaaggcg gtggctgctg ctactgacgc 300  
tgccgtagag tctcggtgcg cggcgtagct ctactgagtc gtttatgtgt tgtgctttgt 360  
gtgtgcatgc ttgtgtctgg gggcatgcag tgcagtcgag tactatatgc tgtatgcgtc 420  
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggatgtcatg 480  
tttatgatga ggaataaatt gcagtgttca ggtg

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1501873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln  
1 5 10 15  
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu  
20 25 30  
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser  
35 40 45  
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Arg Ser Arg  
50 55 60  
Ala Pro  
65

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1501874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:

Met	Ala	Asp	His	His	Arg	Gly	Ala	Thr	Gly	Xaa	Xaa	Gly	Gly	Tyr	Gly
1				5					10					15	
Asp	Leu	Gln	Arg	Gly	Gly	Gly	Met	His	Gly	Glu	Ala	Gln	Gln	Gln	Gln
			20					25					30		
Lys	Gln	Gly	Ala	Met	Met	Thr	Ala	Leu	Lys	Ala	Ala	Thr	Ala	Ala	Thr
			35				40					45			
Ser	Leu	Asn	His	Cys	Arg	Arg	Gly	Gly	Ile	Trp	Pro	Leu	Lys	Ala	Val
			50			55				60					
Ala	Ala	Ala	Thr	Tyr	Ala	Ala	Val	Glu	Ser	Arg	Ser	Pro	Arg		
65				70						75					

(2) INFORMATION FOR SEQ ID NO:1989:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1501875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:

Met	His	Gly	Glu	Ala	Gln	Gln	Gln	Gln	Lys	Gln	Gly	Ala	Met	Met	Thr
1				5					10					15	
Ala	Leu	Lys	Ala	Ala	Thr	Ala	Ala	Thr	Ser	Leu	Asn	His	Cys	Arg	Arg
			20					25					30		
Gly	Gly	Ile	Trp	Pro	Leu	Lys	Ala	Val	Ala	Ala	Ala	Thr	Tyr	Ala	Ala
			35			40						45			
Val	Glu	Ser	Arg	Ser	Pro	Arg									
			50			55									

(2) INFORMATION FOR SEQ ID NO:1990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 556 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..556

(D) OTHER INFORMATION: / Ceres Seq. ID 1501884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:

aagggctgcg	cttcgccccg	accaaacgta	ggagacccat	tcacccatct	cctctctttt	60
ctttccaaga	aaagctttct	cttctctgtc	tcagcgccga	cgcttcccaa	ttccttccaa	120
tcgattcttc	gtctcgtctc	cgtgtaatcc	ccagcttgcc	ctctctcgctc	ttccctccca	180
aaacctacag	ctctccctgac	caagctccgg	ggacgaatgg	acggaggagc	cggtctccct	240
ggcacgcmgg	tcccgcgcctc	gccggaggac	gttttccggg	actaccgcgc	gcgccaggcc	300
ggcctaatac	gggcgcctcac	caccgatgtt	gagaagtctc	acgtgatgtg	cgaccacagag	360
aaggataatt	tatgtttata	tggacttccc	aatgagacat	gggaagtaaa	cttgccctgct	420
gaggaggttc	ctctcgaact	ccagagcca	gctctcgaa	ttaattttgc	tcgtgatggg	480
atgaatgaaa	aagattggct	atcacttggt	gcagtgcata	gtgattcttg	gctaattgtct	540
gttgcaattt	attttg					

(2) INFORMATION FOR SEQ ID NO:1991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501885  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:  
Gly Leu Arg Leu Arg Pro Thr Lys Arg Arg Arg Pro Ile His Pro Ser  
1 5 10 15  
Pro Leu Phe Ser Phe Gln Glu Lys Ser Ser Leu Leu Cys Leu Ser Ala  
20 25 30  
Asp Ala Ser Gln Phe Leu Pro Ile Asp Ser Ser Ser Arg Pro Arg Val  
35 40 45  
Ile Pro Ser Leu Pro Ser Ser Leu Phe Pro Pro Lys Thr Leu Arg Leu  
50 55 60  
Pro Asp Gln Ala Pro Gly Thr Asn Gly Arg Arg Ser Arg Leu Pro Trp  
65 70 75 80  
His Xaa Gly Pro Ala Leu Ala Gly Gly Arg Phe Pro Gly Leu Pro Arg  
85 90 95  
Ala Pro Gly Arg Pro Asn Gln Gly Ala His His Arg Cys  
100 105  
(2) INFORMATION FOR SEQ ID NO:1992:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501886  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:  
Met Asp Gly Gly Ala Gly Phe Pro Gly Thr Xaa Val Pro Arg Ser Pro  
1 5 10 15  
Glu Asp Val Phe Arg Asp Tyr Arg Ala Arg Gln Ala Gly Leu Ile Arg  
20 25 30  
Ala Leu Thr Thr Asp Val Glu Lys Phe Tyr Val Met Cys Asp Pro Glu  
35 40 45  
Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn Glu Thr Trp Glu Val  
50 55 60  
Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu Pro Ala Leu  
65 70 75 80  
Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp Trp Leu Ser  
85 90 95  
Leu Val Ala Val His Ser Asp Ser Trp Leu Met Ser Val Ala Phe Tyr  
100 105 110  
Phe  
(2) INFORMATION FOR SEQ ID NO:1993:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:

Met Cys Asp Pro Glu Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn  
1 5 10 15  
Glu Thr Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu  
20 25 30  
Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu  
35 40 45  
Lys Asp Trp Leu Ser Leu Val Ala Val His Ser Asp Ser Trp Leu Met  
50 55 60  
Ser Val Ala Phe Tyr Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1501888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

gagccttttcg gtttttctct gtcttcattgt gtgtttgttta tagagaccctt gccttgctcgg 60  
ggcagcacac ttgggacgcg aggaggaggga gttggtgagc gaactcggga tcagtgggtg 120  
accgcagagt tcttgcttct tcctcttgga ggargagggc tgcagccctgc agggggccgga 180  
gagagcaggga ggaggcggag acatgggtag ctgcctcgaag ctggcgaggga gggcggtgga 240  
gacggacgct ccggtcatgg tgaagataca agaactgctc cgargggcca aggatgtrat 300  
gtcgcttcgc cagggagttg ttacttgcca acctcccgag tcagctatgg ataatgctga 360  
aaagatcatc agggaaacca tagtcagtaa atatgggtct ratgatgggc ttccctgagct 420  
tcgagaagca ctctctgaaa agctaagcag agaggacaag cttaccaaat catctgtcat 480  
ggtcactgct gttgcgaatc aggcttttgc gaacttgctc ctactcttt gt

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1501889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

Met Gly Ser Phe Ala Lys Leu Ala Arg Arg Ala Val Glu Thr Asp Ala  
1 5 10 15  
Pro Val Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa  
20 25 30  
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala  
35 40 45  
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr  
50 55 60  
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys  
65 70 75 80  
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala  
85 90 95  
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys  
100 105 110

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501890  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:  
Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa Met Ser  
1 5 10 15  
Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala Met Asp  
20 25 30  
Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr Gly Ser  
35 40 45  
Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Glu Lys Leu Ser  
50 55 60  
Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala Gly Ala  
65 70 75 80  
Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys  
85 90  
(2) INFORMATION FOR SEQ ID NO:1997:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501891  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:  
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala  
1 5 10 15  
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr  
20 25 30  
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys  
35 40 45  
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala  
50 55 60  
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys  
65 70 75  
(2) INFORMATION FOR SEQ ID NO:1998:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 569 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..569  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501895  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:  
aggatccgag aacatccgcc gcgactccat gctccaggag atcaagctcg cctaccagat 60  
tcttgccac aagtaaccat ctgatatgaa taagagtccc gaagcagaag aaaagttcaa 120  
ggagatcagt gctgcatatg agccaagcgtt ggatctgacc gctgtacttt gtgtcgccgc 180  
ttgaatctac ggttctcttc ttcttgttcc atcccggtgga tctgtcccggt ggtgtgtcaa 240  
gcattcgatt tctgctatta taacatccaa cggtggcggt gaagagcaag gggacagata 300

agcccaaaagg cagcaagggg aacgtcgaca aggaccccaa caagcctgac toccaacatt 360  
ttttgtccgc cgggtgctgta gcggaagccc aaaggcagca aggggaacgt cgacaaggac 420  
cccaacaagg ctgactccca acattttttg tccgccgggt ctgtarcgcc ggcgtgtgtg 480  
arctccccca tgctgggctc tgggatgctc ccaggcgccg gggttcggcg agacggggac 540  
tgawctgggt ctgggctctg ggatgctcc

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

Gly Ser Glu Asn Ile Arg Arg Asp Ser Met Leu Gln Glu Ile Lys Ser 1 10  
Ala Tyr Gln Ile Leu Ala His Lys Tyr His Pro Asp Met Asn Lys Ser 20 15  
Pro Glu Ala Glu Glu Lys Phe Lys Glu Ile Ser Ala Ala Tyr Glu Pro 30 45  
Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala 40 50 55 60

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

Met Leu Gln Glu Ile Lys Ser Ala Tyr Gln Ile Leu Ala His Lys Tyr 1 10  
His Pro Asp Met Asn Lys Ser Pro Glu Ala Glu Glu Lys Phe Lys Glu 20 15  
Ile Ser Ala Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys 30 45  
Val Ala Ala 40 50

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

Met Asn Lys Ser Pro Glu Ala Glu Glu Lys Phe Lys Glu Ile Ser Ala 1 10  
Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala 20 25 30

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

ccatccagtc	ctggagcgtg	cgcggctgcs	cttgcategc	atctccgtcg	tcgtctcctgc	60
ccacggaatc	cgtccaattc	ccccagccgc	ccgtcgctct	tttctataaa	attcactccg	120
ccaccaaatc	tcgaatcccc	atcgcgctgc	ttttccacgc	accccgacgc	cgacgccgac	180
gccacgcgcg	ctccctcccc	agtcgccact	ccccctccgc	ggccgcggac	agagatccgg	240
ggcgcgcgcg	gatggcgaa	atcgacatgg	cgaagatcct	ggcggacctg	gaccgcggcg	300
ccagcggcgg	ncgacgcgcg	ggtgcccaag	accaaagctg	tatgcacgct	cgccccggcc	360
tcccgcaccg	tgccatgct	cgagaagctg	ctccgcgcgc	gcgatgaact	cgcgcgcttc	420
aacttctccc	ac					

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

Pro	Ser	Ser	Pro	Gly	Ala	Cys	Ala	Ala	Xaa	Leu	Ala	Ser	His	Leu	Arg
1				5					10					15	
Arg	Arg	Pro	Arg	Pro	Arg	Asn	Pro	Ser	Asn	Ser	Pro	Arg	Arg	Pro	Ser
				20				25					30		
Ser	Phe	Ser	Ile	Lys	Phe	Thr	Pro	Pro	Pro	Asn	Leu	Glu	Ser	Pro	Ser
				35				40				45			
Arg	Cys	Phe	Ser	Thr	Asp	Pro	Asp	Ala	Asp	Ala	Asp	Ala	Thr	Ala	Ala
				50				55			60				
Pro	Ser	Pro	Val	Pro	Thr	Pro	Leu	Pro	Gly	Pro	Arg	Thr	Glu	Ile	Arg
				65				70			75			80	
Gly	Ala	Ala	Arg	Trp	Arg	Thr	Ser	Thr	Trp	Arg	Arg	Ser	Trp	Arg	Thr
				85				90					95		
Trp	Thr	Ala	Ala	Pro	Ala	Ala	Xaa	Asp	Ala	Arg	Val	Pro	Lys	Thr	Lys
				100				105					110		
Leu	Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	Arg	Thr	Val	Pro	Met	Leu	Glu
				115				120				125			
Lys	Leu	Leu	Arg	Xaa	Gly	Met	Asn	Val	Ala	Arg	Phe	Asn	Phe	Ser	His
				130				135				140			

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

Ile Gln Ser Trp Ser Leu Arg Gly Cys Xaa Cys Ile Ala Ser Pro Ser  
1 5 10 15  
Ser Ser Ser Pro Thr Glu Ser Val Gln Phe Pro Thr Pro Val Val  
20 25 30  
Leu Phe Tyr Lys Ile His Ser Ala Thr Lys Ser Arg Ile Pro Ile Ala  
35 40 45  
Leu Leu Phe His Arg Pro Arg Arg Arg Arg Arg His Arg Arg Ser  
50 55 60  
Leu Pro Ser Pro His Ser Pro Ser Arg Ala Ala Asp Arg Asp Pro Gly  
65 70 75 80  
Arg Arg Ala Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu  
85 90 95  
Asp Arg Gly Ala Ser Gly Xaa Arg Arg Ala Gly Ala Gln Asp Gln Ala  
100 105 110  
Arg Met His Ala Arg Pro Gly Leu Pro His Arg Ala His Ala Arg Gly  
115 120 125  
Ala Ala Pro Arg Xaa His Glu Arg Arg Ala Leu Gln Leu Leu Pro  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1501902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

aagctctctgc ttttccactgc ctctgcgtctc gcgtctgcgt ctgcgtctgc actgcttcgc 60  
gtctccctcc ccccgctctc gccccgggaa aaaaaaaagc aaaaacacggc catggaaggc 120  
tacgaccgcg agttctacca gttaacggac cagctgcgcc tgcagacggc cgcttctctcg 180  
ggcctctccc tcggcgactc catctggctc cccgcgcgcc gccgcaacaa cagcaacgac 240  
gtctctcttg ccgctctcggc gtgcgccgcc gacgcgcgcg ccaagaccaa cgcgctcgtc 300  
ggcctcaagc tcaacgacggc agggcccgcc ctcctcggtc ccgggaagct ggcttccggc 360  
ggcgggcgca ccaaggccga ccgctacaac aacaacaacc tctccaacac cgacaacaag 420  
accgtgtac

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

Lys Leu Leu Leu Phe His Cys Ser Ala Ser Ala Ser Ala Ser  
1 5 10 15  
Ala Leu Leu Arg Val Ser Leu Pro Pro Pro Pro Arg Glu Lys Lys  
20 25 30  
Lys Gln Asn Thr Ala Met Glu Gly Tyr Asp Arg Glu Phe Tyr Gln Phe  
35 40 45

Ser Asp Gln Leu Arg Leu Gln Thr Ala Ala Phe Ser Gly Leu Ser Leu  
50 55 60  
Gly Asp Ser Ile Trp Ser Pro Ala Gly Arg Arg Asn Asn Ser Asn Asp  
65 70 75 80  
Val Leu Phe Ala Ala Ser Ala Ser Pro Ala Asp Ala Ala Lys Thr  
85 90 95  
Asn Ala Val Val Gly Leu Lys Leu Asn Asp Gly Gly Pro Gly Leu Ile  
100 105 110  
Gly Ser Gly Lys Leu Ala Phe Gly Gly Gly Thr Lys Ala Asp Arg  
115 120 125  
Tyr Asn Asn Asn Leu Ser Asn Thr Asp Asn Lys Thr Val Tyr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2007:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Ser Ser Cys Phe Ser Thr Ala Leu Arg Leu Arg Leu Arg Leu  
1 5 10 15  
His Cys Phe Ala Ser Pro Ser Pro Arg Leu Arg Pro Gly Lys Lys Lys  
20 25 30  
Ser Lys Thr Arg Pro Trp Lys Ala Thr Thr Ala Ser Ser Thr Ser Ser  
35 40 45  
Ala Thr Ser Cys Ala Cys Arg Arg Pro Pro Ser Arg Ala Ser Pro Ser  
50 55 60  
Ala Thr Pro Ser Gly Pro Pro Pro Ala Gly Ala Thr Thr Ala Thr Thr  
65 70 75 80  
Ser Ser Ser Pro Pro Arg Arg Arg Pro Pro Thr Pro Pro Arg Pro  
85 90 95  
Thr Pro Ser Ser Ala Ser Ser Ser Thr Thr Glu Gly Pro Ala Ser Ser  
100 105 110  
Ala Pro Gly Ser Trp Pro Ser Ala Ala Ala Pro Arg Pro Thr Ala  
115 120 125  
Thr Thr Thr Thr Ser Pro Thr Pro Thr Thr Arg Pro Cys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2008:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Ala Pro Ala Phe Pro Leu Leu Cys Val Cys Val Cys Val Cys Val Cys  
1 5 10 15  
Thr Ala Ser Arg Leu Pro Pro Pro Ala Ser Ala Pro Gly Lys Lys Lys  
20 25 30  
Ala Lys His Gly His Gly Arg Leu Arg Pro Arg Val Leu Pro Val Gln  
35 40 45  
Arg Pro Ala Ala Pro Ala Asp Gly Arg Leu Leu Gly Pro Leu Pro Arg

50 55 60  
Arg Leu His Leu Val Pro Arg Arg Pro Ala Gln Gln Gln Arg Arg  
65 70 75 80  
Pro Leu Arg Arg Leu Gly Val Ala Arg Arg Arg Arg Gln Asp Gln  
85 90 95  
Arg Arg Arg Arg Pro Gln Ala Gln Arg Arg Arg Ala Arg Pro His Arg  
100 105 110  
Leu Arg Glu Ala Gly Leu Arg Arg Arg His Gln Gly Arg Pro Leu  
115 120 125  
Gln Gln Gln Gln Pro Leu Gln His Arg Gln Gln Asp Arg Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

aaatatctct gcacactatg acctgagtaa tgatttcttt gctctttttc tggatccgac 60  
gatgacttac tcttggtgga ttttcaakgm rraagatgag agtttagaag cagcgacasta 120  
cgtaaaccttg acaatctaat taataaggct aaggtggatc cggggcatac tgccttgac 180  
attggctgtg gttggggctc attggcaata cgtttggtga agagaactgg ctgcaagtgc 240  
acaggaatta cattatcgga ggagcaactg aaatatggaa agagaaaggt gaaagaattt 300  
ggattagagg accgcataac tcttcctgctt tgtgattacc gtcaaatacc gaacggccag 360  
aagtttgata ggattathag ttgtgggatg cttgaacacg ttggccatga gttctacgaa 420  
gatttcttgc ccttcctgga gtaicatttg gccgaacacg gctacttgt cctccagtc 480  
atcgcggtcc cagaggaact gtacgacaaa atgag

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

Asn Ile Ser Ala His Tyr Asp Leu Ser Asn Asp Phe Ala Leu Phe  
1 5 10 15  
Leu Asp Pro Thr Met Thr Tyr Ser Cys Gly Ile Phe Xaa Xaa Xaa Asp  
20 25 30  
Glu Ser Leu Glu Ala Ala Xaa Tyr Val Asn Leu Thr Ile  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:  
Met Leu Glu His Val Gly His Glu Phe Tyr Glu Asp Phe Phe Ala Ser  
1 5 10 15  
Cys Glu Tyr His Leu Ala Glu His Gly Leu Leu Val Leu Gln Ser Ile  
20 25 30  
Ala Val Pro Glu Glu Leu Tyr Asp Lys Met  
35 40

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..35  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

Met Ser Ser Thr Lys Ile Ser Leu Pro Pro Ala Ser Ile Ile Trp Pro  
1 5 10 15  
Asn Thr Ala Tyr Leu Ser Ser Ser Pro Ser Arg Ser Gln Arg Asn Cys  
20 25 30  
Thr Thr Lys  
35

(2) INFORMATION FOR SEQ ID NO:2013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..549  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

acaacaagca gaagcagaag cagaagctag cagctagtag acgagcgcagc agtagctagc 60  
tagctagcta tctagagagc tcatcatatc gctgctcgct ctcatccacc attatagaga 120  
agagcagatc gagctgcagc tggcagaggc cgagttgttg ctagctagct cctgcttgct 180  
aaatttgcat cgtatccgat ccattccatg aagaagtcgt cgatgatggc gcccatgacg 240  
atcattggcga gaggttgccgc tgtgctcgct ctctcgtcgc ctgccatggc ttccgcgcga 300  
ggagcagctg ggcctggacat gaattcttac ggcagcacgt gccgcgcgct ggagggccatc 360  
gtcaaggagg agatgggtggc gatcctcaag gcggcgccga cgctggccgc cccgctgctc 420  
cgctccatt tcacgactg ctctgctcagg ggctgcgcag cctccgtgct cctggactgc 480  
actcccacca gcacggcgga gaaggacgcc accccgaacc tcacctccg gggcttcggc 540  
tcctgtcag

(2) INFORMATION FOR SEQ ID NO:2014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..114  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:

Met Lys Lys Ser Met Met Ala Pro Met Thr Ile Met Ala Arg Val  
1 5 10 15

Ala Ala Val Leu Val Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly  
20 25 30  
Ala Ala Gly Leu Asp Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val  
35 40 45  
Glu Ala Ile Val Lys Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro  
50 55 60  
Thr Leu Ala Gly Pro Leu Leu Arg Leu His Phe His Asp Cys Phe Val  
65 70 75  
Arg Gly Cys Asp Ala Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr  
85 90 95  
Ala Glu Lys Asp Ala Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser  
100 105 110  
Val Gln

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1501924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val  
1 5 10 15  
Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp  
20 25 30  
Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys  
35 40 45  
Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro  
50 55 60  
Leu Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala  
65 70 75 80  
Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr Ala Glu Lys Asp Ala  
85 90 95  
Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser Val Gln  
100 105

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
  - (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val Leu  
1 5 10 15  
Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp Met  
20 25 30  
Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys Glu  
35 40 45  
Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro Leu  
50 55 60  
Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala Ser

65 70 75 80  
Val Leu Leu Asp Ser Thr Pro Thr Ser Thr Ala Glu Lys Asp Ala Thr  
85 90 95  
Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser Val Gln  
100 105

(2) INFORMATION FOR SEQ ID NO:2017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..555
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2017:

ctggctcgcc	gtcattctct	tcctcttcgc	gtgctcgtrc	tcgtgctcgt	gctctccgcc	60
ctccccctcc	gccacctcgc	gcggaacgga	acccaggccg	ccgcccagccc	agccaccgct	120
aggcgaccgc	gcggcatggt	ggcgctttta	cactacctat	gctagtttgc	ctgatgctac	180
atttccacga	tggttaagct	gactatgata	gcgcgtgtca	ctgatggcct	tccattgtcg	240
gagggattag	atgatatgtc	ggatctgaaa	gatgctgact	tctacaagca	gcaagcaaaa	300
ctgtttgtca	agaacttgtc	cacagggcag	catgaggcgt	caaggatgtc	aattgagaca	360
ggaccatacc	ttttccacta	catcatagaa	ggccgtgttt	gctatttgac	tttgtgtgac	420
cgttcttatt	ccaagaaact	tgcattccag	tatctcgaag	atctcaaaaa	tgaatttgac	480
aaagtcaatg	gcaggcaaat	tgaacacagc	gcaaggccat	atgsatttat	taaatttgat	540
gcattcatat	gaag					

(2) INFORMATION FOR SEQ ID NO:2018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2018:

Met	Val	Lys	Leu	Thr	Met	Ile	Ala	Arg	Val	Thr	Asp	Gly	Leu	Pro	Leu	
1				5					10					15		
Ser	Glu	Gly	Leu	Asp	Asp	Ser	Arg	Asp	Leu	Lys	Asp	Ala	Asp	Phe	Tyr	
			20					25					30			
Lys	Gln	Gln	Ala	Lys	Leu	Leu	Phe	Lys	Asn	Leu	Ser	Arg	Gly	Gln	His	
			35				40					45				
Glu	Ala	Ser	Arg	Met	Ser	Ile	Glu	Thr	Gly	Pro	Tyr	Leu	Phe	His	Tyr	
			50			55					60					
Ile	Ile	Glu	Gly	Arg	Val	Cys	Tyr	Leu	Thr	Leu	Cys	Asp	Arg	Ser	Tyr	
65				70				75						80		
Pro	Lys	Lys	Leu	Ala	Phe	Gln	Tyr	Leu	Glu	Asp	Leu	Lys	Asn	Glu	Phe	
			85					90					95			
Glu	Lys	Val	Asn	Gly	Ser	Gln	Ile	Glu	Thr	Ala	Ala	Arg	Pro	Tyr	Xaa	
			100				105						110			
Phe	Ile	Lys	Phe	Asp	Ala	Phe	Ile	Gln	Lys							
			115													

(2) INFORMATION FOR SEQ ID NO:2019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1501928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

```
Met Ile Ala Arg Val Thr Asp Gly Leu Pro Leu Ser Glu Gly Leu Asp
1           5           10           15
Asp Ser Arg Asp Leu Lys Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys
20           25           30
Leu Leu Phe Lys Asn Leu Ser Arg Gly Gln His Glu Ala Ser Arg Met
35           40           45
Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly Arg
50           55           60
Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu Ala
65           70           75           80
Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn Gly
85           90           95
Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe Asp
100          105          110
Ala Phe Ile Gln Lys
115
```

(2) INFORMATION FOR SEQ ID NO:2020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

```
Met Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly
1           5           10           15
Arg Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu
20           25           30
Ala Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn
35           40           45
Gly Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe
50           55           60
Asp Ala Phe Ile Gln Lys
65           70
```

(2) INFORMATION FOR SEQ ID NO:2021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1501930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

```
aagtcctctt gtgtttttta taggcttgag agcttggaa agcggggggg ggaggaagcg      60
gaagaggagc ttctgtttgt gttctagagg ggagtcagt tccatggcgg caggcctctg      120
tccctcggg ggtctctcaa ggcgcttgaa gctgatatcc accatgccaa caccctggcg      180
catgctatgc acagggcgta trggggtgcc tgcgcagatg naggctgtcc tacagctcca      240
tggtcccaat ctttctcaac cttatccaat ggatggactg cagctgtctc ctgtcataca      300
```

cgctccctag ctaccttgcc ctgctcgagg ttctcgtcta caaggtttat gtcgatgaag 360  
atgcctccat atccaccata gaaaggagg cgagcctgaa ggaattctac actatcatat 420  
accctttctt gcaacaactg gaggacaact tgatggacaa ggactgcaag gacaaagggt 480  
ggctctgtgc tgc

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1501931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

Ser Leu Phe Val Phe Phe Ile Gly Leu Arg Ala Trp Asn Ser Gly Gly  
1 5 10 15  
Trp Arg Lys Arg Lys Arg Ser Phe Val Leu Cys Ser Arg Gly Glu Ser  
20 25 30  
Cys Ser Met Ala Ala Gly Leu Cys Pro Ser Gly Gly Leu Ser Arg Arg  
35 40 45  
Leu Lys Leu Ile Ser Thr Met Pro Thr Pro Trp Arg Met Leu Tyr Thr  
50 55 60  
Gly Arg Xaa Gly Val Pro Ala Gln Met Xaa Ala Val Leu Gln Leu His  
65 70 75 80  
Gly Ser Asn Leu Ser Gln Pro Tyr Pro Met Asp Gly Leu Gln Leu Leu  
85 90 95  
Pro Val Ile His Ala Pro  
100

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met Phe His Gly Gly Arg Pro Leu Ser Leu Arg Gly Ser Leu Lys Ala  
1 5 10 15  
Leu Glu Ala Asp Ile His His Ala Asn Thr Leu Ala His Ala Ile His  
20 25 30  
Arg Ala Tyr Xaa Gly Ala Cys Ala Asp Xaa Gly Cys Pro Thr Ala Pro  
35 40 45  
Trp Leu Gln Ser Phe Ser Thr Leu Ser Asn Gly Trp Thr Ala Ala Ala  
50 55 60  
Pro Cys His Thr Arg Ser Leu Ala Thr Leu Ala Cys Ser Arg Phe Ser  
65 70 75 80  
Ser Thr Arg Phe Met Ser Met Lys Met Pro Pro Tyr Pro Pro  
85 90

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1501933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

Met	Ala	Pro	Ile	Phe	Leu	Asn	Leu	Ile	Gln	Trp	Met	Asp	Cys	Ser	Cys		
1				5				10					15				
Ser	Leu	Ser	Tyr	Thr	Leu	Pro	Ser	Tyr	Leu	Gly	Leu	Leu	Glu	Val	Leu		
			20					25					30				
Val	Tyr	Lys	Val	Tyr	Val	Asp	Glu	Asp	Ala	Ser	Ile	Ser	Thr	Ile	Glu		
		35					40					45					
Arg	Arg	Ala	Ser	Leu	Lys	Glu	Phe	Tyr	Thr	Ile	Ile	Tyr	Pro	Phe	Leu		
		50				55					60						
Gln	Gln	Leu	Glu	Asp	Asn	Leu	Met	Asp	Lys	Asp	Cys	Lys	Asp	Lys	Gly		
65					70					75					80		
Trp	Ser	Ala	Ala														

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..586

(D) OTHER INFORMATION: / Ceres Seq. ID 1501949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

ccgccgtcaa	acgtcatccg	aatcccgccc	gcgaccagcg	aagaaggtag	gaagcatccg		60
gaacggagag	gcgcctcccg	cctcgcttcc	ctcccattgg	gcgcgccctc	gcgcgcgtct		120
catcgctctc	gccctctatt	tctccttcat	cgtcccgccc	catccgcgcg	tgccacgcac		180
ctcctccttc	tatctccttc	cagacgcggg	gacgctcgcc	cacggcggcg	gcggcagctg		240
agtcctctgt	cagtacgctt	ctcgaggctg	gcggactcac	cgcatccctg	aaggagactg		300
ggcagcagat	cctcgccggc	gtcgacctca	ccatccgcga	ggcgagatt	catcgattat		360
tggaaaaaaa	cggtctccgc	aagagcacc	tcacgaaagt	tctcgtaggc	catcctcatt		420
atggagtaac	tggtggtaac	attctcttca	agggtaggga	ctgtgttgac	atggagccag		480
aggacagatc	tctagcaggc	cttttcata	gtttccaag	acctattgag	attccttgga		540
gtcagcaatt	ttgattttct	gtccatggct	gtgaatgctc	gcagag			

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1501950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

Pro	Pro	Ser	Asn	Val	Ile	Arg	Ile	Arg	Ala	Ala	Thr	Ser	Glu	Glu	Gly		
1				5					10					15			
Arg	Lys	His	Pro	Glu	Arg	Arg	Arg	Ala	Ser	Cys	Leu	Ala	Phe	Leu	Pro		
			20					25					30				
Trp	Arg	Arg	Pro	Ser	Pro	Pro	Ser	His	Arg	Arg	Arg	Pro	Tyr	Ser	Leu		
		35					40						45				
Leu	His	Arg	Pro	Ala	Pro	Ser	Ala	Ala	Ala	Thr	His	Leu	Leu	Leu	Leu		
		50				55				60							
Ser	Pro	Ser	Arg	Arg	Gly	Asp	Ala	Arg	Pro	Arg	Arg	Arg	Arg	Gln	Leu		
65					70					75					80		

Ser Pro Leu Ser Val Arg Phe Ser Arg Cys Ala Asp Ser Pro His Pro  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Arg Arg Gln Thr Ser Ser Glu Ser Ala Pro Arg Pro Ala Lys Lys Val  
1 5 10 15  
Gly Ser Ile Arg Asn Gly Asp Ala Pro Pro Ala Ser Leu Ser Ser His  
20 25 30  
Gly Ala Ala Pro Arg Arg Arg Leu Ile Val Val Ala Pro Ile Leu Ser  
35 40 45  
Phe Ile Val Pro Pro His Pro Pro Leu Pro Arg Thr Ser Ser Phe Tyr  
50 55 60  
Leu Leu Pro Asp Ala Gly Thr Leu Ala His Gly Gly Gly Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

Met Ala Pro Pro Leu Ala Ala Val Ser Ser Ser Ser Pro Leu Phe Ser  
1 5 10 15  
Pro Ser Ser Ser Arg Pro Ile Arg Arg Cys His Ala Pro Pro Pro Ser  
20 25 30  
Ile Ser Phe Gln Thr Arg Gly Arg Ser Pro Thr Ala Ala Ala Ala Ala  
35 40 45  
Glu Ser Ser Val Ser Thr Leu Leu Glu Val Arg Gly Leu Thr Ala Ser  
50 55 60  
Val Lys Glu Thr Gly Gln Gln Ile Leu Ala Gly Val Asp Leu Thr Ile  
65 70 75  
Arg Glu Gly Glu Ile His Ala Ile Met Gly Lys Asn Gly Ser Gly Lys  
85 90 95  
Ser Thr Leu Thr Lys Val Leu Val Gly His Pro His Tyr Glu Val Thr  
100 105 110  
Gly Gly Thr Ile Leu Phe Lys Gly Glu Asp Leu Val Asp Met Glu Pro  
115 120 125  
Glu Asp Arg Ser Leu Ala Gly Leu Phe Met Ser Phe Gln Ala Pro Ile  
130 135 140  
Glu Ile Pro Trp Ser Gln Gln Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..657  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501976  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029;

agtgccggca	cgccgcgtgt	tcagagaagt	gcctcttttt	taagtcttgt	ttctctccca	60
ccccggcag	gcgaatggag	aaggccagtg	gaggcagcaa	tcctccgcgc	coaccgctcc	120
acatggagga	cttccaactg	gaggggaaga	agcccgctca	gaaccccttt	gtgcccatac	180
gcgcactggt	tactgctgga	gttctgactg	ctggctgtgt	cagtttccga	taagggaaac	240
ctcagctggg	tcagaaaact	atgagggcac	gtgtagttgc	tcaaggcgct	acagtcgctc	300
tgatgattgg	cagtgctttac	tactatggcg	atcaaatcaa	gctgttcaag	aaagggtcga	360
gcccatgac	ttcccatgaa	tattgctgtt	tttggtgtat	ggaggaatgc	ctgttatcac	420
cataaatttc	acctggactc	tgctgccctc	ttttaacatc	attttgacct	gacacgtggt	480
agctaaaca	aaatcgctgt	tggtccgac	ggcaggattg	aaaataaata	attttgtttg	540
ttgatatttg	tcaggatttg	tgggttgat	taattaggct	atatgcatca	attgttatat	600
ctttgtacaa	acacgcgttc	gttgctgtgc	aatcagcgcc	tgaagtgaac	attttgc	

(2) INFORMATION FOR SEQ ID NO:2030:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501977  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

Val	Pro	Ala	Pro	Pro	Leu	Leu	Gln	Lys	Leu	Pro	Leu	Phe	Tyr	Val	Leu
1				5				10					15		
Phe	Leu	Leu	His	Pro	Gly	Asp	Ala	Asn	Gly	Glu	Gly	Gln	Trp	Arg	Gln
				20				25					30		
Gln	Ser	Ser	Ala	Ala	Thr	Ala	Pro	His	Gly	Gly	Leu	Pro	Thr	Gly	Gly
				35				40					45		
Glu	Glu	Ala	Arg	Gln	Glu	Pro	Leu	Cys	Ala	His	Arg	Arg	Thr	Gly	Tyr
				50				55					60		
Cys	Trp	Ser	Ser	Asp	Cys	Trp	Ser	Asp	Gln	Phe	Pro	Ile	Trp	Glu	Leu
				65				70					75		
Ser	Ala	Gly	Ser	Glu	Thr	Asp	Glu	Gly	Thr	Cys	Ser	Cys	Ser	Arg	Arg
				85				90					95		
Tyr	Ser	Arg	Ser	Asp	Asp	Trp	Gln	Cys	Leu	Leu	Leu	Trp	Arg	Ser	Asn
				100				105					110		
Gln	Ala	Val	Gln	Glu	Arg	Val	Glu	Pro	Met	Ile	Phe	Pro			
				115				120					125		

(2) INFORMATION FOR SEQ ID NO:2031:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..121  
(D) OTHER INFORMATION: / Ceres Seq. ID 1501978  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

Cys Arg His Arg Arg Cys Cys Arg Ser Cys Leu Phe Phe Thr Ser Cys

1	5	10	15
Phe Ser Ser Thr Pro Ala Thr Arg Met Glu Lys Gly Ser Gly Gly Ser			
20	25	30	
Asn Pro Pro Pro Pro Pro Leu His Met Glu Asp Phe Gln Leu Glu Gly			
35	40	45	
Lys Lys Pro Val Lys Asn Pro Phe Val Pro Ile Gly Ala Leu Val Thr			
50	55	60	
Ala Gly Val Leu Thr Ala Gly Leu Ile Ser Phe Arg Tyr Gly Asn Ser			
65	70	75	80
Gln Leu Gly Gln Lys Leu Met Arg Ala Arg Val Val Ala Gln Gly Ala			
85	90	95	
Thr Val Ala Leu Met Ile Gly Ser Ala Tyr Tyr Tyr Gly Asp Gln Ile			
100	105	110	
Lys Leu Phe Lys Lys Gly Ser Ser Pro			
115	120		

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

Met Glu Lys Gly Ser Gly Gly Ser Asn Pro Pro Pro Pro Leu His	
1	15
Met Glu Asp Phe Gln Leu Glu Gly Lys Lys Pro Val Lys Asn Pro Phe	
20	30
Val Pro Ile Gly Ala Leu Val Thr Ala Gly Val Leu Thr Ala Gly Leu	
35	45
Ile Ser Phe Arg Tyr Gly Asn Ser Gln Leu Gly Gln Lys Leu Met Arg	
50	60
Ala Arg Val Val Ala Gln Gly Ala Thr Val Ala Leu Met Ile Gly Ser	
65	80
Ala Tyr Tyr Tyr Gly Asp Gln Ile Lys Leu Phe Lys Lys Gly Ser Ser	
85	95
Pro	

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

atgcgcctcg cgccgccttc gacagtccct cgcgttccat ttgcttcggc tcattctcaga	60
tcaagctagc gcacctgaca cccaccacct ccctcccaga tccaccacc cagccatggc	120
caccgccttt gactcccaga cctctctccc cgcgcgcgcg cccttcacg acgacccttt	180
ctctcatttc gacgctcgg cccccgcgcg cgcgcacggc ttcccgacct ccccggaagc	240
ctacgcgcgc tcccccttcg gcatgcccca ctcaacggc gacctcacg acgacccttt	300
cgcgcacact gctgaactcca acggtgggcc catcttcgc cgcgccaccg agatgggccc	360
cgaaggagga ttctgtccc gcgagtgtg cgcacaaaaa gctattcacc ttgaggaaaa	420
agagaagaag gagaaggagc tgaggagcca aatcatcgtt gatgctgaag agtttaag	

(2) INFORMATION FOR SEQ ID NO:2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

Cys Ala Ser Arg Pro Leu Arg Gln Ser Leu Ala Phe His Leu Leu Arg  
1 5 10 15  
Leu Ile Ser Asp Gln Ala Ser Ala Pro Asp Thr His His Leu Pro Pro  
20 25 30  
Arg Ser Thr Thr Pro Ala Met Ala Thr Ala Phe Asp Ser Pro Thr Ser  
35 40 45  
Ser Pro Ala Ala Ala Pro Phe His Asp Asp Pro Phe Leu His Phe Asp  
50 55 60  
Gly Ser Ala Pro Ala Ala Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala  
65 70 75 80  
Tyr Ala Pro Ser Pro Phe Gly Met Pro His Ser Asn Gly Asp Leu His  
85 90 95  
Asp Asp Pro Phe Ala Ala Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu  
100 105 110  
Pro Pro Pro Thr Glu Met Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu  
115 120 125  
Trp Cys Arg Gln Asn Ala Ile His Leu Glu Glu Lys Glu Lys Lys Glu  
130 135 140  
Lys Glu Leu Arg Ser Gln Ile Ile Val Asp Ala Glu Glu Phe Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

Ala Pro Arg Gly Arg Phe Asp Ser Pro Ser Arg Ser Ile Cys Phe Gly  
1 5 10 15  
Ser Ser Gln Ile Lys Leu Ala His Leu Thr Pro Thr Thr Ser Leu Pro  
20 25 30  
Asp Pro Pro Pro Gln Pro Trp Pro Pro Pro Leu Thr Pro Arg Pro Pro  
35 40 45  
Pro Pro Pro Pro Arg Pro Ser Thr Thr Thr Leu Ser Ser Ile Ser Thr  
50 55 60  
Ala Arg Pro Pro Pro Pro Thr Ala Ser Arg Pro Pro Arg Thr Pro  
65 70 75 80  
Thr Arg Pro Pro Pro Ser Ala Cys Pro Thr Pro Thr Ala Thr Ser Thr  
85 90 95  
Thr Thr Leu Ser Pro His Leu Leu Thr Pro Thr Val Gly Pro Ser Phe  
100 105 110  
Arg Arg Pro Pro Arg Trp Ala Ala Arg Arg Asp Ser Cys Ser Ala Ser  
115 120 125  
Gly Ala Asp Lys Met Leu Phe Thr Leu Arg Lys Lys Arg Arg Arg Arg

(2) INFORMATION FOR SEQ ID NO:2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..12

SEQUENCE DESCRIPTION: SEQ ID NO:2036:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:

(2) INFORMATION FOR SEO ID NO:2037:

(A) LENGTH: 713 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1502011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

accaaaggta	ccttgcatct	acacgaacaa	gaagctatcg	atctacgca	caccgaggaa	160
gaagagata	atggcgctcgc	acaggggagt	ctgtatcgcg	tgccacagca	agcctgagtt	120
cgacgcceac	atgacaaagg	cccagggaagc	cggaacatcg	tggtctatcg	agctctatgc	180
cgccgtgacg	gtactctcag	cacacgctga	tgaccattcg	gcattaccac	ggccggctgc	240
aggtctggcgc	cgctcgtggac	gacgattacc	gggtgtatcg	cgtagcagca	ctgatagctg	300
tcgacagact	cacgcttcaag	tactccccgc	gcaccaaccc	cgaggccacc	gctgatgctg	360
tcgggaagtt	tatgggttag	aaaattctcag	ccgagatagc	gaggaaatga	tcgagatttc	420
aagtatcagc	atggctctagg	gactaagcct	ctgatctgtg	taatgaacat	caatacaaac	480
attctgtaac	gggttaactgc	tetacgctct	agagtagggt	tattttttct	ctgatatatt	540
tttaatctcc	tcgacagata	ctctcagctt	cgccatggtt	ttggttccat	tcaccacac	600
ccctagatgc	atgtgttcagc	atttcgcggg	aaataaagaa	attatgctga	aaaggctgta	660
ctgtctctcc	tgctattctc	acagaaaaat	aaataaagaa	cgcccatctt	atc	

(2) INFORMATION FOR SEQ ID NO:2038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1502012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

Pro	Lys	Val	Pro	Cys	Asn	His	Asn	Glu	Gln	Lys	Leu	Ser	Ile	Ser	Pro
1				5				10						15	
Thr	Pro	Arg	Lys	Lys	Arg	Ser	Met	Ala	Ser	Glu	Gln	Gly	Val	Val	Ile
			20				25					30			
Ala	Cys	His	Ser	Lys	Ala	Glu	Phe	Asp	Ala	His	Met	Thr	Lys	Ala	Gln
		35				40					45				
Glu	Ala	Gly	Lys	Leu	Val	Val	Ile	Asp	Phe	Thr	Ala	Ala			
	50				55			60							

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1502013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Met	Thr	Ile	Trp	His	Tyr	His	Gly	Gly	Cys	Gln	Val	Gly	Ala	Val	Val
1			5				10						15		
Asp	Asp	Asp	Tyr	Arg	Val	Phe	Gly	Val	Gln	Arg	Leu	Met	Val	Ile	Asp
			20				25				30				
Ser	Ser	Thr	Phe	Lys	Tyr	Ser	Pro	Gly	Thr	Asn	Pro	Gln	Ala	Thr	Val
		35				40					45				
Met	Met	Leu	Gly	Arg	Tyr	Met	Gly	Val	Lys	Ile	Gln	Ala	Glu	Arg	Trp
	50				55			60							
Arg	Lys														
65															

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1502014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

Met	Leu	Leu	Val	Pro	Phe	His	His	Thr	Pro	Arg	Cys	Ile	Val	Gln	His
1				5				10					15		
Phe	Ala	Gly	Ile	Met	Arg	Ile	Met	Leu	Lys	Arg	His	Asp	Arg	Ser	Ser
		20					25				30				
Cys	Leu	Phe	Tyr	Arg	Lys	Leu	Asn	Lys	Glu	Pro	Pro	Phe	His		
	35				40			45							

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..567  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

ctcgcaaac	cacgtttcaa	aaaaaagaga	ggaaagcaaa	gttccttctt	cctcga	60
aaaaaatcag	tctcgccatg	gagagcagcg	ttggcataga	gaagggccgca	gcgggtggcgg	120
ttgggtgcagg	tgtggggcggg	ggaggtggag	ggtacggcts	cgccgggtgg	gagacggccga	180
agcgcgagga	gtaccgcac	ccggcgacgc	tgccgtgcc	cgccggcgccg	aggaagggccg	240
tgccggactt	cggaagcgg	cgccggcccg	cccaagaacg	gctacttcca	cgccggcgac	300
ctggagggc	tcttcgcct	cgccggcgcc	cgccaggcct	tctgcgcgtg	acttggcrgc	360
gacttgattt	tttggggagg	gaagttgtaga	tagcttgccg	gtctcgctct	gtttgactct	420
ttctagtggg	ggtgttttagt	ggccscgggt	gtattaggga	ggcagtaggg	tggttttagg	480
gagtagtagg	taggttaggtg	gtggactctt	aatcataag	catactgttt	ggttaagctg	540
atgaaatcct	tatatatgtt	tctctg				

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..121  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Ser	Gln	Thr	His	Val	Ser	Lys	Lys	Arg	Glu	Glu	Ser	Lys	Val	Pro	Ser
1			5					10					15		
Ser	Leu	Glu	Lys	Lys	Asn	Gln	Ser	Arg	His	Gly	Glu	Gln	Arg	Trp	His
			20					25					30		
Arg	Glu	Gly	Arg	Ser	Gly	Gly	Gly	Trp	Cys	Arg	Cys	Gly	Arg	Gly	Arg
			35				40					45			
Trp	Arg	Val	Arg	Xaa	Arg	Arg	Val	Gly	Asp	Ala	Glu	Ala	Arg	Gly	Xaa
			50				55				60				
Pro	His	Pro	Gly	Asp	Ala	Ala	Val	Pro	Arg	Gly	Ala	Glu	Glu	Gly	Arg
			65				70				75				80
Ala	Gly	Leu	Arg	Glu	Ala	Ala	Gln	Pro	Xaa	Pro	Arg	Thr	Ala	Thr	Ser
			85						90					95	
Ser	Arg	Arg	Thr	Trp	Arg	Arg	Ser	Ser	Arg	Ser	Arg	Arg	Ala	Ala	Arg
			100					105					110		
Pro	Ser	Ala	Arg	Asp	Leu	Xaa	Arg	Thr							
			115				120								

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Arg	Lys	Pro	Thr	Phe	Gln	Lys	Lys	Glu	Arg	Lys	Ala	Lys	Phe	Leu	Leu
1				5				10					15		
Pro	Ser	Lys	Lys	Lys	Ile	Ser	Leu	Ala	Met	Glu	Ser	Ser	Val	Gly	Ile
			20					25					30		
Glu	Lys	Ala	Ala	Ala	Val	Ala	Val	Gly	Ala	Gly	Val	Gly	Gly	Gly	Gly
			35				40					45			

Gly Gly Tyr Gly Xaa Gly Gly Trp Glu Thr Pro Lys Arg Glu Glu Xaa  
50 55 60  
Arg Ile Pro Ala Thr Leu Pro Cys Pro Ala Ala Pro Arg Lys Ala Val  
65 70 75 80  
Pro Asp Phe Gly Lys Arg Arg Ser Xaa Ala Gln Glu Arg Leu Leu Pro  
85 90 95  
Ala Ala Gly Pro Gly Gly Ala Leu Arg Ala Ala Pro Pro Gly  
100 105 110  
Leu Leu Arg Val Thr Trp Xaa Gly Leu Asp Phe Leu Gly Arg Glu Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

Met Glu Ser Ser Val Gly Ile Glu Lys Ala Ala Val Ala Val Gly  
1 5 10 15  
Ala Gly Val Gly Gly Gly Gly Tyr Gly Xaa Gly Gly Trp Glu  
20 25 30  
Thr Pro Lys Arg Glu Glu Xaa Arg Ile Pro Ala Thr Leu Pro Cys Pro  
35 40 45  
Ala Ala Pro Arg Lys Ala Val Pro Asp Phe Gly Lys Arg Arg Ser Xaa  
50 55 60  
Ala Gln Glu Arg Leu Leu Pro Ala Ala Gly Pro Gly Gly Ala Leu Arg  
65 70 75 80  
Ala Arg Ala Ala Pro Pro Gly Leu Leu Arg Val Thr Trp Xaa Gly Leu  
85 90 95  
Asp Phe Leu Gly Arg Glu Leu  
100

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

ggggtagcga ttacaccttg acacctaaagg ccagagattg gagagagaaa gaagcagctg 60  
agtggagcaa gaaagaagag gtcattggcg tgtagtctat cagctgagtg ggaagaagtg 120  
gagcaatggt gggggcgctg gccagcgcgcg acggcgccgc cgaaggagcg ctccgaggt 180  
ggcgaggggc ggccggccaag cgatcgggcc tctcatgcgc ctctctcttc tctacggcg 240  
cctctccctc ccgcctcctc tccaagatca tctcccactc cgcactgaat gcgcctgatg 300  
gagagcagca aaagatggag gaacccacca gcaccagagt ggctgacaag aatctatgtg 360  
caatatgttt ggaactcctc agcacagca tcagcagcga tgttgacagt ggtgagcgcg 420  
cagcaatcta cacagcgag tgctcccact cattccactt yctatgcac gcctccaaca 480  
tccggcatgg caacgtcagc tgccctatct gccgtgcaca atggtctgag ctaccacgtg 540  
ac

(2) INFORMATION FOR SEQ ID NO:2046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1502024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

Met	Val	Gly	Gly	Cys	Ala	Ser	Gly	Asp	Gly	Ala	Ala	Glu	Gly	Thr	Leu
1			5					10					15		
Ala	Arg	Trp	Arg	Arg	Ala	Ala	Ala	Lys	Arg	Ile	Gly	Leu	Ser	Cys	Ala
			20					25				30			
Ser	Phe	Phe	Ser	Tyr	Ala	Ala	Ser	Pro	Ser	Pro	Pro	Pro	Ser	Lys	Ile
		35					40					45			
Ile	Ser	His	Ser	Ala	Leu	Asn	Ala	Pro	Asp	Gly	Glu	Gln	Gln	Lys	Met
	50				55						60				
Glu	Glu	Pro	Thr	Ser	Thr	Arg	Val	Ala	Asp	Lys	Asn	Leu	Cys	Ala	Ile
65				70					75					80	
Cys	Leu	Glu	Leu	Leu	Ser	Thr	Ser	Ile	Ser	Ser	Asp	Val	Asp	Ser	Gly
			85						90					95	
Glu	Ala	Ala	Ala	Ile	Tyr	Thr	Ala	Gln	Cys	Ser	His	Ser	Phe	His	Xaa
			100				105						110		
Leu	Cys	Ile	Ala	Ser	Asn	Ile	Arg	His	Gly	Asn	Val	Ser	Cys	Pro	Ile
		115					120					125			
Cys	Arg	Ala	Gln	Trp	Ser	Glu	Leu	Pro	Arg	Asp					
	130						135								

(2) INFORMATION FOR SEQ ID NO:2047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1502025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

Met	Arg	Leu	Met	Glu	Ser	Ser	Lys	Arg	Trp	Arg	Asn	Pro	Pro	Ala	Pro
1			5						10					15	
Glu	Trp	Leu	Thr	Arg	Ile	Tyr	Val	Gln	Tyr	Val	Trp	Asn	Ser	Ser	Ala
			20						25				30		
Arg	Ala	Ser	Ala	Ala	Met	Leu	Thr	Val	Val	Arg	Arg	Gln	Gln	Ser	Thr
		35					40					45			
Gln	Arg	Ser	Ala	Pro	Thr	His	Ser	Thr	Xaa	Tyr	Ala	Ser	Pro	Pro	Thr
	50				55					60					
Ser	Gly	Met	Ala	Thr	Ser	Ala	Ala	Leu	Ser	Ala	Val	His	Asn	Gly	Leu
65				70					75					80	
Ser	Tyr	His	Val												

(2) INFORMATION FOR SEQ ID NO:2048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..81  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502026  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:  
Met Glu Ser Ser Lys Arg Trp Arg Asn Ser Pro Pro Ala Pro Glu Trp Leu  
1 5 10 15  
Thr Arg Ile Tyr Val Gln Tyr Val Trp Asn Ser Ser Ala Arg Ala Ser  
20 25 30  
Ala Ala Met Leu Thr Val Val Arg Arg Gln Gln Ser Thr Gln Arg Ser  
35 40 45  
Ala Pro Thr His Ser Thr Xaa Tyr Ala Ser Pro Pro Thr Ser Gly Met  
50 55 60  
Ala Thr Ser Ala Ala Leu Ser Ala Val His Asn Gly Leu Ser Tyr His  
65 70 75 80  
val

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..502

(D) OTHER INFORMATION: / Ceres Seq. ID 1502027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

acagcacagc agagaacgca ggcagaggca ccataccagt caaccaccac cgcttcgttc 60  
tcctcccaca ccgctcgccct tcgctcctct ctggttccca tcctctatca tcccgcagct 120  
ccagttctcc acacctcacg tctataaata ataaataagg cgcccgcggt gcccatcaat 180  
tcgtgtcacc gcgtcccagc agcgcaaatc attccgcgcg acgcaaaaac cctagcccag 240  
ccaccgatcc ctctcatggc aaccaccacc acccaggcga gcctctctct ccagaagcag 300  
ctaagagatc tcgcgaagca cccggtggat gggttctctg ctgggctggt cgacgacagc 360  
aatgtcttcg agtggcaggt caccatcatc ggaaccgcctg acactctata tgatggaggt 420  
tacttcaatg caataatgag ctccccacaa aattacccaa acagcccgcg atcagtcaga 480  
tttacctctg aaatgkggca tc

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1502028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Gln His Ser Arg Glu Arg Arg Gln Arg His His Thr Ser Gln Pro Pro  
1 5 10 15  
Pro Leu Arg Ser Pro Pro Thr Pro Leu Ala Phe Ala Ser Phe Trp Phe  
20 25 30  
Pro Ser Ser Ile Ile Pro Glu Leu Gln Phe Ser Thr Pro His Val Tyr  
35 40 45  
Lys

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..51  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502029  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:  
Ser Thr Ala Glu Asn Ala Gly Arg Gly Thr Ile Pro Val Asn His His  
1 5 10 15  
Arg Phe Val Leu Leu Pro His Arg Ser Pro Ser Pro Ser Gly Ser  
20 25 30  
His Leu Leu Ser Ser Pro Ser Ser Ser Pro His Leu Thr Ser Ile  
35 40 45  
Asn Asn Lys  
50

(2) INFORMATION FOR SEQ ID NO:2052:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:

Met Ala Thr Thr Thr Thr Gln Ala Ser Leu Leu Leu Gln Lys Gln Leu  
1 5 10 15  
Arg Asp Leu Ala Lys His Pro Val Asp Gly Phe Ser Ala Gly Leu Val  
20 25 30  
Asp Asp Ser Asn Val Phe Glu Trp Gln Val Thr Ile Ile Gly Pro Pro  
35 40 45  
Asp Thr Leu Tyr Asp Gly Gly Tyr Phe Asn Ala Ile Met Ser Phe Pro  
50 55 60  
Gln Asn Tyr Pro Asn Ser Pro Pro Ser Val Arg Phe Thr Ser Glu Met  
65 70 75 80  
Xaa His

(2) INFORMATION FOR SEQ ID NO:2053:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 526 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..526  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

aattttctta tccccctcta tctgtctcac ctccgacctc gcgcgagacg agcaagccca 60  
agtatggccg gagcagcagc agccgcccgt gcgtccgggg tctcgcccg gccggccgcg 120  
ccgatgaggg cttctgcggg acgccgcgct cggtctgcgg tggtagcggg ccgcgatatcc 180  
ctcgagaagg gcgagaaggc gtacacgggt cagaagtcgc aggagatctt caacgcgcgc 240  
aaggagctga tgccctgagg tgtttaactc ccagtcctgt ccttcaaatc tgttggtggg 300  
cagccagtag tgttcgactc tgttaaagggt tctcgatatg gggatgttga tgggaatgag 360  
tacattgatt acgttggttc ctggggctct gcaatcatcg gccatgcaga tgataaggtt 420  
aatgctgcatt tgattgaanac tctgaagaaa ggaactagct ttggtgtccc atgtttgtcg 480  
gagaacgtat tggtctgagat ggtcatctct gccgtgccaa gtatcg

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..175

SEQUENCE DESCRIPTION:

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5                                  10

Arg	Ala	Ser	Pro	Ser	Met	Ala	Gly	Ala	Ala	Ala	Ala	Val	Ala	Ser
			20					25					30	
Gly	Val	Ser	Ala	Arg	Pro	Ala	Ala	Pro	Met	Arg	Ala	Ser	Ala	Gly
			35				40					45		Arg
Arg	Ala	Arg	Leu	Ser	Val	Val	Arg	Ala	Ala	Ile	Ser	Leu	Glu	Lys
			50				55				60			Gly
Glu	Lys	Ala	Tyr	Thr	Val	Gln	Lys	Ser	Glu	Glu	Ile	Phe	Asn	Ala
					70					75				Ala
Lys	Glu	Leu	Met	Pro	Gly	Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	Phe
				85					90				95	Lys
Ser	Val	Gly	Gly	Gln	Pro	Val	Val	Phe	Asp	Ser	Val	Lys	Gly	Ser
			100					105					110	Arg
Met	Trp	Asp	Val	Asp	Gly	Asn	Glu	Tyr	Ile	Asp	Tyr	Val	Gly	Ser
		115					120					125		Trp
Gly	Pro	Ala	Ile	Ile	Gly	His	Ala	Asp	Asp	Lys	Val	Asn	Ala	Ala
			130				135				140			Leu
Ile	Glu	Thr	Leu	Lys	Lys	Gly	Thr	Ser	Phe	Gly	Ala	Pro	Cys	Leu
	145				150					155				Leu
Glu	Asn	Val	Leu	Ala	Glu	Met	Val	Ile	Ser	Ala	Val	Pro	Ser	Ile
				165					170					175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..154

SEQUENCE DESCRIPTION:

5 10

Pro	Ala	Ala	Pro	Met	Arg	Ala	Ser	25	Ala	Gly	Arg	Arg	Ala	Arg	Leu	Ser
Val	Val	Arg	Ala	Ala	Ile	Ser	Leu	40	Glu	Lys	Gly	Glu	Lys	Ala	Tyr	Thr
Val	Gln	Lys	Ser	Glu	Glu	Ile	Phe	55	Asn	Ala	Ala	Lys	45	Leu	Met	Pro
Gly	Gly	Val	Asn	Ser	Pro	Val	Arg	Ala	Phe	Lys	Ser	Val	Gly	Gly	Gln	80
Pro	Val	Val	Phe	Asp	Ser	Val	Lys	Gly	Ser	Arg	Met	Trp	Asp	Val	Asp	95
Gly	Asn	Glu	Tyr	Ile	Asp	Tyr	Val	Gly	Ser	Trp	Gly	Pro	Ala	Ile	Ile	110
Gly	His	Ala	Asp	Asp	Lys	Val	Asn	Ala	Ala	Leu	Ile	Glu	Thr	Leu	Lys	125

115 120 125  
Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala  
130 135 140  
Glu Met Val Ile Ser Ala Val Pro Ser Ile  
145 150

(2) INFORMATION FOR SEQ ID NO:2056:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser Val Val Arg Ala  
1 5 10 15  
Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr Val Gln Lys Ser  
20 25 30  
Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro Gly Gly Val Asn  
35 40 45  
Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln Pro Val Val Phe  
50 55 60  
Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp Gly Asn Glu Tyr  
65 70 75 80  
Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile Gly His Ala Asp  
85 90 95  
Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys Lys Gly Thr Ser  
100 105 110  
Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala Glu Met Val Ile  
115 120 125  
Ser Ala Val Pro Ser Ile  
130

(2) INFORMATION FOR SEQ ID NO:2057:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 474 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..474  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

aaggcaggcg actgcactgc acgcatgcac tgacctgacg acgcgcgccca cagtccactc 60  
cacactcagg catggcgatg ggcgcgcgctt ccattcctact gatgatgggtt tcgctggagg 120  
ccctgcttct cgcgcgcgcgc gccgcgcgcgc ggaccatcgc tetgcccagc gatgtcggag 180  
gcgttgtctgc agaccttgtc acggcgatgg cgaaggcgag ggcaagggca aagcatcagc 240  
ttcgcgacga ggagaggccg tggggggaat gctgcgactt ggccgtatgc gtcaagacgt 300  
accgcctaac ttgctcgtgc ttgcgacggg ttgagcgctg ctccgacgcc tgtaaggagt 360  
gcgtggaaac ggaggactcg cgccacgtct gcgtcgacag gtaccgtggc gaccccgagg 420  
ccaggtgccca cgacgaggac gggaggagcg gcggacccgc tgacgcagac gctg

(2) INFORMATION FOR SEQ ID NO:2058:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

Met	Ala	Met	Gly	Ala	Ala	Ser	Ile	Leu	Leu	Met	Met	Val	Ser	Leu	Glu
1			5						10					15	
Ala	Leu	Leu	Leu	Ala	Ala	Ala	Ala	Gly	Gly	Thr	Ile	Arg	Leu	Pro	
		20				25						30			
Ser	Asp	Val	Gly	Gly	Val	Ala	Ala	Asp	Leu	Val	Thr	Ala	Met	Ala	Arg
		35				40					45				
Ala	Arg	Ala	Arg	Ala	Lys	His	Gln	Leu	Arg	Asp	Glu	Glu	Arg	Pro	Trp
	50				55						60				
Gly	Glu	Cys	Cys	Asp	Leu	Ala	Val	Cys	Val	Lys	Thr	Tyr	Pro	Leu	Thr
	65				70					75				80	
Cys	Ser	Cys	Phe	Asp	Arg	Val	Glu	Arg	Cys	Ser	Asp	Ala	Cys	Lys	Glu
			85						90				95		
Cys	Val	Glu	Thr	Glu	Asp	Ser	Arg	His	Val	Cys	Val	Asp	Arg	Tyr	Arg
		100					105						110		
Gly	Asp	Pro	Gly	Pro	Arg	Cys	His	Asp	Glu	Asp	Gly	Arg	Ser	Gly	Gly
		115					120					125			
Pro	Ala	Asp	Asp	Asp	Ala										

(2) INFORMATION FOR SEQ ID NO:2059:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1502037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

Met	Gly	Ala	Ala	Ser	Ile	Leu	Leu	Met	Met	Val	Ser	Leu	Glu	Ala	Leu
1			5						10				15		
Leu	Leu	Ala	Ala	Ala	Ala	Gly	Gly	Thr	Ile	Arg	Leu	Pro	Ser	Asp	
		20				25						30			
Val	Gly	Gly	Val	Ala	Ala	Asp	Leu	Val	Thr	Ala	Met	Ala	Arg	Ala	Arg
		35				40						45			
Ala	Arg	Ala	Lys	His	Gln	Leu	Arg	Asp	Glu	Glu	Arg	Pro	Trp	Gly	Glu
	50				55						60				
Cys	Cys	Asp	Leu	Ala	Val	Cys	Val	Lys	Thr	Tyr	Pro	Leu	Thr	Cys	Ser
	65				70				75					80	
Cys	Phe	Asp	Arg	Val	Glu	Arg	Cys	Ser	Asp	Ala	Cys	Lys	Glu	Cys	Val
			85						90				95		
Glu	Thr	Glu	Asp	Ser	Arg	His	Val	Cys	Val	Asp	Arg	Tyr	Arg	Gly	Asp
		100					105						110		
Pro	Gly	Pro	Arg	Cys	His	Asp	Glu	Asp	Gly	Arg	Ser	Gly	Gly	Pro	Ala
		115					120					125			
Asp	Asp	Asp	Ala												

(2) INFORMATION FOR SEQ ID NO:2060:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

Met Met Val Ser Leu Glu Ala Leu Leu Leu Ala Ala Ala Ala Ala Gly  
1 5 10 15  
Gly Thr Ile Arg Leu Pro Ser Asp Val Gly Gly Val Ala Ala Asp Leu  
20 25 30  
Val Thr Ala Met Ala Arg Ala Arg Ala Arg Ala Lys His Gln Leu Arg  
35 40 45  
Asp Glu Glu Arg Pro Trp Gly Glu Cys Cys Asp Leu Ala Val Cys Val  
50 55 60  
Lys Thr Tyr Pro Leu Thr Cys Ser Cys Phe Asp Arg Val Glu Arg Cys  
65 70 75 80  
Ser Asp Ala Cys Lys Glu Cys Val Glu Thr Glu Asp Ser Arg His Val  
85 90 95  
Cys Val Asp Arg Tyr Arg Gly Asp Pro Gly Pro Arg Cys His Asp Glu  
100 105 110  
Asp Gly Arg Ser Gly Gly Pro Ala Asp Asp Ala  
115 120

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..895  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

atcgaaaaaa aaaactcttc tccccgagtc ctctctcttc cggggtattg aattcgaacc 60  
aaaaaatcaa aacaactcag cgattcgatt cgcggcgagt caagcgggat gccgcgcgcg 120  
acggctccgg cgcgcgacct aaccccgccg cggagaggtg cctctccgaa gctgctcgct 180  
gcggcgctcg tcgcctcggg ggtgcagttc ggcggggcgc tgaagctgtc gttgctgacc 240  
ccgtacgtgc aggagctggg catcccgcaac gccttgcca gtcctgtctg gctgtcgctg 300  
ccgctgtcgc gctctctcgt ccagcccttc gtcggccacc tctccgacgc catcgccccc 360  
gccgcttcgc cgctcgggcg ccgcaggccc ttcctcgccg ccggcgccgc gtgcctcgcc 420  
gcagccgtgc tcaccgtcgg ctctctccgt gacctcgccc gactcttcgg cgacgcagtc 480  
accccgggct caacgcgcct cggcgccatc tgcgtctacc ttgtaggatt ctggctgtct 540  
gacgtgggca acaacggcac gcaggggccc tgcaggggct tcctcgccga cctcacagag 600  
aatgacccaa ggaggagagg cgggacacac cgataagctc gctcatttac cattacaggc 660  
atcatcaaat ctggaaaact ttgtgtgggt ggagaagagc acgctgggag ctcttgaagt 720  
ctgtgtgtct ttgtgtgggt tgccccgttg agctattttt tgccttgtct ccaaatcttt 780  
tgttgttcaa ttcaactcga atgatgtgac gcacgtatgc atgtatgtat ttgtatgtat 840  
gtggatcatt tgtagagagc ttaagcaatg aataaaaagt acaggagtta cgttc

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Arg Lys Lys Lys Leu Leu Ser Pro Ser Pro Leu Leu Ser Gly Val Leu

1	5	10	15
Asn Ser Asn Gln Lys Ile Lys Thr Thr Gln Arg Phe Asp Ser Arg Arg	20	25	30
Val Lys Arg Asp Ala Ala Ala His Gly Ser Gly Gly Asp Leu Asn Pro	35	40	45
Ala Ala Glu Gly Ala Pro Pro Glu Ala Ala Ala Cys Gly Val Gly Arg	50	55	60
Leu Arg Gly Ala Val Arg Leu Gly Ala Ala Ala Val Val Ala Asp Pro	65	70	75
Val Arg Ala Gly Ala Gly His Pro Ala Arg Leu Cys Gln Ser Arg Leu	85	90	95
Ala Val Arg Ser Ala Val Arg Pro Pro Arg Pro Ala Pro Arg Arg Pro	100	105	110
Pro Leu Arg Pro His Arg Pro Arg Arg Phe Ala Ala Arg Ala Pro Gln	115	120	125
Ala Leu His Arg Arg Arg Arg Arg Val His Arg Arg Ser Arg Ala His	130	135	140
Arg Arg Leu Leu Arg			

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

Met Pro Pro Arg Thr Ala Pro Ala Ala Thr Ser Thr Pro Pro Arg Lys	1	5	10	15
Val Pro Leu Arg Lys Leu Leu Arg Ala Ala Ser Val Ala Cys Gly Val	20	25	30	
Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln	35	40	45	
Glu Leu Gly Ile Pro His Ala Phe Ala Ser Leu Val Trp Leu Cys Gly	50	55	60	
Pro Leu Ser Gly Leu Leu Val Gln Pro Leu Val Gly His Leu Ser Asp	65	70	75	80
Arg Ile Gly Pro Ala Ala Ser Pro Leu Gly Arg Arg Arg Pro Phe Ile	85	90	95	
Ala Ala Gly Ala Ala Cys Ile Ala Ala Val Leu Thr Val Gly Phe	100	105	110	
Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp Asp Val Thr Pro Gly Ser	115	120	125	
Thr Arg Leu Gly Ala Ile Cys Val Tyr Leu Val Gly Phe Trp Leu Leu	130	135	140	
Asp Val Gly Asn Asn Gly Thr Gln Gly Pro Cys Arg Ala Phe Leu Ala	145	150	155	160
Asp Leu Thr Glu Asn Asp Pro Arg Arg Arg Gly Thr His Arg	165	170	175	

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..490  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

atcttctgtct	ctctccgact	ctccctcgcc	cgcgcacctt	tccgcgcccgc	ctccttccctt	60
tccttcgctgt	ctctggcgcg	cgaagcgatc	aaaaggcgcc	ggccactaga	ggcgagtgcg	120
tcgcatgttaa	acgaccacca	gctgctgtga	tctcaaaagg	gagcgagaga	caaaggagag	180
gcgagcaggt	cgtggcgcca	gcaatcgttg	cgaatccgcg	cgggattctg	tcctctgcac	240
cactgcttcc	cgctttcctg	cccggcggaa	gtggtataat	tctccaacgc	gggtgactgt	300
attgcctctc	gctctcggtg	ggtgggggga	tggacgagcg	agaggagatg	caggtggaga	360
ggctgcacga	ggaggccgat	gcggggggag	cgcacacgga	caagcttcagc	tacgagatat	420
tcctcatcct	cgagagcaag	ttcctgttctg	gctataccga	cccgcaccag	ctctggctgc	480
ccaagccagc						

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..49  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

Ile	Phe	Val	Ser	Leu	Arg	Leu	Ser	Leu	Ala	Arg	Ala	Pro	Phe	Arg	Ala
1		5					10						15		
Ala	Ser	Phe	Leu	Ser	Ser	Arg	Ala	Leu	Ala	Arg	Ala	Arg	Ile	Lys	Arg
		20					25						30		
Arg	Arg	Pro	Leu	Glu	Ala	Ser	Glu	Ser	His	Val	Asn	Asp	His	Gln	Leu
		35					40						45		
Leu															

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

Met	Asp	Glu	Ala	Glu	Glu	Met	Gln	Val	Glu	Arg	Leu	His	Glu	Glu	Ala
1		5						10					15		
Asp	Ala	Gly	Gly	Ala	Asp	Thr	Asp	Lys	Leu	Ser	Tyr	Glu	Ile	Phe	Ser
		20						25					30		
Ile	Leu	Glu	Ser	Lys	Phe	Leu	Phe	Gly	Tyr	Thr	Asp	Pro	His	Gln	Leu
		35					40						45		
Trp	Leu	Pro	Lys	Pro											
		50													

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..47  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502059  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:  
Met Gln Val Glu Arg Leu His Glu Glu Ala Asp Ala Gly Gly Ala Asp  
1 5 10 15  
Thr Asp Lys Leu Ser Tyr Glu Ile Phe Ser Ile Leu Glu Ser Lys Phe  
20 25 30  
Leu Phe Gly Tyr Thr Asp Pro His Gln Leu Trp Leu Pro Lys Pro  
35 40 45  
(2) INFORMATION FOR SEQ ID NO:2068:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 566 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..566  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502066  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:  
aaaaatcaaa gtacgctcgt gctgccccaa ctcggaact ccccatcagc tcaccccgat 60  
ctagggtttg ggcacccctcc gcttacgcgc ctccccacca agcaaatgtg agggcccgcg 120  
gcattctcct tcgggcgtca tggcggtac agggcaggag ggggatgacg tcgaccacta 180  
cgaggtaact tgcttccgt cgggggagga aggcgcggcg ctgaccatcg agcatatcga 240  
gaagccctac cgagcgcagt cgcgctcgcg ccaccccgat aagcgccccg acgaccccaa 300  
cgccaccgac gacttcagc tctctcagag ttctacaaa ctctcccgcg acgattccct 360  
tcgcgcgcag ttgcagcgcg gctctccgcg ccgcgcgcag ccgcgcgcgc gcgcgcgcgc 420  
cacggcggtt aagcgccgga aggcgcgtct cgacctcgag gagcgcgagc gcgcgcgcgc 480  
cgnngggcac ccgcgcgac ccgagagact cgccmagcgc gagggccara gatggccsc 540  
gacattgagc gcgagctcgc agcggt  
(2) INFORMATION FOR SEQ ID NO:2069:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502067  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:  
Met Ala Ala Thr Gly Gln Glu Gly Asp Asp Val Asp His Tyr Glu Val  
1 5 10 15  
Leu Cys Leu Pro Ser Gly Glu Glu Gly Ala Ala Leu Thr Ile Glu His  
20 25 30  
Ile Glu Lys Ala Tyr Arg Thr Gln Ser Arg Leu Arg His Pro Asp Lys  
35 40 45  
Arg Pro Asp Asp Pro Asn Ala Thr Ala Asp Phe Gln Leu Leu Ser Ser  
50 55 60  
Ser Tyr Lys Leu Leu Arg Asp Glu Ser Leu Arg Arg Gln Phe Asp Ala  
65 70 75 80  
Arg Leu Arg Gly Arg Arg Glu Ala Ala Ala Arg Ala Ala Thr Gly  
85 90 95  
Val Lys Arg Arg Lys Ala Val Ser Asp Leu Glu Glu Arg Glu Arg Ala  
100 105 110  
Xaa Xaa Xaa Gly His Pro Xaa Asp Pro Glu Glu Leu Ala Xaa Arg Glu  
115 120 125  
Ala Xaa Arg Trp Xaa Pro Thr Leu Ser Ala Ser Ser Gln Arg

130 135 140

(2) INFORMATION FOR SEQ ID NO:2070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1502074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

aagaccacca	ctgcgcatt	ggccagctag	agccaaccag	aagagcttgc	agtactgag	60
agtgtttgag	agagagagga	tgatgggtgg	cagcggcagg	gctgctctgc	tgctggccct	120
ggtggccgtg	agcctggcgc	tggagatcca	ggccgacgcc	gggtacgggt	acaccccgac	180
gccgacgcgc	gccaccccg	ccccgaagcc	ggagaagccc	cccaccaagg	ggcccaaagc	240
ggagaagccc	ccaagagagc	acaagccgcc	caaggagcac	gggccaagc	cggagaagcc	300
gcccaaggag	cacaagccga	cgccgcccac	gtacaccccg	agccccaac	ccacgcgcgc	360
gacgtacact	cccacccgca	cgccccccaa	gccgacgcca	cccacataga	ctcccgcccc	420
tacgcccac	aaaccacact	ccactctcc	gacgtacac	cttct		

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1502075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Arg	Pro	Pro	Leu	Arg	His	Trp	Pro	Ala	Arg	Ala	Asn	Gln	Lys	Ser	Leu	
1			5						10					15		
Gln	Leu	Leu	Arg	Val	Phe	Glu	Arg	Glu	Arg	Met	Met	Gly	Gly	Ser	Gly	
			20					25				30				
Arg	Ala	Ala	Leu	Leu	Leu	Ala	Leu	Val	Ala	Val	Ser	Leu	Ala	Val	Glu	
			35					40				45				
Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr	Pro	Thr	Pro	Thr	Pro	Ala	
			50			55					60					
Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Thr	Lys	Gly	Pro	Lys	Pro	
			65			70				75				80		
Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro	Lys	Glu	His	Gly	Pro	Lys	
			85							90				95		
Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	
			100					105					110			
Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Thr	Pro	Thr	Pro	
			115					120					125			
Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ala	Pro	Thr	Pro	His	Lys	
			130					135					140			
Pro	Thr	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro							
			145					150								

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

Met	Met	Gly	Gly	Ser	Gly	Arg	Ala	Ala	Leu	Leu	Leu	Ala	Leu	Val	Ala
1				5					10					15	
Val	Ser	Leu	Ala	Val	Glu	Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr
			20					25					30		
Pro	Thr	Pro	Thr	Pro	Ala	Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro
			35				40					45			
Thr	Lys	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro
			50				55				60				
Lys	Glu	His	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro
65					70				75					80	
Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr
			85					90						95	
Thr	Pro	Thr	Pro	Thr	Pro	Pro	Lys	Pro	Thr	Pro	Thr	Tyr	Thr	Pro	Thr
			100				105						110		
Ala	Pro	Thr	Pro	His	Lys	Pro	Thr	Pro	Thr	Pro	Thr	Tyr	Thr	Pro	Thr
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1502077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

Met	Gly	Gly	Ser	Gly	Arg	Ala	Ala	Leu	Leu	Ala	Leu	Val	Ala	Val	
1				5				10				15			
Ser	Leu	Ala	Val	Glu	Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr	Pro
			20					25				30			
Thr	Pro	Thr	Pro	Ala	Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Thr
			35				40					45			
Lys	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro	Lys
			50				55				60				
Glu	His	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Thr
65					70				75					80	
Pro	Pro	Thr	Tyr	Thr	Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Thr	Thr
			85					90						95	
Pro	Thr	Pro	Thr	Pro	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ala
			100				105						110		
Pro	Thr	Pro	His	Lys	Pro	Thr	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Thr
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 591 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1502086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

atccaggcat	ccagcaaatc	cagcgggtcc	gtactcatct	gcttcacetc	cgggctccgg	60
ctacggcgcc	actcttctct	ggcaaccgga	ccacagaaac	ctctaggcga	cgaatcgagc	120
aggtagagga	gtaatcaggc	atccatggct	gagcatcttg	cgtccatett	tgccacggag	180
aaggaccgcg	tgaactgccc	cttctacttc	aagatcggcg	catgcsccac	ggcgaccggg	240
gtctccgcct	gcacaacaag	ccttccatct	ccccgacgct	gtgctctgc	aacatgtacc	300
agcggcggga	catgatcacc	ccgggcgtgg	acgcgcaggg	caaccccatc	gacccggagc	360
ggatccagga	ggacttcgag	gactttctacg	aggacatctt	cgtggagctg	agcaagcacg	420
gcgagatcga	gagcctccac	gtctgcgaca	acctgcggga	ccacatgac	gggaacctgt	480
acgtggagtt	ccgcgaggag	gagcaggcgg	scgcgcctct	gcargcgctg	cargcccgcc	540
tactactcgg	gcgcgcccat	catcgccgag	ttctgcggg	tgactgactt	c	

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1502087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

Met	Xaa	His	Gly	Asp	Arg	Cys	Ser	Arg	Leu	His	Asn	Lys	Pro	Ser	Ile	
1			5				10				15					
Ser	Pro	Thr	Leu	Leu	Leu	Cys	Asn	Met	Tyr	Gln	Arg	Pro	Asp	Met	Ile	
			20				25				30					
Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly	Asn	Pro	Ile	Asp	Pro	Glu	Arg	Ile	
			35				40				45					
Gln	Glu	Asp	Phe	Glu	Asp	Phe	Tyr	Glu	Asp	Ile	Phe	Val	Glu	Leu	Ser	
			50				55				60					
Lys	His	Gly	Glu	Ile	Glu	Ser	Leu	His	Val	Cys	Asp	Asn	Leu	Ala	Asp	
65			70				75				80					
His	Met	Ile	Gly	Asn	Val	Tyr	Val	Glu	Phe	Arg	Glu	Glu	Glu	Gln	Ala	
			85				90				95					
Xaa	Arg	Ala	Leu	Xaa	Ala	Leu	Xaa	Gly	Arg	Leu	Leu	Leu	Gly	Pro	Pro	
			100				105				110					
His	His	Arg	Arg	Val	Leu	Ala	Gly	Asp								
			115				120									

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1502088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

Met	Tyr	Gln	Arg	Pro	Asp	Met	Ile	Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly	
1			5				10				15					
Asn	Pro	Ile	Asp	Pro	Glu	Arg	Ile	Gln	Glu	Asp	Phe	Glu	Asp	Phe	Thr	
			20				25				30					
Glu	Asp	Ile	Phe	Val	Glu	Leu	Ser	Lys	His	Gly	Glu	Ile	Glu	Ser	Leu	
			35				40				45					
His	Val	Cys	Asp	Asn	Leu	Ala	Asp	His	Met	Ile	Gly	Asn	Val	Tyr	Val	
			50				55				60					
Glu	Phe	Arg	Glu	Glu	Glu	Gln	Ala	Xaa	Arg	Ala	Leu	Xaa	Ala	Leu	Xaa	
65			70				75				80					

Gly Arg Leu Leu Leu Gly Pro Pro His His Arg Arg Val Leu Ala Gly  
85 90 95  
Asp

(2) INFORMATION FOR SEQ ID NO:2077:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

Met Ile Thr Pro Gly Val Asp Ala Gln Gly Asn Pro Ile Asp Pro Glu  
1 5 10 15  
Arg Ile Gln Glu Asp Phe Glu Asp Phe Tyr Glu Asp Ile Phe Val Glu  
20 25 30  
Leu Ser Lys His Gly Glu Ile Glu Ser Leu His Val Cys Asp Asn Leu  
35 40 45  
Ala Asp His Met Ile Gly Asn Val Tyr Val Glu Phe Arg Glu Glu Glu  
50 55 60  
Gln Ala Xaa Arg Ala Leu Xaa Ala Leu Xaa Gly Arg Leu Leu Leu Gly  
65 70 75 80  
Pro Pro His His Arg Arg Val Leu Ala Gly Asp  
85 90

(2) INFORMATION FOR SEQ ID NO:2078:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..314  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

aaccatttgg acacccgatcc atccatccat ccagcccccgt acgtgtctctcg ctggcccgctcc 60  
gtatatatag agagaggcat cggagatttgc ccgccacgtt gccatcgcgc gcrgcgcccg 120  
ccggccaagg ccaacacatgc tggcgagggc tcttcgcgcg cgcccggtgct ccagcgccgt 180  
ttgcatcgcc cgcgcacatc caagarcmgc cgcgcgtcgc gccaggccgg nggacgacga 240  
ggacgacgac gacggtcgcg gcggcgccgg cagaggccgc tntctaaagg gtcarcggcg 300  
gcggccgctcg cagg

(2) INFORMATION FOR SEQ ID NO:2079:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..104  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Asn His Leu Asp Thr Asp Pro Ser Ile His Pro Ala Pro Tyr Val Ser  
1 5 10 15  
Arg Trp Pro Ser Val Tyr Ile Glu Arg Gly Ile Gly Asp Xaa Pro Pro

20 25 30  
Arg Cys His Arg Ala Xaa Arg Pro Pro Ala Lys Ala Asn His Ala Gly  
35 40 45  
Glu Gly Ser Ser Ala Ala Ala Val Leu Gln Arg Arg Leu His Arg Pro  
50 55 60  
Arg Thr Ser Lys Xaa Xaa Arg Arg Arg Gly Gln Ala Xaa Gly Arg Arg  
65 70 75 80  
Gly Arg Arg Arg Arg Ser Arg Arg Arg Arg Gln Arg Pro Xaa Ser Asn  
85 90 95  
Gly Ser Xaa Ala Ala Ala Val Ala

(2) INFORMATION FOR SEQ ID NO:2080:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..94  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

Pro Phe Gly His Arg Ser Ile His Pro Ser Ser Pro Val Arg Val Ser  
1 5 10 15  
Leu Ala Val Arg Ile Tyr Arg Glu Arg His Arg Arg Xaa Ala Ala Thr  
20 25 30  
Leu Pro Ser Arg Xaa Ala Pro Ala Gly Gln Gly Gln Pro Cys Trp Arg  
35 40 45  
Gly Leu Leu Arg Arg Gly Arg Ala Pro Ala Ala Phe Ala Ser Pro Ala  
50 55 60  
His Ile Gln Xaa Xaa Pro Pro Ser Arg Pro Gly Arg Xaa Thr Thr Arg  
65 70 75 80  
Thr Thr Thr Thr Val Ala Ala Ala Ala Glu Ala Ala Xaa  
85 90

(2) INFORMATION FOR SEQ ID NO:2081:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Leu Ala Arg Ala Pro Pro Pro Arg Pro Cys Ser Ser Gly Val Cys  
1 5 10 15  
Ile Ala Arg Ala His Pro Arg Xaa Ala Ala Val Ala Ala Arg Pro Xaa  
20 25 30  
Asp Asp Glu Asp Asp Asp Asp Gly Arg Gly Gly Gly Arg Gly Arg  
35 40 45  
Xaa Leu Thr Gly Xaa Arg Arg Arg Pro Ser Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:2082:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1036 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1036

(D) OTHER INFORMATION: / Ceres Seq. ID 1502094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

```
acccatagtgt catgccacca tgggaagggt tcgtatttga gcaccgatta tgcaggttta      60
tcatgagaaaa tcttttatct taccatgatgt ttcaagggtg cttgcttgcc ttatatgagaa      120
ggatgtcaaag tttagaactc acacagccctc atacaggagc ctactcggat tgcaggcatc      180
atctcatgctt ccagttccatc tctatgaagg ccctactttt ctagaagaaa ccagagaaaa      240
ctgccgttat atagcagaaa agtatgaaaa tcaaggatat ccgttctctc ttgaaaaggga      300
tgccttgtag agggcttcaa ttgaacaatg gctccacaac gaggagcatg ctttcaaccc      360
tccgagccgg gccttgttct ttcatttggc ctttccctg ggtgaaggag aagatgatga      420
tatttgatgtt catacaagga agctagaaga ggttctggaa gtttatgagc aaaggctcag      480
tgacagcgaa ttctctgttg gaaacaagtt cactcttgcc gacctgtgtc acctgccaaa      540
ttcccactat atcaaaagcat ctacaagatt tctttacctt tatgattcga ggaataatgt      600
aaggagggtg tgggatgcta ttctgaccg gagtcttggg aagaaaagtc tgaggtatat      660
gaagagcgtg gaggagaaga acaacaaga agaactcaag aagcagcagc agcagcagga      720
agaggctcct agaactccca ccgaccacaac tcgggtagac tcgagaaaagc agagcagaac      780
agagcctcgg acaatattgg ttctcctcgc tgataacgag tcatcagctt cgatagtctc      840
tcgaacaaag aagcctcttc ctgggtgatc actagtgtct actacaacaa ttgattgttg      900
tggtatgcca gccacaaatt gatgggtgatg gtcgtcttag tgggtgttgt ctgtctttt      960
attgtttggt tctttaacaa gagttatatt ttacctctt gaccaaaagag ttgtttaaca      1020
ggatagtcac tgtacg
```

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1502095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

```
Pro Tyr Val His Ala Thr Met Glu Gly Leu Arg Ile Gly Ala Pro Ile
1      5      10
Met Gln Val Tyr His Glu Lys Ser Phe Ile Leu Pro Asp Val Ser Arg
20     25     30
Val Leu Ala Cys Leu Tyr Glu Lys Asp Val Lys Phe Glu Thr His Thr
35     40     45
Ala Ser Tyr Arg Ser Leu Leu Gly Leu Gln Ala Ser Ser His Ala Pro
50     55     60
Val Pro Phe Tyr Glu Gly Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile
65     70     75     80
Cys Arg Tyr Ile Ala Glu Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu
85     90     95
Leu Gly Lys Asp Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu His
100    105    110
Asn Glu Glu His Ala Phe Asn Pro Pro Ser Arg Ala Leu Phe Phe His
115    120    125
Leu Ala Phe Pro Leu Gly Gly Glu Asp Asp Asp Ile Asp Val His
130    135    140
Thr Arg Lys Leu Glu Glu Val Leu Glu Val Tyr Glu Gln Arg Leu Ser
145    150    155    160
Asp Ser Glu Phe Leu Val Gly Asn Lys Phe Thr Leu Ala Asp Leu Val
165    170    175
His Leu Pro Asn Ser His Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr
180    185    190
Leu Tyr Asp Ser Arg Lys Asn Val Arg Arg Trp Trp Asp Ala Ile Ser
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..300  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

Met	Glu	Gly	Leu	Arg	Ile	Gly	Ala	Pro	Ile	Met	Gln	Val	Tyr	His	Glu
1			5						10				15		
Lys	Ser	Phe	Ile	Leu	Pro	Asp	Val	Ser	Arg	Val	Leu	Ala	Cys	Leu	Tyr
			20					25					30		
Glu	Lys	Asp	Val	Lys	Phe	Glu	Thr	His	Thr	Ala	Ser	Tyr	Arg	Ser	Leu
		35					40					45			
Leu	Gly	Leu	Gln	Ala	Ser	Ser	His	Ala	Pro	Val	Pro	Phe	Tyr	Glu	Gly
		50				55					60				
Pro	Thr	Phe	Leu	Glu	Glu	Ser	Arg	Glu	Ile	Cys	Arg	Tyr	Ile	Ala	Glu
65				70						75				80	
Lys	Tyr	Glu	Asn	Gln	Gly	Tyr	Pro	Phe	Leu	Leu	Gly	Lys	Asp	Ala	Leu
			85						90					95	
Glu	Arg	Ala	Ser	Ile	Glu	Gln	Trp	Leu	His	Asn	Glu	Glu	His	Ala	Phe
			100					105					110		
Asn	Pro	Pro	Ser	Arg	Ala	Leu	Phe	His	Leu	Ala	Phe	Pro	Leu	Gly	
			115				120					125			
Glu	Gly	Glu	Asp	Asp	Asp	Ile	Asp	Val	His	Thr	Arg	Lys	Leu	Glu	Glu
		130				135					140				
Val	Leu	Glu	Val	Tyr	Glu	Gln	Arg	Leu	Ser	Asp	Ser	Glu	Phe	Leu	Val
145					150					155				160	
Gly	Asn	Lys	Phe	Thr	Leu	Ala	Asp	Leu	Val	His	Leu	Pro	Asn	Ser	His
			165						170				175		
Tyr	Ile	Lys	Ala	Ser	Asn	Lys	Phe	Leu	Tyr	Leu	Tyr	Asp	Ser	Arg	Lys
			180					185					190		
Asn	Val	Arg	Arg	Trp	Trp	Asp	Ala	Ile	Ser	Asp	Arg	Ser	Ser	Trp	Lys
		195				200						205			
Lys	Val	Leu	Arg	Tyr	Met	Lys	Ser	Val	Glu	Glu	Lys	Asn	Lys	Gln	Glu
		210				215					220				
Glu	Leu	Lys	Lys	Gln	Gln	Gln	Gln	Glu	Glu	Ala	Pro	Arg	Thr	Ser	
225				230						235				240	
Thr	Asp	Pro	Thr	Arg	Val	Asp	Ser	Arg	Lys	Gln	Ser	Arg	Thr	Glu	Pro
			245						250				255		
Arg	Thr	Ile	Leu	Val	Pro	Pro	Ala	Asp	Asn	Glu	Ser	Ser	Ala	Ser	Ile
			260					265					270		

Val Pro Arg Thr Lys Lys Pro Leu Pro Gly Asp His Leu Val Ser Thr  
275 280 285  
Gln Gln Ile Asp Gly Val Gly Met Pro Ala Thr Asn  
290 295 300

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

Met Gln Val Tyr His Glu Lys Ser Phe Ile Leu Pro Asp Val Ser Arg  
1 5 10 15  
Val Leu Ala Cys Leu Tyr Glu Lys Asp Val Lys Phe Glu Thr His Thr  
20 25 30  
Ala Ser Tyr Arg Ser Leu Leu Gly Leu Gln Ala Ser Ser His Ala Pro  
35 40 45  
Val Pro Phe Tyr Glu Gly Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile  
50 55 60  
Cys Arg Tyr Ile Ala Glu Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu  
65 70 75 80  
Leu Gly Lys Asp Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu His  
85 90 95  
Asn Glu Glu His Ala Phe Asn Pro Pro Ser Arg Ala Leu Phe His  
100 105 110  
Leu Ala Phe Pro Leu Gly Glu Gly Asp Asp Asp Ile Asp Val His  
115 120 125  
Thr Arg Lys Leu Glu Glu Val Leu Glu Val Tyr Glu Gln Arg Leu Ser  
130 135 140  
Asp Ser Glu Phe Leu Val Gly Asn Lys Phe Thr Leu Ala Asp Leu Val  
145 150 155 160  
His Leu Pro Asn Ser His Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr  
165 170 175  
Leu Tyr Asp Ser Arg Lys Asn Val Arg Arg Trp Trp Asp Ala Ile Ser  
180 185 190  
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu  
195 200 205  
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu  
210 215 220  
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys  
225 230 235 240  
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn  
245 250 255  
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly  
260 265 270  
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala  
275 280 285

Thr Asn  
290

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..833  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

atcttagaag	gaaacaggaa	caggcagctc	tgaagactg	aaactcacg	ccatggccat	60
cctgggcgcc	ctcaggctcg	cgccgtctcc	acccgccctc	gccggcgctg	cgccaccggc	120
tacgtcgccg	tctgcggctg	tacgctctct	cgtgcacttc	cacctcgcca	atgccggcgc	180
cgccgcgctc	ngtcgccgcc	tcgctctctg	ccgccgaccc	cgccgtggct	tccattggag	240
gaggaccgta	cggaagcag	gtgacgggg	ggcaggacct	caccggcaag	gacttcagcg	300
gccagacact	catcaagcag	gacttcaaga	cgtctatact	gaggcaggcg	aacttcaaa	360
gcgcgaacct	gctcggcgcg	agcttctctg	atgcagacct	cacaagcgct	gatctctctg	420
acgctgatct	tagaggcgct	gatttgtcgc	tggcgaaatt	aacgaaggca	aacttatcaa	480
atgccaaact	agaaggggca	cttgccactg	ggaacacttc	tttcaaaggt	gccgacataa	540
ctggggcaga	ttttaccgat	gtgccgctgc	gagatgatca	acgggagtat	ccttgcaaaa	600
tcgctgacgg	agtaaatcca	accactggaa	acccaacaaa	ggagactctg	ttctgcagct	660
gactcgacgga	aggacctggg	acttgtgact	tattcaacgt	cttgataaac	ttgcactctg	720
tgctgtaagc	acgtgaggaa	tgtaaatatg	gttatagagg	gttcctagaa	ataataactg	780
gtaattacgt	gtaaatcaac	caacaataaa	agtgtgtgct	gcccttgtaa	tgt	

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..119  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

Met	Ala	Ile	Leu	Gly	Ala	Leu	Arg	Leu	Ala	Pro	Ser	Pro	Pro	Ala	Leu	
1				5					10					15		
Ala	Gly	Ala	Ala	Pro	Pro	Ala	Thr	Ser	Pro	Ser	Ala	Ala	Val	Arg	Ser	
				20				25					30			
Ser	Val	His	Phe	His	Leu	Ala	Asn	Ala	Gly	Ala	Ala	Ala	Leu	Xaa	Arg	
				35			40					45				
Arg	Leu	Ala	Pro	Arg	Arg	Arg	Pro	Arg	Arg	Gly	Phe	His	Trp	Arg	Arg	
				50			55				60					
Thr	Val	Arg	Glu	Ala	Gly	Asp	Ala	Gly	Ala	Gly	Pro	His	Arg	Gln	Gly	
				65			70				75			80		
Leu	Gln	Arg	Pro	Asp	Thr	His	Gln	Ala	Gly	Leu	Gln	Asp	Val	Tyr	Thr	
				85			90				95					
Glu	Ala	Gly	Glu	Leu	Gln	Arg	Arg	Glu	Pro	Ala	Arg	Arg	Glu	Leu	Leu	
				100			105				110					
Arg	Cys	Arg	Pro	His	Lys	Arg										
				115												

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

Met	Pro	Ala	Pro	Pro	Arg	Xaa	Val	Ala	Ala	Ser	Leu	Leu	Ala	Ala	Asp	
1				5						10					15	

Pro Ala Val Ala Phe Ile Gly Gly Gly Pro Tyr Gly Lys Gln Val Thr  
20 25 30  
Arg Gly Gln Asp Leu Thr Gly Lys Asp Phe Ser Gly Gln Thr Leu Ile  
35 40 45  
Lys Gln Asp Phe Lys Thr Ser Ile Leu Arg Gln Ala Asn Phe Lys Gly  
50 55 60  
Ala Asn Leu Leu Gly Ala Ser Phe Phe Asp Ala Asp Leu Thr Ser Ala  
65 70 75 80  
Asp Leu Ser Asp Ala Asp Leu Arg Gly Ala Asp Leu Ser Leu Ala Asn  
85 90 95  
Leu Thr Lys Ala Asn Leu Ser Asn Ala Asn Leu Glu Gly Ala Leu Ala  
100 105 110  
Thr Gly Asn Thr Ser Phe Lys Gly Ala Asp Ile Thr Gly Ala Asp Phe  
115 120 125  
Thr Asp Val Pro Leu Arg Asp Asp Gln Arg Glu Tyr Leu Cys Lys Ile  
130 135 140  
Ala Asp Gly Val Asn Ser Thr Thr Gly Asn Pro Thr Lys Glu Thr Leu  
145 150 155 160  
Phe Cys Ser

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1502130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

atctctatct catcgctcatc attagaaaagg ccgaagcctt ctccgttctt cctcgacgcg 60  
tctcttccac agcccgcaacc tctatccctc gtctgggtatc gtctctccca caccctctcg 120  
ccccaaacca gaaaaaccct cgaaaaagcgg cggcggcgcg acatggcgga ggctcagggtc 180  
ccagctgctg cggttgccgc ggcgaccctt gaggtggcga cggtgaccga gggcgaggcc 240  
gctaaggagg cgaagggtcc gcataagctg caccgcagat ggaccttctg gtacgacatc 300  
cagtcacaag ccaagcccgcg cgctgcgtgg ggcacctccc tcaaaaaggc gtacaccttc 360  
gacacgcgtc aggagttttg gggcttgtat gatcatgttt tccgtccaaag caagttgcctt 420  
ggaaactgctg attttcacct attcaaggct ggagtagagc caaaatgg

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1502131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Ile Ser Ile Ser Ser Ser Ser Leu Glu Arg Pro Lys Pro Ser Pro Phe  
1 5 10 15  
Leu Leu Asp Ala Ser Leu Pro Gln Pro Gln Pro Leu Ser Leu Val Trp  
20 25 30  
Tyr Arg Leu Ser His Thr Pro Leu Pro Gln Pro Arg Lys Thr Leu Glu  
35 40 45  
Lys Arg Arg Arg Asp Met Ala Glu Val Glu Ala Pro Ala Ala Ala  
50 55 60  
Val Ala Ala Ala Thr Pro Glu Val Ala Thr Val Thr Glu Gly Gly Ala

65	Ala	Thr	Glu	Ala	Lys	Gly	Pro	His	Lys	Leu	His	Arg	Gln	Trp	Thr	Phe
				85						90					95	
Trp	Tyr	Asp	Ile	Gln	Ser	Lys	Pro	Lys	Pro	Gly	Ala	Ala	Trp	Gly	Thr	
			100					105					110			
Ser	Leu	Lys	Lys	Ala	Tyr	Thr	Phe	Asp	Thr	Val	Glu	Glu	Phe	Trp	Gly	
		115					120					125				
Leu	Tyr	Asp	His	Val	Phe	Arg	Pro	Ser	Lys	Leu	Pro	Gly	Thr	Ala	Asp	
	130					135					140					
Phe	His	Leu	Phe	Lys	Ala	Gly	Val	Glu	Pro	Lys	Trp					
145				150						155						

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

Met	Ala	Glu	Val	Glu	Ala	Pro	Ala	Ala	Val	Ala	Ala	Ala	Thr	Pro
1			5						10				15	
Glu	Val	Ala	Thr	Val	Thr	Glu	Gly	Gly	Ala	Ala	Thr	Glu	Ala	Lys
			20					25				30		
Pro	His	Lys	Leu	His	Arg	Gln	Trp	Thr	Phe	Trp	Tyr	Asp	Ile	Gln
		35					40				45			
Lys	Pro	Lys	Pro	Gly	Ala	Ala	Trp	Gly	Thr	Ser	Leu	Lys	Lys	Ala
		50				55					60			
Thr	Phe	Asp	Thr	Val	Glu	Glu	Phe	Trp	Gly	Leu	Tyr	Asp	His	Val
			70						75				80	
Arg	Pro	Ser	Lys	Leu	Pro	Gly	Thr	Ala	Asp	Phe	His	Leu	Phe	Lys
			85					90					95	
Gly	Val	Glu	Pro	Lys	Trp									
			100											

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

aaacaaaat	catttcaccc	ccggaaccgg	acgccgaacg	gcagtgctgc	aaaagtcggg	60
acaaagctcg	cgccgcccac	cgcaccgcgat	ccgcctcggc	caggcgctgct	gccgtccgct	120
cccttctccc	gcgcgctgcg	ctccgcctac	gcccgggccg	acccgctgga	cccagcgctgc	180
gcgcgtccac	tcggacgcgc	cgccgccttc	tcgggttgag	gcggagggtgc	ttggggacc	240
gcgcccatgg	cgagcgccgg	caacagcggc	agcggggacg	acgatgcagg	agggaaagctc	300
ctggcgcatc	gctaccagaa	ggcgaggttc	ctcgccgagg	gcacgatgag	agtcgtcttc	360
aaggccatcg	acacaaagac	tggaataaca	gtcgcggtaa	agcgaatccg	gataggaaa	420
gacaagaagg	aaggtgtcaa	cttcactgcg	ttgagggaaa	ttaaactact	taaggagctg	480
aaagatccta	atattataga	gctgattgat	tgt			

(2) INFORMATION FOR SEQ ID NO:2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

Asn	Gln	Asn	His	Phe	Ile	Pro	Gly	Thr	Gly	Arg	Arg	Thr	Ala	Val	Leu
1			5					10						15	
Gln	Lys	Ser	Gly	Gln	Ser	Ser	Arg	Arg	Pro	Pro	His	Pro	Ile	Arg	Leu
			20				25						30		
Ala	Gln	Ala	Cys	Cys	Arg	Pro	Leu	Pro	Ser	Pro	Ala	Pro	Ser	Pro	Pro
			35				40					45			
Pro	Thr	Pro	Gly	Pro	Thr	Arg	Trp	Thr	Gln	Arg	Ala	Pro	Leu	His	Ser
			50				55				60				
Asp	Ala	Pro	Pro	Pro	Ser	Arg	Val	Glu	Ala	Glu	Val	Leu	Gly	Asp	Pro
65						70				75				80	
Pro	Pro	Trp	Arg	Ala	Pro	Ala	Thr	Ala	Ala	Ala	Gly	Thr	Thr	Met	Gln
						85				90				95	
Glu	Gly	Ser	Ser	Trp	Arg	Ile	Ala	Thr	Arg	Arg	Ala	Arg	Ser	Ser	Ala
							105						110		
Arg	Ala	Arg	Met	Glu	Ser	Ser	Ser	Arg	Pro	Ser	Thr	Pro	Arg	Leu	Glu
							120					125			
Ile	Gln	Ser	Arg												
															130

(2) INFORMATION FOR SEQ ID NO:2094:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Thr	Lys	Ile	Ile	Ser	Ser	Pro	Glu	Pro	Asp	Ala	Glu	Arg	Gln	Cys	Cys
1														15	
Lys	Ser	Pro	Asp	Lys	Ala	Arg	Ala	Ala	His	Arg	Thr	Arg	Ser	Ala	Ser
														30	
Pro	Arg	Arg	Ala	Ala	Val	Arg	Ser	Leu	Pro	Arg	Arg	Arg	Arg	Leu	Arg
														45	
Leu	Arg	Pro	Gly	Arg	Pro	Ala	Gly	Pro	Ser	Val	Arg	Arg	Ser	Thr	Arg
														60	
Thr	Arg	Arg	Arg	Pro	Leu	Gly	Leu	Arg	Arg	Arg	Cys	Leu	Gly	Thr	Arg
65														80	
Pro	His	Gly	Glu	Arg	Arg	Gln	Gln	Arg	Gln	Arg	Gly	Arg	Arg	Cys	Arg
														95	
Arg	Glu	Ala	Pro	Gly	Gly	Ser	Leu	Pro	Glu	Gly	Arg	Gly	Pro	Arg	Arg
														110	
Gly	His	Val	Trp	Ser	Arg	Leu	Gln	Gly	His	Arg	His	Gln	Asp	Trp	Lys
														125	
Tyr	Ser	Arg	Gly	Lys	Ala	Asn	Pro	Asp	Arg	Lys	Gly	Gln	Glu	Gly	Arg
														140	
Cys	Gln	Leu	His	Cys	Val	Glu	Gly	Asn							
145															150

(2) INFORMATION FOR SEQ ID NO:2095:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502136  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:  
Met Ala Ser Ala Gly Asn Ser Gly Ser Gly Asp Asp Ala Gly Gly  
1 5 10 15  
Lys Leu Leu Ala Asp Arg Tyr Gln Lys Gly Asp Val Leu Gly Gly  
20 25 30  
Thr Tyr Gly Val Val Phe Lys Ala Ile Asp Thr Lys Thr Gly Asn Thr  
35 40 45  
Val Ala Val Lys Arg Ile Arg Ile Gly Lys Asp Lys Lys Glu Gly Val  
50 55 60  
Asn Phe Thr Ala Leu Arg Glu Ile Lys Leu Leu Lys Lys Asp  
65 70 75 80  
Pro Asn Ile Ile Glu Leu Ile Asp Cys  
85

(2) INFORMATION FOR SEQ ID NO:2096:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 522 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..522  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502153  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:  
aatccctccc gatcagatcc ctgcacaatg gcactccagg cagcctacga gtacctgcag 60  
caggccctcg gccatggcgc gtggctcgcc acgcagacgc tgacgtctgt gtcacatgcc 120  
gtacccaccg tactactgct gctagcgtcc ctgcacaaga gcacgtcgct gtcggtagg 180  
ggcaagccgc cgctccctcc ctgcgcgcgc ggcacccctcc ccatctgggg gcacctacac 240  
cacatcgggc ccagagacca catctcgctc caggagctgt tggccaahta cgggcacac 300  
gggttcctgt tcctccgcgc cggcgcgcgt cccacccctga tcgtgtcgtc gccacgcgcc 360  
gccgaggccg tgatgcgcac ccacgaccac atcttcgcgt cccgcgcgtg gtccatggcc 420  
tcccacatcc tcgctataca cactgcgcac gtggccttc cgcgcctcgg cgaatactgg 480  
cagcagacca ggaagctgat gaacacgcac ctgctcagca ac

(2) INFORMATION FOR SEQ ID NO:2097:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 174 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..174  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502154  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:  
Asn Pro Ser Arg Ser Asp Pro Ser Thr Met Ala Leu Gln Ala Ala Tyr  
1 5 10 15  
Glu Tyr Leu Gln Gln Ala Val Gly His Gly Ala Trp Ser Ser Thr Gln  
20 25 30  
Thr Leu Thr Leu Leu Leu Ile Ala Val Pro Thr Val Leu Leu Leu Leu  
35 40 45

Ala Ser Leu Ala Lys Ser Thr Ser Ser Ser Gly Arg Gly Lys Pro Pro  
50 55 60  
Leu Pro Pro Ser Pro Pro Gly Thr Leu Pro Ile Val Gly His Leu His  
65 70 75 80  
His Ile Gly Pro Gln Thr His Ile Ser Leu Gln Glu Leu Val Ala Lys  
85 90 95  
Tyr Gly His Asn Gly Phe Leu Phe Leu Arg Ala Gly Ala Val Pro Thr  
100 105 110  
Leu Ile Val Ser Ser Pro Ser Ala Ala Glu Ala Val Met Arg Thr His  
115 120 125  
Asp His Ile Phe Ala Ser Arg Pro Trp Ser Met Ala Ser His Ile Leu  
130 135 140  
Arg Tyr Asn Thr Cys Asp Val Ala Phe Ser Pro Leu Gly Glu Tyr Trp  
145 150 155 160  
Gln Gln Thr Arg Lys Leu Met Asn Thr His Leu Leu Ser Asn  
165 170

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1502155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Ala Leu Gln Ala Ala Tyr Glu Tyr Leu Gln Gln Ala Val Gly His  
1 5 10 15  
Gly Ala Trp Ser Ser Thr Gln Thr Leu Leu Leu Ile Ala Val  
20 25 30  
Pro Thr Val Leu Leu Leu Leu Ala Ser Leu Ala Lys Ser Thr Ser Ser  
35 40 45  
Ser Gly Arg Gly Lys Pro Pro Leu Pro Pro Ser Pro Gly Thr Leu  
50 55 60  
Pro Ile Val Gly His Leu His His Ile Gly Pro Gln Thr His Ile Ser  
65 70 75 80  
Leu Gln Glu Leu Val Ala Lys Tyr Gly His Asn Gly Phe Leu Phe Leu  
85 90 95  
Arg Ala Gly Ala Val Pro Thr Leu Ile Val Ser Ser Pro Ser Ala Ala  
100 105 110  
Glu Ala Val Met Arg Thr His Asp His Ile Phe Ala Ser Arg Pro Trp  
115 120 125  
Ser Met Ala Ser His Ile Leu Arg Tyr Asn Thr Cys Asp Val Ala Phe  
130 135 140  
Ser Pro Leu Gly Glu Tyr Trp Gln Gln Thr Arg Lys Leu Met Asn Thr  
145 150 155 160  
His Leu Leu Ser Asn  
165

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..626

(D) OTHER INFORMATION: / Ceres Seq. ID 1502165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

aaagccgaaa	aggagaaagt	accccggttcc	gtcggccgca	gtgccgcacc	tgcacccacc	60
gcacgcccag	tcacgcccc	cctggaccag	ccaacgtgac	actccaccgc	cgccggcgcc	120
gcggcagccc	gtagcaaccg	ccaccgcctg	cccatctcct	ctctatcccg	cgcgcgatgg	180
ccgcgtactt	caaccactcc	tcgtcctacc	cgccgcgcgc	tccccgccgc	ggcacttccc	240
cgtacggcgc	gtaccgccac	gctaccgcgc	cgccgcgcgc	accccgccgc	gcttacggcg	300
cctactacga	cgccgcagag	caggccctcc	cgccgcggga	cgaggtccgc	acccttctca	360
tcgctggcct	ccccgccgac	gccaagccgc	gcgaagtcta	caacctcttc	cgcgatttcc	420
ccggatacgt	ctctctccac	ctccgcacgg	gcaaatcctc	tcaggcggtat	gcgtttgctg	480
tgttttcgaga	tcaacagctt	gcactagctg	ctttgagctg	cacaaatgga	atggattttg	540
atcttgagaaa	aaattgttct	cttcatgtag	atctcgcaaa	atccaattcc	agatcaaaag	600
gcttgagatc	agatgatact	tcacct				

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

Lys	Pro	Lys	Arg	Lys	Tyr	Pro	Val	Pro	Ser	Ala	Ala	Val	Pro	His
1			5				10					15		
Leu	His	Pro	Pro	His	Ala	Glu	Ser	Arg	Pro	Pro	Trp	Thr	Ser	Gln
		20					25					30		Arg
Asp	Thr	Pro	Pro	Pro	Pro	Ala	Pro	Arg	Gln	Pro	Val	Ala	Thr	Ala
		35					40					45		Thr
Ala	Cys	Pro	Ser	Pro	Leu	Tyr	Pro	Ala	Pro	His	Gly	Arg	Val	Leu
		50				55				60				Gln
Pro	Leu	Leu	Val	Leu	Pro	Ala	Ala	Ala	Ser	Pro	Ala	Gly	His	Phe
		65				70				75				80
Val	Arg	Arg	Val	Pro	Pro	Arg	Leu	Pro	Ala	Gly	Ala	Gly	Thr	Pro
			85				90						95	Gly
Arg	Leu	Arg	Arg	Leu	Leu	Arg	Pro	Arg	Arg	Ala	Gly	Pro	Pro	Gly
			100				105						110	Ala
Gly	Arg	Gly	Pro	His	Pro	Leu	His	Arg	Trp	Pro	Pro	Arg	Arg	Gln
			115				120						125	
Ala	Ala	Arg	Ser	Leu	Gln	Pro	Leu	Pro	Arg	Phe	Pro	Arg	Ile	Arg
			130				135					140		Leu
Leu	Pro	Pro	Pro	His	Gly	Gln	Ile	Leu	Ser	Gly	Val	Cys	Val	Cys
			145			150				155				Cys
Val	Cys	Arg	Ser	Thr	Val	Cys	Thr	Ser	Cys	Leu	Glu	Cys	His	Lys
			165					170					175	Trp
Asn	Gly	Ile												

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met Ala Ala Tyr Phe Asn His Ser Ser Ser Tyr Pro Pro Pro Pro Pro

Gly	Lys	Gly	Val	Arg	Ser	Thr	Gly	Asp	Ile	Val	Asn	Ala	Met	Ala	Gly
1			5					10					15		
Gly	Gly	Ala	Thr	Val	Cys	Val	Thr	Gly	Ala	Gly	Gly	Phe	Ile	Ala	Ser
			20					25					30		
Trp	Val	Val	Lys	Leu	Leu	Leu	Ser	Arg	Gly	Tyr	Thr	Val	His	Gly	Thr
			35				40					45			
Val	Arg	His	Leu	Ser	Asp	Glu	Lys	Thr	Gly	His	Leu	Lys	Arg	Leu	Gly
	50					55				60					
Asn	Ala	Ala	Gly	Asn	Leu	Arg	Ile	Phe	Lys	Ala	Asp	Leu	Leu	Asp	Tyr
65				70						75				80	

Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val Phe His Val  
85 90 95  
Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu Leu Gln Met  
100 105 110  
Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys Ala Ala Ser  
115 120 125  
Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met Val Ala Val  
130 135 140  
Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

Met Ala Gly Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe  
1 5 10 15  
Ile Ala Ser Trp Val Val Lys Leu Leu Ser Arg Gly Tyr Thr Val  
20 25 30  
His Gly Thr Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys  
35 40 45  
Arg Leu Glu Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu  
50 55 60  
Leu Asp Tyr Asp Ala Met Ala Ala Val Val Gly Cys Gln Gly Val  
65 70 75 80  
Phe His Val Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu  
85 90 95  
Leu Gln Met Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys  
100 105 110  
Ala Ala Ser Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met  
115 120 125  
Val Ala Val Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..843
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

tcttcaccca	cattataaag	atctccact	tcgcactttc	gccgccgcct	ctctcctttc	60
cgagcaggag	cgggacaagg	taagcagcaa	tcgcagggaac	cctagcgcgc	ccgcacccgc	120
aggaatgggt	atcgacctcg	tcgcgggttg	gaggrrrkaag	aagaccaagc	gcactgcgcc	180
caagtctgac	gatgtctacc	tcaagctcct	cgctcaagctc	taccgtttcn	ttggtcagga	240
ggaccaagag	caatttcaac	gctgtcattc	tcaagaggct	tttcatgagt	aaaaccaacc	300
gaccaccaat	ctccatgcgc	cgccctgtca	agtttatgga	aggaaggagg	aagaacattg	360
ctgtcatttg	tggcacagtc	acagatgaca	aaaggatcca	ggaggtttcca	gcaatgaagg	420
ttactgcctt	gaggttcacg	gagacagcaa	gggccaggat	tgccaatgct	ggtggcgagt	480
gcctcacatt	tgaccagctt	gctcttcgtg	ctccacttgg	cgagaacacg	gtcctcttga	540

ggggccccc aaatgcccgaggcagtgaggcactttggcaaggctcctggagtgccgc600  
acagccacac caagccgatatgtgcgtcccaagggaaggaa gttcgagaag gctcgtggca660  
ggaggaacac ccgtggattc aaggttttaaa acaaattgtg gccctccgtg ttccatcag720  
catmstgcaa ccgttgtgtt tgatcagtcg acagtaatta gtcatactc tgtaccgaga780  
ttmstgacac aatttgttgt cctggytga attytsgaag atatttgatg tcgtctccyt840  
att

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

Met	Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Val	Xaa	Leu	Val	Arg
1			5					10				15		
Arg	Thr	Lys	Ser	Asn	Phe	Asn	Ala	Val	Ile	Leu	Lys	Arg	Leu	Phe
			20					25				30		
Ser	Lys	Thr	Asn	Arg	Pro	Pro	Ile	Ser	Met	Arg	Arg	Leu	Val	Lys
			35				40					45		
Met	Glu	Gly	Lys	Glu	Lys	Asn	Ile	Ala	Val	Ile	Val	Gly	Thr	Val
			50				55					60		
Asp	Asp	Lys	Arg	Ile	Gln	Glu	Val	Pro	Ala	Met	Lys	Val	Thr	Ala
			65				70				75			80
Arg	Phe	Thr	Glu	Thr	Ala	Arg	Ala	Arg	Ile	Val	Asn	Ala	Gly	Gly
			85					90					95	
Cys	Leu	Thr	Phe	Asp	Gln	Leu	Ala	Leu	Arg	Ala	Pro	Leu	Gly	Asn
			100					105					110	
Thr	Val	Leu	Leu	Arg	Gly	Pro	Lys	Asn	Ala	Arg	Glu	Ala	Val	Arg
			115					120					125	
Phe	Gly	Lys	Ala	Pro	Gly	Val	Pro	His	Ser	His	Thr	Lys	Pro	Tyr
			130				135						140	
Arg	Ser	Lys	Gly	Arg	Lys	Phe	Glu	Lys	Ala	Arg	Gly	Arg	Arg	Asn
			145				150				155			160
Arg	Gly	Phe	Lys	Val										
				165										

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

Met	Ser	Lys	Thr	Asn	Arg	Pro	Pro	Ile	Ser	Met	Arg	Arg	Leu	Val	Lys
1			5					10					15		
Phe	Met	Glu	Gly	Lys	Glu	Lys	Asn	Ile	Ala	Val	Ile	Val	Gly	Thr	Val
			20					25					30		
Thr	Asp	Asp	Lys	Arg	Ile	Gln	Glu	Val	Pro	Ala	Met	Lys	Val	Thr	Ala
			35				40						45		
Leu	Arg	Phe	Thr	Glu	Thr	Ala	Arg	Ala	Arg	Ile	Val	Asn	Ala	Gly	Gly
			50				55					60			
Glu	Cys	Leu	Thr	Phe	Asp	Gln	Leu	Ala	Leu	Arg	Ala	Pro	Leu	Gly	Glu

65 70 75 80  
Asn Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg  
85 90 95  
His Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr  
100 105 110  
Val Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn  
115 120 125  
Ser Arg Gly Phe Lys Val  
130

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala  
1 5 10 15  
Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro  
20 25 30  
Ala Met Lys Val Thr Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg  
35 40 45  
Ile Val Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu  
50 55 60  
Arg Ala Pro Leu Gly Glu Asn Thr Val Leu Leu Arg Gly Pro Lys Asn  
65 70 75 80  
Ala Arg Glu Ala Val Arg His Phe Gly Lys Ala Pro Gly Val Pro His  
85 90 95  
Ser His Thr Lys Pro Tyr Val Arg Ser Lys Gly Arg Lys Phe Glu Lys  
100 105 110  
Ala Arg Gly Arg Arg Asn Ser Arg Gly Phe Lys Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 819 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..819

(D) OTHER INFORMATION: / Ceres Seq. ID 1502193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

aaatcccac gaaaaacctt aaccctcgct acccgggcgg ggetacaaagc tcttcgtcgg 60  
ttcagcaacca tgargccacc ggctagaggga ggacgtgggt ggaggggtgg caggttcgat 120  
ggcgggggccc tctgtgcggg cggcggttgc atcgtccccc ggcctaacgt tctcttcctt 180  
ctcgcgctcg cgggcttccct cctctggccc gcggaccggc acatctccct ggcccgcctc 240  
cacctagcgc acgtctccgt cgtggcacgc cctgcgctcg ccgtcactat atccggcaag 300  
ctcaaggttc gcgttcgcaa tcttgacctc ttgcgctcgc actacaccgc cctcgacgtc 360  
gctatcgctc accgcgggtgc gggcgcttgg ccggtaacat ccggcgggcg acgggtccgg 420  
gcgcgcgctg tctcgtacgt cgacgcacac ctgcagctcg acggcatacg cgtcgtcgag 480  
gacgcgatgt acctgctcga ggacctgcgc caaggatccg tgcccctcga caccatcgcc 540  
gaggtcgagg gccacctcca ctctcctttc ctacagatcc cgggtcaaggg gagaatatct 600  
tgcgtaatgc atattaatcc acacaaccaa accatagtac atcaggactg ctatcctcga 660  
tgaattgctt atggcgtgga aatgtggaag ggtgtaaagt atgttgccct gcgaatggat 720

cggttgattt gtttctaacc ttgtcttcca gtcgtggttg taaaagtaag aaccaactaa 780  
gggggtgtttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

Met	Xaa	Pro	Pro	Ala	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Arg	Phe
1				5					10							15
Asp	Gly	Gly	Gly	Leu	Cys	Arg	Gly	Gly	Gly	Arg	Cys	Ile	Val	Pro	Cys	Leu
				20					25					30		
Thr	Val	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Gly	Phe	Leu	Leu	Trp	Pro	Ala	
				35				40					45			
Asp	Pro	Asp	Ile	Ser	Leu	Ala	Arg	Leu	His	Leu	Ala	His	Val	Ser	Val	
				50				55				60				
Val	Ala	Arg	Pro	Ala	Val	Ala	Val	Thr	Ile	Ser	Ala	Thr	Leu	Lys	Val	
				65				70				75			80	
Arg	Val	Arg	Asn	Pro	Asp	Leu	Phe	Ala	Leu	Asp	Tyr	Thr	Arg	Leu	Asp	
				85				90						95		
Val	Ala	Ile	Gly	Tyr	Arg	Gly	Ala	Gly	Leu	Gly	Arg	Val	Thr	Ser	Gly	
				100				105					110			
Gly	Gly	Arg	Val	Arg	Ala	Arg	Ala	Val	Ser	Tyr	Val	Asp	Ala	Asn	Leu	
				115				120					125			
Gln	Leu	Asp	Gly	Ile	Arg	Val	Val	Glu	Asp	Ala	Met	Tyr	Leu	Leu	Glu	
				130				135				140				
Asp	Leu	Ala	Gln	Gly	Ser	Val	Pro	Phe	Asp	Thr	Ile	Ala	Glu	Val	Glu	
				145				150				155			160	
Gly	His	Leu	His	Phe	Leu	Phe	Leu	Ser	Ile	Pro	Val	Lys	Gly	Arg	Ile	
				165				170						175		
Ser	Cys	Val	Met	His	Ile	Asn	Pro	His	Asn	Gln	Thr	Ile	Val	His	Gln	
				180				185						190		
Asp	Cys	Tyr	Pro	Glu												
				195												

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

ataaatcaac	cgccggtgaa	gtctagtctg	ctcgtcgtct	gggtccaccac	ctcagctccg	60
ccgcttgccc	gttttggctc	tctccctccc	gggtctctggc	ttctttctaca	cgctaccgctc	120
tcacagccgt	aaacgcccct	cccggatccc	gctagtctgc	caccgcgcgc	cgccccgcgc	180
cttttgcctc	catcatggcc	gctcgtctga	ccgccaccctc	cgctccacgac	ttcatctgtca	240
aggatgcgag	cgggcaagac	gttgacctca	gcacctacaa	gggggaaggtt	cttctcattgt	300
ttaacgtcgc	atcccagtg	ggcttaacca	actccaaacta	cactgagctgt	gcccagctct	360
atgagaagta	caaggaccac	ggctttgaaa	tctctggcttt	cccattgcaac	cagtttggtgt	420
ggcaggagcc	tggtaccaat	aaggagattg	tccagtttgc	ctgcacacgc	ttcaaggctgt	480
agtaccatc	ttcgacaagg	ttgatgtc				

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..104

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

Met	Ala	Ala	Ser	Ser	Thr	Ala	Thr	Ser	Val	His	Asp	Phe	Ile	Val	Lys
1			5					10						15	
Asp	Ala	Ser	Gly	Lys	Asp	Val	Asp	Leu	Ser	Thr	Tyr	Lys	Gly	Lys	Val
			20					25					30		
Leu	Leu	Ile	Val	Asn	Val	Ala	Ser	Gln	Cys	Gly	Leu	Thr	Asn	Ser	Asn
			35					40					45		
Tyr	Thr	Glu	Leu	Ala	Gln	Leu	Tyr	Glu	Lys	Tyr	Lys	Asp	Gln	Gly	Phe
			50			55				60					
Glu	Ile	Leu	Ala	Phe	Pro	Cys	Asn	Gln	Phe	Gly	Gly	Gln	Glu	Pro	Gly
			65			70				75				80	
Thr	Asn	Lys	Glu	Ile	Val	Gln	Phe	Ala	Cys	Thr	Arg	Phe	Lys	Ala	Glu
			85						90					95	
Tyr	Pro	Ser	Ser	Thr	Arg	Leu	Met								
			100												

(2) INFORMATION FOR SEQ ID NO:2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..523

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

attggcagct	atgaatgctc	agccacaatgc	gtatgtatac	atcacggcca	cggtcacgct	60
tcccccttct	gcaagcaaac	ctaaccaaacg	ctctgcggct	cttcttcgaa	tcacaactct	120
ccccgatccc	caaaaatcgaa	cccaagtoga	aaccttaaac	tggcccttct	cgatgtcggc	180
cgccacaacc	gccccaaccc	ctgcggtggc	caccccgatg	gcgcgcgctc	cgctgtaccc	240
ggctcctccc	acgatctccg	cctccgtggc	cgcgctcgct	gaggaaagg	acgacctcta	300
tgcccgctcc	aagtgcctcc	agcgccacat	ggagttcgct	gagatccagg	aggagtaagt	360
taaaagacga	cagaagaacc	tcaagcgcca	actcctccgt	gcgcaggagg	aggccaagcg	420
gatccagctc	gtaccgntcg	tcatcgggcca	gtttatggag	atggctcgacg	gcaacaacgg	480
catcggtggg	tctactacgg	gcagcaacta	ctatgtgcgg	atc		

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..174

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

Leu	Ala	Arg	Met	Asn	Ala	Gln	Pro	His	Ala	Tyr	Val	Tyr	Ile	Thr	Ala
1			5					10						15	

Thr Phe Thr Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala  
20 25 30  
Ala Leu Leu Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln  
35 40 45  
Val Glu Thr Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala  
50 55 60  
Pro Thr Pro Ala Val Ala Thr Pro Met Ala Pro Pro Ser Tyr Pro  
65 70 75 80  
Ala Ser Ser Thr Ile Ser Ala Ser Val Ala Ser Val Glu Glu Glu  
85 90 95  
Asp Asp Leu Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe  
100 105 110  
Val Glu Ile Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys  
115 120 125  
Arg Glu Leu Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val  
130 135 140  
Pro Xaa Val Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly  
145 150 155 160  
Ile Val Gly Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile  
165 170

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala Thr Phe Thr  
1 5 10 15  
Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala Ala Leu Leu  
20 25 30  
Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln Val Glu Thr  
35 40 45  
Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala Pro Thr Pro  
50 55 60  
Ala Val Ala Thr Pro Met Ala Pro Pro Pro Ser Tyr Pro Ala Ser Ser  
65 70 75 80  
Thr Ile Ser Ala Ser Val Ala Ala Ser Val Glu Glu Glu Asp Asp Leu  
85 90 95  
Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe Val Glu Ile  
100 105 110  
Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys Arg Glu Leu  
115 120 125  
Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val Pro Xaa Val  
130 135 140  
Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly Ile Val Gly  
145 150 155 160  
Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile  
165 170

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1502223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

Met	Ser	Ala	Ala	Thr	Thr	Ala	Pro	Thr	Pro	Ala	Val	Ala	Thr	Pro	Met
1			5					10					15		
Ala	Pro	Pro	Pro	Ser	Tyr	Pro	Ala	Ser	Ser	Thr	Ile	Ser	Ala	Ser	Val
			20				25					30			
Ala	Ala	Ser	Val	Glu	Glu	Glu	Asp	Asp	Leu	Tyr	Gly	Arg	Leu	Lys	Ser
		35					40				45				
Leu	Gln	Arg	His	Met	Glu	Phe	Val	Glu	Ile	Gln	Glu	Glu	Tyr	Val	Lys
	50					55					60				
Asp	Glu	Gln	Lys	Asn	Leu	Lys	Arg	Glu	Leu	Leu	Arg	Ala	Gln	Glu	Glu
65				70					75					80	
Val	Lys	Arg	Ile	Gln	Ser	Val	Pro	Xaa	Val	Ile	Gly	Gln	Phe	Met	Glu
			85					90					95		
Met	Val	Asp	Gly	Asn	Asn	Gly	Ile	Val	Gly	Ser	Thr	Thr	Gly	Ser	Asn
			100				105						110		
Tyr	Tyr	Val	Arg	Ile											
			115												

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1058

(D) OTHER INFORMATION: / Ceres Seq. ID 1502224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

ctcacacgccc	ggccgcccgcg	caagagccgt	ggccccgtcg	acgtccgccc	gcacaggact	60
ctccgagtgt	gggattgagc	cgtagttttt	tttttttggt	ggctcgggcc	gatatccggt	120
actgtatgag	gggttcccaac	tactagactt	taagatcgct	gatttcaatgg	aggcctccga	180
ggcagcacct	gcagcggcgg	ccaccgtcat	ggaagcagag	gatgtgagcg	gcgggaaggg	240
ccaatggtac	gtccttgggg	agcgggcgct	gatggtgcgc	tacacgcggg	agcacgtgcc	300
gcgtaccacc	gactggatgc	aggaccgggc	gctgctggag	gccaccgggt	cggagccccc	360
ctccctctcg	caggagttcg	aggtcccacc	ytcatggacc	ctcgaccctc	taaagcacac	420
cttcatagtg	ttggataagg	agctcataga	gggagagttc	gtgccgggca	acccgcacat	480
tgaagctatg	gktggkgatg	tgaacatata	tatgaatgac	tctgatgatg	tgcagatcgc	540
ggagatagag	attatgatag	ctgaacataa	gascgctggg	aagggtatgt	gtcaagaagc	600
aattcttactg	atgatggcat	ttgcagtaga	gaaatatgga	attcacacgt	tcagggcaaa	660
aattagcgaa	tcaaatatgg	catcgcttaa	gctcttcagg	aagttgggct	tcaaggatgc	720
tctcatcagt	gtggtgttca	aggaggtgac	tctggaggca	cccgtgact	cactcccgtt	780
gaagtttctc	ctgaccatgt	gagacttggt	acgtttgaca	tgccccaaat	taattccatg	840
cadagcacac	aagaagctaa	tgctgtttgt	ctgtactatc	tgaccataat	ttactcgggc	900
tgatattgta	tgaaaaaaat	gaataaaca	gttgcaacagt	tgtgattcaa	ttgcattaga	960
ccagtcgggt	ttttcatgtc	actattttga	agaccccata	tcttataaac	aaatgtagac	1020
aaagttttatc	tcataatttt	tttatagtat	ctcccgtc			

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1502225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

Met Glu Ala Ser Glu Ala Ala Pro Ala Ala Ala Thr Val Met Glu  
1 5 10 15  
Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu Gly Glu  
20 25 30  
Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His  
35 40 45  
Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro  
50 55 60  
Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp  
65 70 75 80  
Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly  
85 90 95  
Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val  
100 105 110  
Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu  
115 120 125  
Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gln Glu  
130 135 140  
Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His  
145 150 155 160  
Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu  
165 170 175  
Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys  
180 185 190  
Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro  
195 200 205  
Leu Thr Ile Gly Asp Trp  
210

(2) INFORMATION FOR SEQ ID NO:2119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1502226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:

Met Glu Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu  
1 5 10 15  
Gly Glu Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg  
20 25 30  
Tyr His Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser  
35 40 45  
Glu Pro Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr  
50 55 60  
Leu Asp Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile  
65 70 75 80  
Glu Gly Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa  
85 90 95  
Asp Val Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu  
100 105 110  
Ile Glu Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly  
115 120 125  
Gln Glu Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly  
130 135 140  
Ile His Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu

145 150 155 160  
Lys Leu Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val  
165 170 175  
Phe Lys Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg  
180 185 190  
Phe Pro Leu Thr Ile Gly Asp Trp  
195 200

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His Asp Trp Met  
1 5 10 15  
Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro Leu Ser Leu  
20 25 30  
Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp Pro Leu Lys  
35 40 45  
His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly Glu Phe Val  
50 55 60  
Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val Asn Ile Tyr  
65 70 75 80  
Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu Ile Met Ile  
85 90 95  
Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu Ala Ile Leu  
100 105 110  
Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His Thr Phe Arg  
115 120 125  
Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu Phe Arg Lys  
130 135 140  
Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys Glu Val Thr  
145 150 155 160  
Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro Leu Thr Ile  
165 170 175  
Gly Asp Trp

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

acatccatcc atccatccat ccatccatcc ctaaaaatca aggtctacaca ccaacttact 60  
ttctaggtct caaattaaat ggctctctcg tctctctct tctgtctggc gtcgatggcg 120  
gtggcgggac tctttgtcgt cggctcgtgt ggcggcgcgc tcaccttcac gatcgggcaag 180  
gaectcagct ccaccaaaact atccctcgtc actaacgttg ccatctccga ggtgtcggtc 240  
aaggagaagg gcgccctgga ctggtcggat gatctcaagg agtcgccagc caaaaccttc 300  
acccctcgata gcaaggagcc gattaagggc cccatctcgc tcgcttcgc tgtgaaagggt 360

gggtggctacc gcgtcgctcga tgacgtcctac cctgccgact tcaagcctgg ctctgtttac 420  
cagacaggcg aacaaatctg agtaattggt tctgctgcgt gcagattata ttgatctcta 480  
aaataaatgt ttgacagaga ctaattaagc acmcaaacaa agcaaggcmc taattcattt 540  
cctatgttta ctttgttgga ggcaactgca aaacaatgta ttgatgcat gttctectct 600  
cacatatgtt gbtgggtgtgc tgtatatata attaatyycc

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

Ile His Pro Ser Ile His Pro Ser Ile Pro Lys Asn Gln Gly Tyr Thr  
1 5 10 15  
Pro Thr Tyr Phe Leu Gly Leu Lys Leu Asn Gly Leu Leu Val Leu Leu  
20 25 30  
Leu Ala Ala Gly Val Asp Gly Gly Gly Thr Leu Cys Arg Arg Leu  
35 40 45  
Val Trp Arg Arg Ala His Leu His Asp Arg Gln Gly Leu Gln Leu His  
50 55 60  
Gln Thr Ile Pro Arg His  
65 70

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1502230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Ala Ser Ser Ser Ser Ser Leu Leu Leu Ala Ser Met Ala Val Ala  
1 5 10 15  
Ala Leu Phe Val Val Gly Ser Cys Gly Gly Ala Leu Thr Phe Thr Ile  
20 25 30  
Gly Lys Asp Ser Ser Ser Thr Lys Leu Ser Leu Val Thr Asn Val Ala  
35 40 45  
Ile Ser Glu Val Ser Val Lys Glu Lys Gly Ala Leu Asp Trp Ser Asp  
50 55 60  
Asp Leu Lys Glu Ser Pro Ala Lys Thr Phe Thr Leu Asp Ser Lys Glu  
65 70 75 80  
Pro Ile Lys Gly Pro Ile Ser Val Arg Phe Ala Val Lys Gly Gly Gly  
85 90 95  
Tyr Arg Val Val Asp Asp Val Ile Pro Ala Asp Phe Lys Pro Gly Ser  
100 105 110  
Val Tyr Gln Thr Gly Glu Gln Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

Met	Ala	Val	Ala	Ala	Leu	Phe	Val	Val	Gly	Ser	Cys	Gly	Gly	Ala	Leu
1				5					10					15	
Thr	Phe	Thr	Ile	Gly	Lys	Asp	Ser	Ser	Ser	Thr	Lys	Leu	Ser	Leu	Val
			20					25					30		
Thr	Asn	Val	Ala	Ile	Ser	Glu	Val	Ser	Val	Lys	Glu	Lys	Gly	Ala	Leu
			35				40					45			
Asp	Trp	Ser	Asp	Asp	Leu	Lys	Glu	Ser	Pro	Ala	Lys	Thr	Phe	Thr	Leu
	50					55					60				
Asp	Ser	Lys	Glu	Pro	Ile	Lys	Gly	Pro	Ile	Ser	Val	Arg	Phe	Ala	Val
	65				70					75				80	
Lys	Gly	Gly	Gly	Tyr	Arg	Val	Val	Asp	Asp	Val	Ile	Pro	Ala	Asp	Phe
			85						90					95	
Lys	Pro	Gly	Ser	Val	Tyr	Gln	Thr	Gly	Glu	Gln	Ile				
			100					105							

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1502270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

cggttgcttc	gcttcgcttt	gsscgcgatt	cgatccaggc	tttggttgga	ggcatggcct	60
cgtcgccgcg	gagcagctac	gactgctcct	tcaaggtcct	gcttatcggg	gattcggccg	120
tcggcaagag	cagcctctct	gtcagctctg	tctccgcgcg	tcacatcgac	gacgacatog	180
cgccaaccat	aggggtggat	tttaaaatca	aattttctcag	tgtgggtggg	aaagaactaa	240
aactgacaat	atgggacact	gcgggtcaag	agagggttca	gacaattacc	agctcttaot	300
acaggggtgc	tcatgggatt	attttagttt	atgacgttac	aaagagggag	agtttcacaa	360
atttggtcga	tgtgtggacc	aaggaaaatag	agttacactc	aacaaaataag	gaatgcatca	420
aaatgcttgt	tggaataaaa	gtggacaagg	atgaggacag	aatgggtgaca	aaagaagaag	480

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Gly	Ala	Ser	Leu	Arg	Phe	Xaa	Arg	Asp	Ser	Ile	Gln	Ala	Leu	Val	Gly
1				5				10						15	
Gly	Met	Ala	Ser	Ser	Pro	Ala	Ser	Ser	Tyr	Asp	Cys	Ser	Phe	Lys	Val
			20					25					30		
Leu	Leu	Ile	Gly	Asp	Ser	Ala	Val	Gly	Lys	Ser	Ser	Leu	Leu	Val	Ser
			35				40					45			
Phe	Val	Ser	Ala	Ala	His	Ile	Asp	Asp	Asp	Ile	Ala	Pro	Thr	Ile	Gly
	50					55					60				

Val	Asp	Phe	Lys	Ile	Lys	Phe	Leu	Ser	Val	Gly	Gly	Lys	Lys	Leu	Lys
65					70					75				80	
Leu	Thr	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr
				85					90					95	
Ser	Ser	Tyr	Tyr	Arg	Gly	Ala	His	Gly	Ile	Ile	Leu	Val	Tyr	Asp	Val
				100				105					110		
Thr	Lys	Arg	Glu	Ser	Phe	Thr	Asn	Leu	Ala	Asp	Val	Trp	Thr	Lys	Glu
				115			120						125		
Ile	Glu	Leu	His	Ser	Thr	Asn	Lys	Glu	Cys	Ile	Lys	Met	Leu	Val	Gly
				130			135				140				
Asn	Lys	Val	Asp	Lys	Asp	Glu	Asp	Arg	Met	Val	Thr	Lys	Glu	Glu	
145				150						155					

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met	Ala	Ser	Ser	Pro	Ala	Ser	Ser	Tyr	Asp	Cys	Ser	Phe	Lys	Val	Leu
1				5				10					15		
Leu	Ile	Gly	Asp	Ser	Ala	Val	Gly	Lys	Ser	Ser	Leu	Leu	Val	Ser	Phe
				20				25				30			
Val	Ser	Ala	Ala	His	Ile	Asp	Asp	Asp	Ile	Ala	Pro	Thr	Ile	Gly	Val
				35			40					45			
Asp	Phe	Lys	Ile	Lys	Phe	Leu	Ser	Val	Gly	Gly	Lys	Lys	Leu	Lys	Leu
				50			55				60				
Thr	Ile	Trp	Asp	Thr	Ala	Gly	Gln	Glu	Arg	Phe	Arg	Thr	Ile	Thr	Ser
				65			70			75			80		
Ser	Tyr	Tyr	Arg	Gly	Ala	His	Gly	Ile	Ile	Leu	Val	Tyr	Asp	Val	Thr
				85			90					95			
Lys	Arg	Glu	Ser	Phe	Thr	Asn	Leu	Ala	Asp	Val	Trp	Thr	Lys	Glu	Ile
				100			105					110			
Glu	Leu	His	Ser	Thr	Asn	Lys	Glu	Cys	Ile	Lys	Met	Leu	Val	Gly	Asn
				115			120					125			
Lys	Val	Asp	Lys	Asp	Glu	Asp	Arg	Met	Val	Thr	Lys	Glu	Glu		
				130			135				140				

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..344
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

gaccgcgcgg	cagggggaagc	ttagcacgga	cgggaccagc	tgacgaccag	gccatgggga	60
agtacatgcg	caaggggcaag	atgtccgggg	aggtggccgt	catggaggtc	cccggcggcg	120
cgctgctkkg	tgctccgcacc	gtctccgcac	gtctcgctgt	cagaggggcg	agaggccgct	180
cgacaagggg	gacgcggatg	acgccgcggg	acagttacct	gagctcagga	gccggangna	240
gaagcctcat	aaggaccatc	acggcgtgcc	gtgcgcgcgc	cccgcggcgc	cagccaagag	300
gggcgcgggg	aggaaggcgc	cctccgcgcg	gcgcgcgcgc	cacg		

(2) INFORMATION FOR SEQ ID NO:2129:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 114 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..114  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502286  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:  
Pro Arg Gly Arg Gly Ser Leu Ala Arg Thr Gly Pro Ala Asp Asp Gln  
1                  5                  10                  15  
Ala Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala  
                  20                  25                  30  
Val Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro  
                  35                  40                  45  
Ala Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr  
                  50                  55                  60  
Arg Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg  
65                  70                  75                  80  
Ser Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro  
                  85                  90                  95  
Gln Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg  
                  100                  105                  110  
Arg Thr

(2) INFORMATION FOR SEQ ID NO:2130:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 97 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..97  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502287  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:  
Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val  
1                  5                  10                  15  
Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala  
                  20                  25                  30  
Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg  
                  35                  40                  45  
Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser  
                  50                  55                  60  
Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro Gln  
65                  70                  75                  80  
Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg Arg  
                  85                  90                  95  
Thr

(2) INFORMATION FOR SEQ ID NO:2131:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 93 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..93  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502288  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:  
Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val Met Glu Val Pro  
1 5 10 15  
Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala Arg Ser Arg Cys  
20 25 30  
Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg Met Thr Pro Pro  
35 40 45  
Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser Leu Ile Arg Thr  
50 55 60  
Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Gln Pro Arg Gly Ala  
65 70 75 80  
Pro Gly Gly Arg Pro Pro Pro Pro Pro Arg Arg Thr  
85 90

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1502297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

ctcacgcaag kntntgcctc cggttaagcc acaaacacac agacaccatg gccttccccg 60  
ggactccggc gaggaaagatc gtaccaggcg gcttcaccgc agcacgaacc gccgtggcca 120  
gcgssgcgct cttagctctcg acctggacgg cgccggcgac tttttctggg gccctgtggca 180  
gtctatcaag gcgaaggccg ccgaggcagc ggccctacct cgtgcctctc tcgcggcgct 240  
ggcggagaag gcggacgaga ttttccccgc ggagaccgcg tcggagagcgc tccggcagtg 300  
gatgcgcgtc gcgcgtcacg ttgtgattcc cgcccctagt ggtcgccctc gtgctttgct 360  
gtgctggcg ctgctgtgct t

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1502298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Ser Arg Lys Xaa Xaa Pro Pro Val Lys Pro Gln Thr His Arg His His  
1 5 10 15  
Gly Leu Pro Arg Asp Ser Gly Glu Glu Asp Arg Thr Arg Arg Leu His  
20 25 30  
Arg Ser Thr Asn Arg Arg Gly Gln Xaa Ala Leu Ser Phe Asp Leu  
35 40 45  
Asp Gly Ala Gly Asp Phe Phe Trp Gly Leu Trp Gln Leu Ile Lys Ala  
50 55 60  
Lys Ala Ala Glu Ala Ala Tyr Leu Ala Ala Leu Phe Ala Ala Leu  
65 70 75 80  
Ala Glu Lys Ala Asp Glu Ile Phe Pro Pro Glu Thr Arg Ser Glu Thr  
85 90 95  
Leu Arg Gln Trp Met Arg Val Ala Val Thr Val Val Ile Pro Gly Pro  
100 105 110

Ser Gly Arg Pro Arg Ala Leu Leu Leu Leu Ala Leu Leu Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

His Ala Xaa Xaa Cys Leu Arg Leu Ser His Lys His Thr Asp Thr Met  
1 5 10 15  
Ala Phe Pro Gly Thr Pro Ala Arg Lys Ile Val Pro Gly Gly Thr  
20 25 30  
Ala Ala Arg Thr Ala Val Ala Ser Xaa Ala Leu Leu Ala Ser Thr Trp  
35 40 45  
Thr Ala Pro Ala Thr Phe Ser Gly Ala Cys Gly Ser Ser Ser Arg Arg  
50 55 60  
Arg Pro Pro Arg Gln Arg Pro Thr Ser Leu Pro Ser Ser Arg Arg Trp  
65 70 75 80  
Arg Arg Arg Arg Thr Arg Ser Ser Arg Arg Arg Pro Ala Arg Arg Arg  
85 90 95  
Ser Gly Ser Gly Cys Ala Ser Pro Ser Pro Trp  
100 105

(2) INFORMATION FOR SEQ ID NO:2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

Met Ala Phe Pro Gly Thr Pro Ala Arg Lys Ile Val Pro Gly Gly Phe  
1 5 10 15  
Thr Ala Ala Arg Thr Ala Val Ala Ser Xaa Ala Leu Leu Ala Ser Thr  
20 25 30  
Trp Thr Ala Pro Ala Thr Phe Ser Gly Ala Cys Gly Ser Ser Ser Arg  
35 40 45  
Arg Arg Pro Pro Arg Gln Arg Pro Thr Ser Leu Pro Ser Ser Arg Arg  
50 55 60  
Trp Arg Arg Arg Arg Thr Arg Ser Ser Arg Arg Arg Pro Ala Arg Arg  
65 70 75 80  
Arg Ser Gly Ser Gly Cys Ala Ser Pro Ser Pro Trp  
85 90

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1502315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

ctgtttcaaa atcctgggtc cgccattggg ggcgggtgagg ccaccctagt agaggctaga	60
ggatgatata caaggcgatc gacacgttct acctgacaga tgagcagctc cgtgactcgc	120
catcacggaa ggaaggatc gacgagggcca ccgagactgc gcttcsstc tatggctgtg	180
acctcatcca ggagagcggc atctctctca ggcaccaca agcagtgtat gccacggcac	240
aagtattgtt ccactcgctt tactgcaaga aatcatttgt tcgatttagt gcaagagagag	300
ttgctgctag ctgtgtttgg ctggcaggga agttggagga gagtccaggg aaatcaaggc	360
atattatatt tgtcttccac agaattggaat gtaggagaga aaacttgcca attgaatttt	420
tagatgtttt ttcaaagaaa tattcggaac tgaggc	

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1502316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

Met Ile Tyr Thr Ala Ile Asp Thr Phe Tyr Leu Thr Asp Glu Gln Leu	
1 5 10 15	
Arg Asp Ser Pro Ser Arg Lys Asp Gly Ile Asp Glu Ala Thr Glu Thr	
20 25 30	
Ala Leu Xaa Xaa Tyr Gly Cys Asp Leu Ile Gln Glu Ser Gly Ile Leu	
35 40 45	
Leu Arg Leu Pro Gln Ala Val Met Ala Thr Ala Gln Val Leu Phe His	
50 55 60	
Arg Phe Tyr Cys Lys Lys Ser Phe Val Arg Phe Ser Ala Lys Arg Val	
65 70 75	
Ala Ala Ser Cys Val Trp Leu Ala Gly Lys Leu Glu Glu Ser Pro Arg	
85 90 95	
Lys Ser Arg His Ile Phe Val Phe His Arg Met Glu Cys Arg Arg	
100 105 110	
Glu Asn Leu Pro Ile Glu Phe Leu Asp Val Phe Ser Lys Lys Tyr Ser	
115 120 125	
Glu Leu Arg	
130	

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

Met Asa Thr Ala Gln Val Leu Phe His Arg Phe Tyr Cys Lys Lys Ser	
1 5 10 15	
Phe Val Arg Phe Ser Ala Lys Arg Val Ala Ala Ser Cys Val Trp Leu	
20 25 30	
Ala Gly Lys Leu Glu Glu Ser Pro Arg Lys Ser Arg His Ile Phe	
35 40 45	
Val Phe His Arg Met Glu Cys Arg Arg Glu Asn Leu Pro Ile Glu Phe	
50 55 60	

Leu Asp Val Phe Ser Lys Lys Tyr Ser Glu Leu Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:

gatttggctc	ttgccatgga	ggtgcgcgtc	tccccacgcg	gtgcccacgc	cggcctcctc	60
tgctgcagct	ccactcccg	ctgcctcggc	ctccgctccc	gctccgcccac	cgctccgagc	120
cgccgcgcaa	ggccactcct	tgccgcgaga	accggggacag	ccggagcgac	gaggagaccg	180
cgccggassc	aaatcatcat	cggtcggcgc	gccgggggnak	agcggggcgcc	ggcgcaacag	240
gaagcagcag	cagcagcagc	agcagacggc	ggcgaaaggaa	gaagaagaag	aggaggagga	300
agatgaggac	gacgaggagg	agcgtgacgc	gacgatcccg	gagtggtgac	gaaccggatg	360
atgcggcggg	gtgggcgcgt	cggtgggcgt	tccgctggcg	ctgggcgtgg	ggtttcttcc	420
cggtgttcta	ctacctgaag	gcgktggcga	aggtggacgt	gccgacgtgg	atcccctt	

(2) INFORMATION FOR SEQ ID NO:2140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

Asp	Leu	Ala	Leu	Ala	Met	Glu	Val	Pro	Leu	Ser	Pro	Pro	Arg	Ala	His
1						5				10				15	
Ala	Gly	Leu	Leu	Cys	Cys	Ser	Ser	Thr	Pro	Val	Val	Leu	Gly	Leu	Arg
						20				25				30	
Ser	Arg	Ser	Ala	Thr	Ala	Pro	Ser	Arg	Arg	Ala	Arg	Pro	Leu	Leu	Ala
						35				40				45	
Arg	Gly	Thr	Gly	Thr	Ala	Gly	Ala	Thr	Arg	Arg	Pro	Arg	Arg	Xaa	Gln
						50				55				60	
Asp	His	His	Gly	Arg	Ala	Ala	Gly	Xaa	Xaa	Arg	Ala	Ala	Ala	Gln	Gln
						65				70				75	
Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Gly	Gly	Glu	Gly	Arg	Arg	Arg
						85				90				95	
Arg	Gly	Gly	Gly	Arg											
						100									

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Ile Trp Leu Leu Pro Trp Arg Cys Arg Ser Pro His Arg Val Pro Thr

1 5 10 15  
Pro Ala Ser Ser Ala Ala Ala Pro Leu Pro Ser Ser Ser Ala Ser Ala  
20 25 30  
Pro Ala Pro Pro Pro Leu Arg Ala Ala Ala Gln Gly His Ser Leu Pro  
35 40 45  
Ala Glu Pro Gly Gln Pro Glu Arg Arg Gly Asp Arg Gly Gly Xaa Lys  
50 55 60  
Ile Ile Thr Val Gly Arg Pro Gly Xaa Ser Gly Arg Arg Arg Asn Arg  
65 70 75 80  
Lys Gln Gln Gln Gln Gln Gln Thr Ala Ala Lys Glu Glu Glu Glu  
85 90 95  
Glu Glu Glu Glu Asp Glu Asp Asp Glu Glu Glu Arg Asp Ala Thr Ile  
100 105 110  
Pro Glu Trp  
115

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1502366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

Phe Gly Ser Cys His Gly Gly Ala Ala Leu Pro Thr Ala Cys Pro Arg  
1 5 10 15  
Arg Pro Pro Leu Leu Gln Leu His Ser Arg Arg Pro Arg Pro Pro Leu  
20 25 30  
Pro Leu Arg His Arg Ser Glu Pro Pro Arg Lys Ala Thr Pro Cys Pro  
35 40 45  
Gln Asn Arg Asp Ser Arg Ser Asp Glu Glu Thr Ala Ala Xaa Xaa Arg  
50 55 60  
Ser Ser Arg Ser Gly Gly Arg Xaa Xaa Ala Gly Gly Gly Ala Thr Gly  
65 70 75 80  
Ser Ser Ser Ser Ser Ser Ser Arg Arg Arg Arg Arg Lys Lys Lys Lys  
85 90 95  
Arg Arg Arg Lys Met Arg Thr Thr Arg Arg Ser Val Thr Arg Arg Ser  
100 105 110  
Arg Ser Gly Asp Glu Pro Asp Asp Ala Ala Gly Trp Ala Arg Arg Trp  
115 120 125  
Gly Phe Arg Trp Arg Trp Ala Trp Gly Phe Phe Pro Val Phe Tyr Tyr  
130 135 140  
Leu Lys Ala Xaa Ala Lys Val Asp Val Pro Thr Trp Ile Pro  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1502367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

ttaacttgat tgatttagct gggagtgagc gtcttgctaa aagtggctcc acaggtgatc  
gcttgaagga aactcagtca atcaataaaa gcttgtcggc tttagcgcat gtaactcttcg

60  
120

cgatcgcaaa aggagatgac cacgttccgt tcagaaattc aaaacttaca tacctattgc 180  
agccttgct tggagggtgac tcgaaagctc tcatgtttgt caacatttca ccggagcatc 240  
ctccgttggt gagacgatat ghtcgttgag gtttgcttca aggggtgaatg cttgtgagat 300  
tggaatacca agacgtcaca cataagcccg tcctcttgct ctaggctgaa ttatgggtga 360  
aggtagctgt agggatcatg ataattgtat atataatgtg ttggttttgt ccgatttgg 420  
ccacaaaggt gatgcccaac aaaattcttg taactgtac agtgtaggtg atgtgtg

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Asn Leu Ile Asp Leu Ala Gly Ser Glu Arg Leu Ala Lys Ser Gly Ser  
1 5 10 15  
Thr Gly Asp Arg Leu Lys Glu Thr Gln Ser Ile Asn Lys Ser Leu Ser  
20 25 30  
Ala Leu Ser Asp Val Ile Phe Ala Ile Ala Lys Gly Asp Asp His Val  
35 40 45  
Pro Phe Arg Asn Ser Lys Leu Thr Tyr Leu Leu Gln Pro Cys Leu Gly  
50 55 60  
Gly Asp Ser Lys Ala Leu Met Phe Val Asn Ile Ser Pro Glu His Pro  
65 70 75 80  
Pro Leu Val Arg Arg Tyr Xaa Arg  
85

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..388

(D) OTHER INFORMATION: / Ceres Seq. ID 1502373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

attaacagcc aggaagctgg cgtcttgctt gtccttgctt ttttccacc cggctacc 60  
cgtcgctgcc gccgctttcc cegtggnttc agagctcgag tcggctagct agggccgctg 120  
gctaattccc ctgcctttca taagtacaga gatcaggagg cgggcacact ccatccact 180  
accgctcatg gcgaaggctc acctctacgt ccgccgggcc tgcgccgctg tctctgcgct 240  
cgccgccccc gccctcgccc gcgaccccga catgctcgag gacgtctgcc cggctgacta 300  
cgtcccccgc gtgaagctga acgggtttgc gtgcaaggcg aacttttcgg cggacgactt 360  
ctctttcgac gggctgagga acnccggc

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1502374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His  
1 5 10 15  
Pro Ala Thr Pro Val Val Ala Ala Ala Phe Pro Val Xaa Ser Glu Leu  
20 25 30  
Glu Ser Ala Ser  
35

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Met Ala Lys Val His Leu Tyr Val Ala Ala Ala Cys Ala Val Val Leu  
1 5 10 15  
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp  
20 25 30  
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala  
35 40 45  
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Asp Gly Leu Arg  
50 55 60  
Asn Xaa Gly  
65

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu  
1 5 10 15  
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe  
20 25 30  
Asp Gly Leu Arg Asn Xaa Gly  
35

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

ttaactgttg ctgtcaagac actcaacat gatgggttgc aggggcataa agagtgggtg 60  
gcagaagttg attttcttgg aaaccttcag catccacatc tagtgaatt ggttggtcac 120  
tgcatggaag atgaccagag gtgcttctg tatgaattta tgcccctgtg aagtttgagg 180

aatcatcttt ttagaaagtc attgcctcta ccatggggcca ttagaatgaa aattgctctt 240  
gggtgctgcga aaggccctgcg ttttcttcat gaagaagctg aaagaccagt aatctatcgg 300  
gacttcaaaa cctccaatat tcttttagat gcggactata acgcaaaact ctctgatttt 360  
ggacttgcta aagatggccc tgagggtgat aaaacac

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1502382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

Leu Thr Val Ala Val Lys Thr Leu Asn His Asp Gly Leu Gln Gly His  
1 5 10 15  
Lys Glu Trp Val Ala Glu Val Asp Phe Leu Gly Asn Leu Gln His Pro  
20 25 30  
His Leu Val Lys Leu Val Gly Tyr Cys Ile Glu Asp Asp Gln Arg Leu  
35 40 45  
Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe  
50 55 60  
Arg Lys Ser Leu Pro Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu  
65 70 75 80  
Gly Ala Ala Lys Gly Leu Ala Phe Leu His Gly Glu Ala Glu Arg Pro  
85 90 95  
Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp  
100 105 110  
Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu  
115 120 125  
Gly Asp Lys Thr  
130

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1502383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe Arg Lys Ser Leu Pro  
1 5 10 15  
Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu Gly Ala Ala Lys Gly  
20 25 30  
Leu Ala Phe Leu His Glu Glu Ala Glu Arg Pro Val Ile Tyr Arg Asp  
35 40 45  
Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp Tyr Asn Ala Lys Leu  
50 55 60  
Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu Gly Asp Lys Thr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..480  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:  
aagacctagg gttgcttcct tccttttaac ctgcgcgcgc catccgacgc ccatctcctc 60  
caccagcgcc cngccgcgcg ctaaggagaa gagggtcogg cgtctcctt gccccgatgg 120  
cgctccgagaa gaagcagtc cc aaccgatgc gggagatcaa gtgcagaag ctggtcctca 180  
acatatccgt agggagagcg gcgaccgcct caccgcgcgc gccaaaggtgc tggagcagct 240  
cagcgccgac acccccgctc tctccaagcg gaggtacacg gtgcgctcgt tcggcatccg 300  
gcgtaacgag aagatcgctt gctacgtcac ggtcagggcg gacaaggcca tgcagctgct 360  
tgagagcgcg ctcaaggtca aggagtacga gctgctcagg aggaacttca gcgacaccgg 420  
ctgcttcggg ttcggcatcc aagagcacat cgaccttggt atcaagtatg atccatcaac 480

(2) INFORMATION FOR SEQ ID NO:2153:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 159 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..159  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:  
Arg Pro Arg Val Ala Ser Phe Leu Leu Thr Ser Arg Arg His Pro Thr  
1 5 10 15  
Pro Ile Ser Ser Thr Gln Pro Xaa Pro Pro Lys Glu Lys Arg Val  
20 25 30  
Arg Pro Ser Pro Cys Pro Asp Gly Val Arg Glu Glu Ala Val Gln Pro  
35 40 45  
Asp Ala Gly Asp Gln Gly Ala Glu Ala Gly Pro Gln His Ile Arg Arg  
50 55 60  
Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu Glu Gln Leu  
65 70 75  
Ser Gly Gln Thr Pro Val Phe Ser Lys Ala Arg Tyr Thr Val Arg Ser  
85 90 95  
Phe Gly Ile Arg Arg Asn Glu Lys Ile Ala Cys Tyr Val Thr Val Arg  
100 105 110  
Gly Asp Lys Ala Met Gln Leu Leu Glu Ser Gly Leu Lys Val Lys Glu  
115 120 125  
Tyr Glu Leu Leu Arg Arg Asn Phe Ser Asp Thr Gly Cys Phe Gly Phe  
130 135 140  
Gly Ile Gln Glu His Ile Asp Leu Gly Ile Lys Tyr Asp Pro Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2154:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 121 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..121  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:  
Met Ala Ser Glu Lys Lys Gln Ser Asn Pro Met Arg Glu Ile Lys Val

1	5	10	15
Gln Lys Leu Val Leu Asn Ile Ser Val Gly Arg Ala Ala Thr Ala Ser	20	25	30
Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser Ala Ala Arg Pro Pro Ser	35	40	45
Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg Ser Ala Ser Gly Val Thr	50	55	60
Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly Ala Thr Arg Pro Cys Ser	65	70	75
Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser Thr Ser Cys Ser Gly Gly	85	90	95
Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser Ala Ser Lys Ser Thr Ser	100	105	110
Thr Leu Val Ser Ser Met Ile His Gln	115	120	

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile Ser Val Gly	1	5	10	15
Arg Ala Ala Thr Ala Ser Pro Ala Pro Pro Arg Cys Trp Ser Ser Ser	20	25	30	35
Ala Ala Arg Pro Pro Ser Ser Pro Arg Arg Gly Thr Arg Cys Ala Arg	40	45	50	55
Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg Ser Gly	60	65	70	75
Ala Thr Arg Pro Cys Ser Cys Leu Arg Ala Ala Ser Arg Ser Arg Ser	80	85	90	95
Thr Ser Cys Ser Gly Gly Thr Ser Ala Thr Pro Ala Ala Ser Gly Ser	100	105	110	
Ala Ser Lys Ser Thr Ser Thr Leu Val Ser Ser Met Ile His Gln	115	120		

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

attcagccca	tcgtagctc	tcgcgtctc	ctgtctctc	ctagtacac	aagaccacga	60
gggattaagc	gatgacaacc	tctaagctcg	ctgtctctac	ctgtgttgcc	ctgctcggtc	120
cagtgtaag	ccagtcgggt	ggctactact	tctacccaa	cccgacgaa	ccatctccaa	180
ccaccagccc	tcctcttagt	ccgcaactca	tggtcggata	ctacaaggac	aagtgtgccg	240
cttaagtgga	tggtgaagct	attgtcaaga	agcaagtcac	ggccaccgat	gctggcatgc	300
aggcggggct	tggtccgtctc	tattccacg	actgcttcgt	ccgtggatgc	gacggctccg	360
tcctctctga	cacgttcagc	aacgacacac	gcctgacccc	agagaagttc	ggcgtgcccc	420
acttccccag	ctgcgggggc	ttcagaggtga	tcgacgcggc	caaggccgag	atcgagggc	

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

Met	Thr	Thr	Ser	Lys	Leu	Ala	Val	Leu	Thr	Leu	Phe	Ala	Leu	Leu	Gly
1				5					10					15	
Ser	Val	Ser	Cys	Gln	Ser	Gly	Gly	Tyr	Tyr	Phe	Tyr	Pro	Thr	Pro	Gln
				20				25						30	
Gln	Pro	Ser	Pro	Thr	Pro	Ser	Pro	Pro	Ser	Ser	Pro	Gln	Leu	Met	Val
				35				40					45		
Gly	Tyr	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu	Ala	Ile
				50			55					60			
Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln	Ala	Gly	Leu
				65			70				75			80	
Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser
				85				90						95	
Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr	Pro	Glu	Lys
				100				105					110		
Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile	Asp
				115			120						125		
Ala	Ala	Lys	Ala	Glu	Ile	Glu									
				130			135								

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met	Val	Gly	Tyr	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu
1				5					10					15	
Ala	Ile	Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln	Ala
				20				25					30		
Gly	Leu	Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp
				35				40					45		
Gly	Ser	Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr	Pro
				50				55				60			
Glu	Lys	Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu	Val
				65			70				75			80	
Ile	Asp	Ala	Ala	Lys	Ala	Glu	Ile	Glu							
				85											

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..437  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

aacccttttcg	cctcgcgcgc	cgccctgatac	ctccagcgcgc	ctcgcgcgtcg	gctgcgccggc	60
tgccgctcctc	ccgctacgag	ctaggcatct	ccttcgcgga	tccagcatgg	gtaagacacg	120
tggtatggga	gctgggcgca	asstcaagac	ccacaggagg	aaccagaggt	ggtgctgaca	180
aagcctacaa	gaagagccat	cttggaacg	agtggaaaga	accctttgtc	ggatcatctc	240
acgcaaaagg	gatcgtcttc	gaaaagatcg	gcacgcaggc	caagcagcct	aactctgcta	300
ttcgtaagtg	tgctcgtgtt	cagctgggtg	agaacggtga	gaagattgcc	gcctttgtgc	360
cgaacgacgg	ctgcttgtaac	tacatcgagg	aaaacgatga	gggtgctgac	gcgggggttcg	420
gtcgtaaggg	ccacgct					

(2) INFORMATION FOR SEQ ID NO:2160:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

Pro	Phe	Arg	Leu	Arg	Arg	Arg	Leu	Ile	Ala	Pro	Ser	Pro	Ser	
1			5				10				15			
Ala	Ala	Arg	Leu	Pro	Ser	Ser	Arg	Tyr	Glu	Leu	Gly	Ile	Ser	Phe
			20					25			30			
Asp	Pro	Ala	Trp	Val	Arg	His	Val	Val	Trp	Glu	Leu	Gly	Ala	Xaa
			35				40				45			
Arg	Pro	Thr	Gly	Gly	Thr	Arg	Gly	Gly	Ala	Asp	Lys	Ala	Tyr	Lys
			50				55			60				
Ser	His	Leu	Gly	Asn	Glu	Trp	Lys	Lys	Pro	Phe	Ala	Gly	Ser	Ser
			65				70			75				
Ala	Lys	Gly	Ile	Val	Leu	Glu	Lys	Ile	Gly	Ile	Glu	Ala	Lys	Gln
			85				90				95			
Asn	Ser	Ala	Ile	Arg	Lys	Cys	Ala	Arg	Val	Gln	Leu	Val	Lys	Asn
			100				105				110			
Lys	Lys	Ile	Ala	Ala	Phe	Val	Pro	Asn	Asp	Gly	Cys	Leu	Asn	Tyr
			115				120				125			
Glu	Glu	Asn	Asp	Glu	Val	Leu	Ile	Ala	Gly	Phe	Gly	Arg	Lys	Gly
			130				135				140			
Ala														
145														

(2) INFORMATION FOR SEQ ID NO:2161:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 501 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..501  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

aaagtgaata	cagaaacctc	cagccccagg	ccaattcttc	gaccgcgatcg	ccacccaccc	60
catctccatg	gtactctcgc	cgacctcacc	gcgggggaaga	aggtgggtct	cttcgcgctg	120
ccggggscgt	tcacgcccac	ctgcacccag	aagcacctcc	cgggggttctg	ggccaaggcc	180
ggggagctcc	gcgccaaggg	ctcgacaccc	tgccctgcgt	ctccgtcaac	gacgccttcg	240

tgatgcgcgc gtggaaggag agtctgggga tcggggacga ggtgctgctc ctgtcggagc 300  
gcaacggcgc gctggcgccgc gcatgggctc gagctcgacc tctccgacaa gcccgtaggg 360  
tcggcgctcc gttcccgccgc tacgsgctgc tcggggagga cggcgtaggtc aaggtgatac 420  
acctcgagga gggcgccgcgc ttcaccaaca gcagcgccga ggacatgctc aacgcgctct 480  
gaactcgcca cgccatgggtt g

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

Lys Val Asn Thr Glu Thr Ser Ser Pro Arg Pro Ile Pro Arg Pro His  
1 5 10  
Arg His Pro Pro His Leu His Gly Tyr Leu Arg Asp Leu Thr Ala Gly  
20 25 30  
Lys Lys Val Val Leu Phe Ala Val Pro Xaa Xaa Phe Thr Pro Thr Cys  
35 40 45  
Thr Gln Lys His Leu Pro Gly Phe Val Ala Lys Ala Gly Glu Leu Arg  
50 55 60  
Ala Lys Gly Ser Thr Pro Trp Pro Ala Ser Pro Ser Thr Thr Pro Ser  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

Ser Glu Tyr Arg Asn Leu Gln Pro Gln Ala Asn Ser Ser Thr Ala Ser  
1 5 10 15  
Pro Pro Thr Pro Ser Pro Trp Leu Pro Pro Arg Pro His Arg Gly Glu  
20 25 30  
Glu Gly Gly Ala Leu Arg Arg Ala Arg Xaa Val His Ala His Leu His  
35 40 45  
Pro Glu Ala Pro Pro Gly Val Arg Gly Gln Gly Arg Gly Ala Pro Arg  
50 55 60  
Gln Gly Leu Asp Thr Val Ala Cys Val Ser Val Asn Asp Ala Phe Val  
65 70 75 80  
Met Arg Ala Trp Lys Glu Ser Leu Gly Ile Gly Asp Glu Val Leu Leu  
85 90 95  
Leu Ser Asp Gly Asn Gly Glu Leu Ala Arg Ala Trp Ala Arg Ala Arg  
100 105 110  
Pro Leu Arg Gln Ala Arg Gly Val Gly Val Arg Ser Arg Arg Tyr Xaa  
115 120 125  
Leu Leu Ala Glu Asp Gly Val Val Lys Val Ile Asn Leu Glu Glu Gly  
130 135 140  
Gly Ala Phe Thr Asn Ser Ser Ala Glu Asp Met Leu Asn Ala Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:

Met	Ala	Thr	Ser	Ala	Thr	Ser	Pro	Arg	Gly	Arg	Arg	Trp	Cys	Ser	Ser
1			5						10					15	
Pro	Cys	Pro	Xaa	Arg	Ser	Arg	Pro	Pro	Ala	Pro	Arg	Ser	Trp	Ser	Arg
			20						25				30		
Gly	Ser	Trp	Pro	Arg	Pro	Gly	Ser	Ser	Ala	Pro	Arg	Ala	Arg	His	Arg
			35				40						45		
Gly	Leu	Arg	Leu	Arg	Gln	Arg	Arg	Leu	Arg	Asp	Ala	Arg	Val	Glu	Gly
			50			55						60			
Glu	Ser	Gly	Asp	Arg	Gly	Arg	Gly	Ala	Ala	Pro	Val	Gly	Arg	Gln	Arg
			65			70				75				80	
Arg	Ala	Gly	Ala	Arg	Met	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Thr	Ser	Pro
					85				90					95	
Trp	Gly	Arg	Arg	Pro	Val	Pro	Pro	Leu	Xaa	Ala	Ala	Arg	Gly	Gly	Arg
					100				105				110		
Arg	Gly	Gln	Gly	Asp	Gln	Pro	Arg	Gly	Gly	Arg	Arg	Val	His	Gln	Gln
			115			120							125		
Gln	Arg	Arg	Gly	His	Ala	Gln	Arg	Ala	Leu	Asn	Ser	Arg	Arg	His	Gly
			130			135						140			

(2) INFORMATION FOR SEQ ID NO:2165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:

acgatcacac	accactccac	agcagtagca	agagggatag	agcaaggcca	cacacacaca	60
caccactagg	ctaggttagc	cttttagtcg	tcgtcgagga	gcaagaaggg	cgcgacgcga	120
agcaggcaag	caagaagaga	gcgcgatgcg	cgagagctag	cacgcgatgg	cgagggtctt	180
caagatgatg	gttgcgccas	stctgctggc	ctgggccctg	gcctgtgtcg	ccgccgagcc	240
gaggaaatc	aagacgcaga	cgacggagaa	gaaggacgac	gcggtgtgtc	agccgcagac	300
attccccgcc	ttcgaccgcc	tcggcgggcg	gcgtccccgg	cgttcggggg	cctccccggg	360
ggcagcattc	ctgcagcag	cattccccgg	ttcagcat			

(2) INFORMATION FOR SEQ ID NO:2166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

Met Ala Arg Ser Ser Lys Met Met Val Ala Ala Xaa Leu Leu Ala Leu  
1 5 10 15  
Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr  
20 25 30  
Thr Glu Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro  
35 40 45  
Phe Asp Arg Leu Gly Gly Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro  
50 55 60  
Ala Ala Ala Phe Leu Ala Ala Ala Phe Pro Gly Ser Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

Met Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr  
1 5 10 15  
Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Glu Lys Lys Asp Asp  
20 25 30  
Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly  
35 40 45  
Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Phe Leu Ala  
50 55 60  
Ala Ala Phe Pro Gly Ser Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr Ala  
1 5 10 15  
Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp Asp Ala  
20 25 30  
Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly Ala  
35 40 45  
Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Phe Leu Ala Ala  
50 55 60  
Ala Phe Pro Gly Ser Ala  
65 70

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(2) INFORMATION FOR SEQ ID NO:2171:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 120 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..120
      (D) OTHER INFORMATION: / Ceres Seq. ID 1502443
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:
Val His Gly Arg Arg Gly Pro Cys Pro Pro Ala Phe Leu Arg Ser Leu
1          5          10
Asp Leu Arg His Asn Gln Leu Thr Gly Pro Ile Pro Ala Gly Trp Cys
20          25          30
Arg Gly Ser Ser Gly Arg Trp Ser Cys Pro Thr Thr Ser Ser Arg Ala
35          40          45
Pro Ser Arg Ala Thr Thr Xaa Xaa Glu Ile Asn Thr Val Asp Leu Ser

```

50	55	60
His Asn Arg Leu Thr Gly Asp Pro Ser His Leu Phe Arg Arg Arg Pro		
65	70	75
Ala His Ser Ala Arg Trp Thr Cys Arg Gly Thr Thr Ser Thr Ser Thr		80
	85	90
Ser Ala Gly Trp Cys Ser Arg Arg Ser Ser Arg Thr Trp Thr Cys Pro		95
	100	105
Thr Thr Ser Ser Ala Ala Pro Cys		110
	115	120

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

aaaaacctag ccaacctag tccgcccans stntcgccgc cgcacacctc tcccgctgcc	60
ccctctccgc gegggcgcat ccaacggggc cgtctccgcg cgcaaccacg gggggcgcac	120
ggctgagcgt ctggggcccg accccgcccgc tggtgngcgt caectccgcg aaggkcgccg	180
tcggaaaagat saaccacacc gccaacctcg ccgcctctct cgcgcgcctc ggctccag	240
ccgtcgccgt cgacgcccgt gctggcctcc gcaacctega cctctgctc ggctccgaga	300
accggtccca cctaccggcc gccgcacdtcc tgcggggaga ctgccgactc gaccaggcgc	360
tcgtccgcca cgcgcgcgt ccagacactc cacttc	

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

Lys Thr Leu Ala Asn Pro Ser Pro Pro Xaa Xaa Ser Arg Ala Ala Pro	
1	10
Pro Pro Ala Ala Pro Ser Ser Gly Gly Gly Ile His Ala Gly Arg Leu	15
	20
Arg Ala Gln Pro Arg Gly Ala His Gly Xaa Ser Ser Arg Ala Arg Pro	25
	30
Arg Ala Trp Trp Xaa Ser Pro Pro Ala Arg Xaa Ala Ser Glu Arg Xaa	35
	40
Pro Pro Pro Pro Thr Ser Pro Pro Leu Ser Arg Ala Ser Ala Ser Gln	45
65	50
Pro Ser Pro Ser Thr Pro Met Leu Ala Ser Ala Thr Ser Thr Ser Cys	55
	60
Ser Ala Ser Arg Thr Ala Ser Thr Ser Pro Pro Pro Xaa Ser Ser Arg	65
	70
Glu Thr Ala Asp Ser Thr Arg Arg Ser Ser Ala Thr Ala Arg Phe His	75
	80
Asp Leu His Leu	85
	90
	95
	100
	105
	110
	115
	120
	125
	130

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1.497  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502479

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

caaaggatgt	caagaaggag	gctccaaagg	aggcccccaa	gccaaagggtg	gttgaggcac	60
cagcagaaga	gaagcacca	aaagccaaagc	caaagaatcc	tcttgacttg	ctgccaccaa	120
gcaagatggt	ccttgatgac	tgggaaggagc	tatactcaaa	cacaagaact	aacttccggg	180
agggttccat	caaaggtttc	tgggacatgt	acgaccacga	ggctactctt	tgtggttctg	240
tgactacaag	tacaatgatg	agaacaccgt	ctcctttgtg	accctgaaca	aggttggtgg	300
attcctgcag	cggatggacc	tgtgcccga	gtacgccttt	gggaagatgc	tcgtgatagg	360
ctctgagcca	cccttcaagc	tgaagggcct	tgtgctcttc	cgtggccagg	atgttcccaa	420
gtttgtaatg	gacgagggtc	atgacatgga	gctctacgag	tgggaccaag	gtggacatct	480
ctgatgaggc	cagaagg					

- (2) INFORMATION FOR SEQ ID NO:2175:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..80  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502480

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

Gln	Arg	Met	Ser	Arg	Arg	Leu	Gln	Arg	Pro	Pro	Ser	Gln	Arg
1			5				10				15		
Trp	Leu	Arg	His	Gln	Gln	Lys	Arg	Lys	His	Gln	Ser	Gln	Ser
			20				25				30		
Ile	Leu	Leu	Thr	Cys	Cys	His	Gln	Ala	Arg	Trp	Ser	Leu	Met
			35				40				45		
Arg	Gly	Tyr	Thr	Gln	Thr	Gln	Arg	Leu	Thr	Ser	Gly	Arg	Leu
			50				55				60		
Lys	Val	Ser	Gly	Thr	Cys	Thr	Thr	Gln	Arg	Leu	Leu	Phe	Val
			65				70				75		80

- (2) INFORMATION FOR SEQ ID NO:2176:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..92  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502481

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

Lys	Asp	Val	Lys	Lys	Glu	Ala	Pro	Lys	Glu	Ala	Pro	Lys	Pro	Lys	Val
1			5				10				15				
Val	Glu	Ala	Pro	Ala	Glu	Glu	Glu	Ala	Pro	Lys	Pro	Lys	Pro	Lys	Asn
			20				25				30				
Pro	Leu	Asp	Leu	Leu	Pro	Pro	Ser	Lys	Met	Val	Leu	Asp	Asp	Trp	Lys
			35				40				45				
Arg	Leu	Tyr	Ser	Asn	Thr	Lys	Thr	Asn	Phe	Arg	Glu	Val	Ala	Ile	Lys

(2) INFORMATION FOR SEQ ID NO:2177:

(A) LENGTH: 78 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..78

SEQUENCE DESCRIPTION: SEQ ID NO:2177:

Met	Ser	Arg	Arg	Arg	Leu	Gln	Arg	Arg	Pro	Pro	Ser	Gln	Arg	Trp	Leu
1				5					10					15	
Arg	His	Gln	Gln	Lys	Arg	Lys	His	Gln	Ser	Gln	Ser	Gln	Arg	Ile	Leu
			20					25					30		
Leu	Thr	Cys	Cys	His	Gln	Ala	Arg	Trp	Ser	Leu	Met	Thr	Gly	Arg	Gly
		35					40					45			
Tyr	Thr	Gln	Thr	Gln	Arg	Leu	Thr	Ser	Gly	Arg	Leu	Pro	Ser	Lys	Val
	50					55					60				
Ser	Gly	Thr	Cys	Thr	Thr	Gln	Arg	Leu	Leu	Phe	Val	Val	Leu		
65				70						75					

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2178:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1502488

Met Gly Leu Leu Ser Ile Ile Arg Lys Ile Lys Arg Lys Glu Lys Glu  
1 5 10 15

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile  
20 25 30  
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu  
35 40 45  
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile  
50 55 60  
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr  
65 70 75 80  
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile  
85 90 95  
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu  
100 105 110  
Glu Arg Leu Val Gly Ala  
115

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile  
1 5 10 15  
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu  
20 25 30  
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile  
35 40 45  
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr  
50 55 60  
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile  
65 70 75 80  
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu  
85 90 95  
Glu Arg Leu Val Gly Ala  
100

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1502490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile Val Leu Lys Ile  
1 5 10 15  
Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu Gly Phe Asn Ile  
20 25 30  
Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile Trp Asp Val Gly  
35 40 45  
Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr  
50 55 60  
Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile Arg Arg Leu Asp

Gly Ala

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502514

- |              |             |             |             |             |             |     |
|--------------|-------------|-------------|-------------|-------------|-------------|-----|
| aacatctcttaa | tcgaaaaaaa  | gctctctgtct | tcctctctcca | tatttttcac  | tcatttcggcg | 60  |
| ccgcgcgcgc   | cctctctctgt | cactcgcgcac | ggccgcgcgat | aagttgcacg  | agctgcgcggc | 120 |
| aaagagcaac   | acggatctctg | aagcgcgmsst | caaggagcct  | aaatcgcgagc | tcctcctctct | 180 |
| acgcgttcgc   | awgttcacgc  | cgggcggtctc | caacaagctc  | tcctaaaatc  | agattgtgtcg | 240 |
| cacctctcac   | gctcgcgtgc  | tcacctgttat | ctcgcgaagc  | cagaagtctgc | cgctcgcgtga | 300 |
| ggcgtctaca   | gaagaagacg  | ttctcccgct  | cgatctccgc  | cccaagaaga  | ccgcgcgatc  | 360 |
| tcgtagcgcg   | ctcaccaagc  | accagctctc  | cttgaagaac  | gagagggaaa  | agaagcgtga  | 420 |
| gcgaagtatt   | ccatgcgcga  | agtcagctat  | caaggcctcga | at          |             |     |

(i) SEQUENCE CHARACTERISTICS:

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502515

- [illegible]

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1502516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

Met	Ala	Arg	Ile	Lys	Val	His	Glu	Leu	Arg	Gly	Lys	Ser	Lys	Thr	Asp	
1				5						10				15		
Leu	Gln	Ala	Xaa	Xaa	Lys	Glu	Leu	Lys	Ser	Glu	Leu	Ser	Leu	Leu	Arg	
			20					25					30			
Val	Ala	Xaa	Val	Thr	Gly	Gly	Ala	Pro	Asn	Lys	Leu	Ser	Lys	Ile	Lys	
			35				40					45				
Ile	Val	Arg	Thr	Ser	Ile	Ala	Arg	Val	Leu	Thr	Val	Ile	Ser	Gln	Lys	
			50				55				60					
Gln	Lys	Ser	Ala	Leu	Arg	Glu	Ala	Tyr	Lys	Lys	Lys	Lys	Leu	Leu	Pro	
					70				75					80		
Leu	Asp	Leu	Arg	Pro	Lys	Lys	Thr	Arg	Ala	Ile	Arg	Arg	Arg	Leu	Thr	
				85				90						95		
Lys	His	Gln	Leu	Ser	Leu	Lys	Thr	Glu	Arg	Glu	Lys	Lys	Arg	Glu	Lys	
				100				105					110			
Tyr	Phe	Pro	Met	Arg	Lys	Tyr	Ala	Ile	Lys	Ala						
				115			120									

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1502517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

tccattgcag	tgcaggaatc	ggaaggactg	gtacttacat	cacaatccat	actacaattg	60
agcgaaattct	tcttgagat	aaaagctctt	acgatcttgc	caaaactgta	aaghaattta	120
gatcccaacg	acctgggatg	gtccaaacag	aggaacaata	caagttctgc	tacaggggcaa	180
ttgctgtacg	agctgaaga	cctgctaaat	tcagatcatt	gagggtgggc	acatgagacg	240
gacagcaacg	ckkctagcat	ttattacgtt	tttttagaca	tttctatgtg	aagggaacact	300
tacccttttag	aggagtgaat	tagtcaatct	cagttctctt	taaaactatgt	ttgttctagt	360
caaaatctat	gtaataaaaa	atctatcata	tgtgaagcta	tgctatgttt	ttgactaatc	420
gttgctatta	ctaccgt					

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	Tyr	Ile	Thr	Ile	His	
1				5				10					15			
Thr	Thr	Ile	Glu	Arg	Ile	Leu	Leu	Gly	Asp	Lys	Ser	Ser	Tyr	Asp	Leu	
			20					25					30			
Ala	Lys	Thr	Val	Lys	Asn	Phe	Arg	Ser	Gln	Arg	Pro	Gly	Met	Val	Gln	
			35				40					45				
Thr	Glu	Glu	Gln	Tyr	Lys	Phe	Cys	Tyr	Arg	Ala	Ile	Ala	Val	Arg	Ala	

50 55 60  
Glu Arg Pro Ala Lys Phe Arg Ser Leu Arg Trp Val Thr  
65 70 75  
(2) INFORMATION FOR SEQ ID NO:2187:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..469  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502519  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:  
attctccag ccacaaatcg atcggaacg cagccccc tctcttgcg ttttcgcgtc 60  
gtccagatct cagtcgttct tgcctccatg agctaggaat ccgaggtgtc ctctaggcta 120  
agcgaagtgt gcgcggcggc gctaggatgg gttgatata cgggatgatg atgggggtca 180  
ttgttgcggt gcgatcatgg ccggtgtggag ccgcgtcatg gcgcgacgca gcacgaagcg 240  
catcgccaag gctgcggata tcaagggtgt tgggtctctc agcaggagac accctcaggaa 300  
gctgtgcgnt gataacttcc cggagttggat atcttccc cagtttgagc aggttaaatg 360  
gttgacaacg catctgagca aactttggcc tttgttgta gaagctgcaa cagtagtggt 420  
taagggaatc cgttgaacca ctgctagatg attacgggcc tccaggaaat  
(2) INFORMATION FOR SEQ ID NO:2188:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..72  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502520  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:  
Met Gly Leu Ile Ser Gly Met Met Met Gly Val Ile Val Gly Val Ala  
1 5 10 15  
Ser Trp Pro Ala Gly Ala Ala Ser Cys Ala Asp Ala Ala Arg Ser Ala  
20 25 30  
Ser Pro Arg Leu Arg Ile Ser Arg Cys Leu Gly Leu Ser Ala Gly Thr  
35 40 45  
Thr Ser Gly Ser Cys Ala Xaa Ile Thr Ser Arg Ser Gly Tyr Pro Ser  
50 55 60  
Arg Ser Leu Ser Arg Leu Asn Gly  
65 70  
(2) INFORMATION FOR SEQ ID NO:2189:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 79 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502521  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:  
Met Ala Gly Trp Ser Arg Val Met Arg Arg Ser Thr Lys Arg Ile  
1 5 10 15  
Ala Lys Ala Ala Asp Ile Lys Val Leu Gly Ser Leu Ser Arg Asp Asp  
20 25 30

Leu Arg Lys Leu Cys Xaa Asp Asn Phe Pro Glu Trp Ile Ser Phe Pro  
35 40 45  
Gln Phe Glu Gln Val Lys Trp Leu Asn Lys His Leu Ser Lys Leu Trp  
50 55 60  
Pro Phe Val Val Glu Ala Ala Thr Val Val Val Lys Gly Ile Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Met Arg Arg Arg Ser Thr Lys Arg Ile Ala Lys Ala Ala Asp Ile Lys  
1 5 10 15  
Val Leu Gly Ser Leu Ser Arg Asp Asp Leu Arg Lys Leu Cys Xaa Asp  
20 25 30  
Asn Phe Pro Glu Trp Ile Ser Phe Pro Gln Phe Glu Gln Val Lys Trp  
35 40 45  
Leu Asn Lys His Leu Ser Lys Leu Trp Pro Phe Val Val Glu Ala Ala  
50 55 60  
Thr Val Val Val Lys Gly Ile Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

atagacagga agattgaatt tccaaatcct aacgaggatt cacgtttcga tatcttgaag 60  
atccattcaa gaaaaatgaa cttgatgcgt ggcattgac tgaaaaagat cgcggaagaag 120  
atgaatgggg cctcaggagc tgaagctcaa gccgtctgca cagaggctgg aatgtttgct 180  
cttcgtgaga gaagggtgca cgttaccacg gaggacttcg agatggcagt ggccaagggtg 240  
atgaagaaag acacgagaga gaacatgtcc ctgcgcaaaa tctggaagtg aggcctcgtgc 300  
ccaccctttca cgcgcctccc gaagctagtgc gcagtgccct catatccata tcttttacc 360  
aagcagtga atgggtgtaac ggcattgctt ggacaatgtt atctcaagtt gcgcgcgcg

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe  
1 5 10 15

Asp	Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile	
		20						25					30			
Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu	
		35					40					45				
Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg	
		50					55				60					
Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val	
		65				70				75				80		
Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Xaa	Xaa	Trp	Lys	
			85					90						95		

(2) INFORMATION FOR SEQ ID NO:2193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

Met	Asn	Leu	Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	
1																
Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	
Met	Phe	Ala	Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	
Glu	Met	Ala	Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	
Ser	Leu	Arg	Xaa	Xaa	Trp	Lys										

(2) INFORMATION FOR SEQ ID NO:2194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1502530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	
1																
Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	
Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	
Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	
Xaa	Xaa	Trp	Lys													

(2) INFORMATION FOR SEQ ID NO:2195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..511  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502542  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:  
gcaccgcgcc cacagcctcg cgtcgtcgcc ccacagccac ggcgagcassncc gccgatccgc 60  
gagcgagat cgcggaagcca ggcggcgcnag agggagctcg aggcggcgga ggaagcggtt 120  
cgacagctcg ctgatttccc tggggaagag atggggctct cctttggtaa gctgttcaag 180  
cgctcttccg ccaagaagga gatgaggatt ctcatggtcg ggctcgatcg cgccggtaag 240  
accaccatcc tctacaagct caagctcgcc gagatcgta ccacatccc cactatcgga 300  
ttcaatgttg aaactgttga gtataagaac attagcttca ctgtttggga tgttggtggc 360  
caggacaaga tcaggccccc gtggaggcac tactttcaga acacacaggg acttattttt 420  
gttgtagaca gcaacgacag gaaacgtgtt gttgaggcta gagatgagct ccacaggatg 480  
(2) INFORMATION FOR SEQ ID NO:2196:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 170 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..170  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502543  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:  
Ala Pro Arg Pro Gln Pro Arg Val Val Ala Pro Gln Pro Arg Glu Xaa  
1 5 10 15  
Xaa Pro Ile Arg Glu Arg Arg Ser Arg Ser Gln Ala Ala Xaa Arg Glu  
20 25 30  
Leu Glu Ala Ala Glu Glu Gly Val Arg Thr Val Ala Asp Phe Pro Gly  
35 40 45  
Glu Glu Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala  
50 55 60  
Lys Lys Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys  
65 70 75 80  
Thr Thr Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile  
85 90 95  
Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser  
100 105 110  
Phe Thr Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp  
115 120 125  
Arg His Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser  
130 135 140  
Asn Asp Arg Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met  
145 150 155 160  
Leu Asn Glu Asp Glu Leu Arg Asp Ala Val 165 170  
(2) INFORMATION FOR SEQ ID NO:2197:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 120 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..120  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:  
Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
1 5 10 15  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
35 40 45  
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
50 55 60  
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
65 70 75 80  
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
85 90 95  
Arg Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn  
100 105 110  
Glu Asp Glu Leu Arg Asp Ala Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1502545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile  
1 5 10 15  
Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile  
20 25 30  
Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val  
35 40 45  
Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr  
50 55 60  
Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg  
65 70 75 80  
Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu  
85 90 95  
Asp Glu Leu Arg Asp Ala Val  
100

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..488

(D) OTHER INFORMATION: / Ceres Seq. ID 1502573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

aggaggagcg	cgccatggag	cgggggcatc	ctgccgctgc	tccgccgcgc	cacgctgggtg	60
cagacgttgc	gccagcgcaa	ccacgtgtgc	ctgcaggagc	gctccatcac	cgctcccgccc	120
tacgccgacc	cgggcaagat	gcaggcgcac	ctcatcagcc	ccggcacgcc	gcgctccatc	180
ttcgtctact	tcaggggcct	ctttctacgac	atgggcaacg	accgccaggg	cggtctactac	240
gccaggggcc	tcgccgctgc	gtgtgggaga	acttcaagga	caaccgcgtg	ttcgacatct	300
cgacggagca	ccgctgcagc	tactacgagc	acatgcagcg	cgccatcttc	tgcctgtgcc	360

cgctgggggtg ggcgccttgg agcccccggc tggtaggagc ggtggtgttc ggggtcatcc 420  
ccgtcatcat cgccgacgac atcgtgctgc cgttcgcgga cgccatcccc tgggaggaca 480  
tcagcgtg

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

Arg Arg Ser Ala Pro Trp Ser Gly Gly Ile Leu Pro Leu Leu Arg Arg  
1 5 10 15  
Ala Thr Leu Val Gln Thr Phe Gly Gln Arg Asn His Val Cys Leu Gln  
20 25 30  
Asp Gly Ser Ile Thr Val Pro Pro Tyr Ala Asp Pro Gly Lys Met Gln  
35 40 45  
Ala His Leu Ile Ser Pro Gly Thr Pro Arg Ser Ile Phe Val Tyr Phe  
50 55 60  
Arg Gly Leu Phe Tyr Asp Met Gly Asn Asp Pro Glu Gly Gly Tyr Tyr  
65 70 75 80  
Ala Arg Gly Leu Ala Arg Arg Cys Gly Arg Thr Ser Arg Thr Thr Arg  
85 90 95  
Cys Ser Thr Ser Arg Arg Ser Thr Arg Arg Arg Thr Thr Arg Thr Cys  
100 105 110  
Ser Ala Pro Ser Ser Ala Cys Ala Arg Trp Gly Gly Arg Pro Gly Ala  
115 120 125  
Pro Gly Trp Trp Arg Arg Trp Cys Ser Gly Ala Ser Pro Ser Ser Ser  
130 135 140  
Pro Thr Thr Ser Cys Cys Arg Ser Arg Thr Pro Ser Pro Gly Arg Thr  
145 150 155 160  
Ser Ala

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Gly Gly Ala Arg His Gly Ala Gly Ala Ser Cys Arg Cys Ser Ala Ala  
1 5 10 15  
Pro Arg Trp Cys Arg Arg Ser Ala Ser Ala Thr Thr Cys Ala Cys Arg  
20 25 30  
Thr Ala Pro Ser Pro Ser Arg Pro Thr Pro Thr Arg Ala Arg Cys Arg  
35 40 45  
Arg Thr Ser Ser Ala Pro Ala Arg Arg Ala Pro Ser Ser Ser Thr Ser  
50 55 60  
Gly Ala Ser Ser Thr Thr Trp Ala Thr Thr Pro Arg Ala Ala Thr Thr  
65 70 75 80  
Pro Gly Ala Ser Arg Val Gly Val Gly Glu Leu Gln Gly Gln Pro Ala  
85 90 95

Val Arg His Leu Asp Gly Ala Pro Val Asp Val Leu Arg Gly His Ala  
100 105 110  
Ala Arg His Leu Leu Pro Val Pro Ala Gly Val Gly Ala Leu Glu Pro  
115 120 125  
Pro Ala Gly Gly Gly Gly Val Arg Val His Pro Arg His His Arg  
130 135 140  
Arg Arg His Arg Ala Ala Val Arg Gly Arg His Pro Leu Gly Gly His  
145 150 155 160  
Gln Arg

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

Glu Glu Arg Ala Met Glu Arg Gly His Pro Ala Ala Ala Pro Pro Arg  
1 5 10 15  
His Ala Gly Ala Asp Val Arg Pro Ala Gln Pro Arg Val Pro Ala Gly  
20 25 30  
Arg Leu His His Arg Pro Ala Leu Arg Arg Pro Gly Gln Asp Ala Gly  
35 40 45  
Ala Pro His Gln Pro Arg His Ala Ala Leu His Leu Arg Leu Leu Gln  
50 55 60  
Gly Pro Leu Leu Arg His Gly Gln Arg Pro Arg Gly Arg Leu Leu Arg  
65 70 75 80  
Gln Gly Pro Arg Ala Ser Val Trp Glu Asn Phe Lys Asp Asn Pro Leu  
85 90 95  
Phe Asp Ile Ser Thr Glu His Pro Ser Thr Tyr Tyr Glu Asp Met Gln  
100 105 110  
Arg Ala Ile Phe Cys Leu Cys Pro Leu Gly Trp Ala Pro Trp Ser Pro  
115 120 125  
Arg Leu Val Glu Ala Val Val Phe Gly Cys Ile Pro Val Ile Ile Ala  
130 135 140  
Asp Asp Ile Val Leu Pro Phe Ala Asp Ala Ile Pro Trp Glu Asp Ile  
145 150 155 160  
Ser Val

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1502613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

ctctcgtct cgggtctcca gtctcgtgc ttccacaagt ccacaaccgt accagcacca 60  
ccgcgcgatg gegtctctccg cccatccmga tgcgcgccag ccaccatccg cncgcagacc 120  
ggagcccgca cgggaaggcag tccgcgtggt ggtgaagggg cgcgtcacgg ggggtggggtt 180  
ccgcgactgg actcgtctac ggccgagtcg ctccgctcgc cggctgggtc cgaacaggcc 240  
gtgacggcag tgtggaggcc ctctctctccg gagacccccc gaagatcgaa gacatgataa 300

ccccgccgct ccccgctggc cccccagcgc ccaccgtcac cgccgctcgc cgtccackg 360  
ccgagcccggt ggatccgct caccggtctt ggagatcaag ttcaccgtct gaccccccg 420  
tcccgcgaca gggtcgcgtc tcgccccgcg ggtcttgaaac ggtctattcg tgcactacta 480  
ctgcgaatct gcg

(2) INFORMATION FOR SEQ ID NO:2204:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

Leu Ser Val Ser Gly Leu Gln Ser Arg Cys Phe His Lys Ser Thr Thr  
1 5 10 15  
Val Pro Ala Pro Pro Arg His Gly Val Leu Arg Arg Ser Xaa Cys Arg  
20 25 30  
His Ala Thr Ile Arg Xaa Ala Ala Gly Ala Arg Thr Glu Gly Ser Pro  
35 40 45  
Arg Gly Gly Glu Gly Ala Arg His Gly Gly Gly Val Pro Arg Leu Asp  
50 55 60  
Cys Val Thr Ala Glu Ser Leu Gly Ser Pro Ala Gly Ser Ala Thr Ala  
65 70 75 80  
Val Thr Ala Val Trp Arg Pro Ser Ser Pro Glu Thr Pro Arg Arg Ser  
85 90 95  
Lys Thr

(2) INFORMATION FOR SEQ ID NO:2205:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..80  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

Ser Pro Ser Pro Val Ser Ser Leu Ala Ala Ser Thr Ser Pro Gln Pro  
1 5 10 15  
Tyr Gln His His Arg Ala Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala  
20 25 30  
Thr Pro Pro Ser Xaa Pro Gln Pro Glu Pro Ala Arg Lys Ala Val Arg  
35 40 45  
Val Val Val Lys Gly Arg Val Thr Gly Val Gly Phe Arg Asp Trp Thr  
50 55 60  
Ala Ser Arg Pro Ser Arg Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2206:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..58  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met	Ala	Ser	Ser	Ala	Asp	Xaa	Asp	Ala	Ala	Thr	Pro	Pro	Ser	Xaa	Pro
1		5				10				15					
Gln	Pro	Glu	Pro	Ala	Arg	Lys	Ala	Val	Arg	Val	Val	Val	Lys	Gly	Arg
		20				25				30					
Val	Thr	Gly	Val	Gly	Phe	Arg	Asp	Trp	Thr	Ala	Ser	Arg	Pro	Ser	Arg
		35				40				45					
Ser	Ala	Arg	Arg	Leu	Gly	Pro	Gln	Pro	Pro						
	50				55										

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..192  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

aagatcaagc	caccaccacc	gccagcaaga	gcagagaggc	gagaccgcga	gagtgtagct	60
gccaccagca	gcagcagcaa	tgccgcgcgc	cgccaccacc	tctcatctct	cccactgct	120
cctctctctc	cgccagcagg	sscctoccta	cgatgccgcc	tctccttctc	cggccagccc	180
agaaggcccg	gc					

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

Lys	Ile	Lys	Pro	Pro	Pro	Pro	Ala	Arg	Ala	Glu	Arg	Arg	Asp	Arg	
1		5					10			15					
Glu	Ser	Val	Arg	Ala	Thr	Ser	Ser	Ser	Ser	Asn	Gly	Arg	Arg	Arg	His
		20				25				30					
His	Leu	Leu	Ile	Leu	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Ala	Xaa	Xaa
		35				40				45					
Ser	Leu	Arg	Cys	Arg	Leu	Ser	Phe	Leu	Gly	Gln	Pro	Arg	Arg	Pro	Gly
	50				55				60						

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502623  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:  
Arg Ser His His Arg Gln Gln Glu Gln Arg Gly Glu Thr Ala  
1 5 10 15  
Arg Val Tyr Val Pro Pro Ala Ala Ala Met Ala Ala Ala Thr  
20 25 30  
Thr Ser Ser Ser His Leu Leu Leu Ser Arg Gln Gln Xaa Pro  
35 40 45  
Pro Tyr Asp Ala Ala Ser Pro Ser Ala Ser Pro Glu Gly Pro  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Asp Gln Ala Thr Thr Ala Ser Lys Ser Arg Glu Ala Arg Pro Arg  
1 5 10 15  
Glu Cys Thr Cys His Gln Gln Gln Gln Trp Pro Pro Pro Pro  
20 25 30  
Pro Pro His Pro Pro Thr Cys Ser Ser Pro Ala Ser Arg Xaa Leu  
35 40 45  
Pro Thr Met Pro Pro Leu Leu Pro Arg Pro Ala Gln Lys Ala Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1502635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

agtgttgtgt cctagcgccg ccgccgcccc aactcgctt gcgtgactga aagctcgctg 60  
gtttccgtcc acgcgagaa cgagagcatg gacacccagg tgaagcttgc tgttgtgtgt 120  
aaggtgatgg gcaggaccgg ctccaggggg caggbgagcc aggtcagagt taagtcttgg 180  
gatgaccaga accggctcat catgaggaat gtcaaggggc ccgtccgcga ggggtgacac 240  
ctcaccttgc tcgagtcgca gatggatgcc akgagggtgc gctgaagccc tagcgtttct 300  
ggtcatccaa gaacttaact ctgacct

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1502636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

Met Asp Thr Gln Val Lys Leu Ala Val Val Val Lys Val Met Gly Arg

1 5 10 15  
Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys Phe Leu Asp  
20 25 30  
Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro Val Arg Glu  
35 40 45  
Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala Xaa Arg Leu  
50 55 60

Arg

65

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met Gly Arg Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys  
1 5 10 15  
Phe Leu Asp Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro  
20 25 30  
Val Arg Glu Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala  
35 40 45  
Xaa Arg Leu Arg  
50

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met Ser Arg Gly Pro Ser Ala Arg Val Thr Ser Ser Pro Cys Ser Ser  
1 5 10 15  
Pro Arg Trp Met Pro Xaa Gly Cys Ala Glu Ala Leu Ala Phe Leu Val  
20 25 30  
Ile Gln Glu Leu Asn Ser Asp  
35

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

gctgttgcaaa attactgttcc ctctagtctc tactctagacc cccctctctct ctcacacaca 60  
cacacaccccc tatcacttgg actgtgctag tataggtagc cgccgtgttaa tggagcagga 120

gctcagcctt gagtcaccc tcttccaccc ctccgtctctg ccggaaccgc cgggctattt 180  
cgtctgcacg tactgcgacc gcaagttctt cactctgcag gctctcgggtg gccaccagaa 240  
cgcgacacaag tacgagcgcm sstgggcaa gcgcggcgag agatcgccac cgccctgcgc 300  
gcgcacgggg gcgcggccac gcgcacgggc gtccaggacg cgccgctatg ggctctcgcg 360  
atgtcccccgc cagccccaag gcacgggtag cgggtccgac aagagcgcaa caaggatgga 420  
taagcacaag gcgcctgctg atgatgccgc tcce

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

Leu Leu Gln Ile Thr Phe Pro Leu Val Ser Thr Leu Ala Pro Ser Leu  
1 5 10 15  
Ser His Thr His Thr His Pro Tyr His Leu Asp Cys Ala Ser Ile Gly  
20 25 30  
Ser Arg Arg Val Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe  
35 40 45  
His Pro Ser Val Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr  
50 55 60  
Cys Asp Arg Lys Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn  
65 70 75 80  
Ala His Lys Tyr Glu Arg Xaa Leu Ala Lys Arg Arg Arg Ser Pro  
85 90 95  
Pro Pro Cys Ala Arg Thr Gly Arg Pro Pro Pro Arg Ala Ser Arg  
100 105 110  
Thr Arg Arg Tyr Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr  
115 120 125  
Gly Ser Gly Ala Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala  
130 135 140  
Pro Ala Asp Asp Ala Ala Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe His Pro Ser Val  
1 5 10 15  
Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr Cys Asp Arg Lys  
20 25 30  
Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Tyr  
35 40 45  
Glu Arg Xaa Leu Ala Lys Arg Arg Arg Arg Ser Pro Pro Pro Cys Ala  
50 55 60  
Arg Thr Gly Arg Pro Pro Pro Pro Arg Ala Ser Arg Thr Arg Arg Tyr  
65 70 75 80  
Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr Gly Ser Gly Ala

85 90 95  
Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala Pro Ala Asp Asp  
100 105 110  
Ala Ala Pro  
115

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

atcagcagac	caccacccaa	tcacaccagc	tctctctaga	gctagccctc	tcttctccca	60
acacttggtg	atcccctccc	atctctctca	gccttcttca	ctgaatttct	ggccgggtcga	120
tcgtcatgca	cagctacaga	gccatgcacc	cgctacactca	tcactcgtac	cagcaccaca	180
ccgcgcgcgn	gacccaccca	agcacggcca	cggccaccga	catggacatg	gccatggcgca	240
cgagaggagc	gacagtcgat	gctgtctctc	tcctctctgg	ctcctggcac	caccacggca	300
acgcgtcgtc	tcactggcgt	gctcgtctcc	cccgatctcg	gccassgcca	ccaccacctc	360
tatggcagcc	gctgctctct	ccccggcttc	ttacccttgg	gctcaccac	caaagccttt	420
acaataatgc	cgctgcggc	ggtaggggag	c			

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

Ser	Ala	Asp	His	His	Pro	Ile	Thr	Pro	Ala	Leu	Ser	Arg	Ala	Ser	Pro	1
				5					10					15		
Leu	Phe	Leu	Gln	His	Leu	Leu	Ile	Pro	Ser	His	Leu	Leu	Lys	Pro	Ser	20
								25					30			
Ser	Leu	Asn	Phe	Trp	Pro	Val	Asp	Arg	His	Ala	Gln	Leu	Gln	Ser	His	35
								40					45			
Ala	Pro	Val	His	Ser	Ser	Leu	Val	Pro	Ala	Pro	His	Arg	Gly	Xaa	Ala	50
								55					60			
Pro	Thr	Lys	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	Asp	65
								70					75			
Glu	Glu	Asp	Asp	Gln	Ser	Cys	Cys	Ser	Ser	Pro	Ser	Gly	Leu	Leu	Ala	80
								85					90			
Pro	Pro	Arg	Gln	Arg	Ala	Ala	Ser	Ser	Ala	Cys	Ser	Ser	Pro	Pro	Ile	95
								100					105			
Cys	Ala	Xaa	Ala	Thr	Thr	Thr	Ser	Met	Ala	Ala	Ala	Ala	Ser	Ser	Pro	110
								115					120			
Ala	Ser	Tyr	Pro	Trp	Ala	His	Pro	Pro	Lys	Pro	Leu	Gln				125
								130					135			

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

Met	His	Ser	Tyr	Arg	Ala	Met	His	Pro	Tyr	Thr	His	His	Ser	Tyr	Gln
1			5						10					15	
His	His	Thr	Ala	Ala	Xaa	Arg	Pro	Pro	Ser	Thr	Ala	Thr	Ala	Thr	Asp
			20						25					30	
Met	Asp	Met	Ala	Met	Ala	Thr	Arg	Arg	Thr	Thr	Ser	His	Ala	Ala	Pro
			35						40				45		
Leu	Pro	Leu	Ala	Ser	Trp	His	His	His	Gly	Asn	Ala	Leu	Leu	His	Arg
			50						55				60		
Arg	Ala	Arg	Leu	Pro	Arg	Ser	Ala	Pro	Xaa	Pro	Pro	Pro	Pro	Leu	Trp
			65						70				75		80
Gln	Pro	Leu	Pro	Pro	Pro	Leu	Leu	Thr	Leu	Gly	Leu	Thr	His	Gln	
			85						90				95		
Ser	Leu	Tyr	Asn	Ala	Gly	Cys	Gly	Gly	Arg	Gly					
			100						105						

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

Met	His	Pro	Tyr	Thr	His	His	Ser	Tyr	Gln	His	His	Thr	Ala	Ala	Xaa
			5						10					15	
Arg	Pro	Pro	Ser	Thr	Ala	Thr	Ala	Thr	Asp	Met	Asp	Met	Ala	Met	Ala
			20						25				30		
Thr	Arg	Arg	Thr	Thr	Ser	His	Ala	Ala	Pro	Leu	Pro	Leu	Ala	Ser	Trp
			35						40				45		
His	His	His	Gly	Asn	Ala	Leu	Leu	His	Arg	Arg	Ala	Arg	Leu	Pro	Arg
			50						55				60		
Ser	Ala	Pro	Xaa	Pro	Pro	Pro	Pro	Leu	Trp	Gln	Pro	Leu	Pro	Pro	Pro
			65						70				75		80
Pro	Leu	Leu	Thr	Leu	Gly	Leu	Thr	His	Gln	Ser	Leu	Tyr	Asn	Asn	Ala
			85						90				95		
Gly	Cys	Gly	Gly	Arg	Gly										
			100												

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1502653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

ggggaggttag	tggatatcaaa	gggtgataat	ccagatgctg	tgttctctgg	tctaattggct	60
gctggtagaag	caastgtgca	tctgttcacg	gtgcgaatag	gctaggcgca	aattcgcttc	120
ttgacatagt	tggtttttggc	agagcttggtg	caaacagggt	agcagatatt	tctaaaccag	180

gtgagaagca gaaacctctg gaaaaagatg ctggagaaaa gaccatagcc tggttggaca 240  
agctgaggaa tgcgaatggg tcattgccaa cttccaagat ccgtctcaac atgcagcgtg 300  
ttatgcaaaa taatgtctgt gtattccgta cacaagaata cacttgaaga aggtgtgtgag 360  
ctgattagca aaacatggga aggttttcca tgatgtgaag ctacgttgac eggagtctca 420  
tttggaaact tgacctgata gag

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Gly Glu Val Val Asp Ile Lys Gly Asp Asn Pro Asp Ala Val Val Pro  
1 5 10 15  
Gly Leu Met Ala Ala Gly Glu Ala Xaa Val His Leu Phe Met Val Arg  
20 25 30  
Ile Gly

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Arg Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser  
1 5 10 15  
Val Leu Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu  
20 25 30  
Glu Glu Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser Val Leu  
1 5 10 15  
Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu Glu Glu  
20 25 30  
Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..386  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502682  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:  
ttccccctcc ctctgccaat ctggccagct agccagccca gtccccacgc ccattcccatc 60  
ccatctaaaa actgcatcga atctctgcgc ccgcaccgct agactcagcc gacgssatgc 120  
cgccgcccac ctccgctccc cgctctgcgc ttcccgcaat ggcccgatcc cagaccagga 180  
ccagctccca gggagacetc gacttcccggt cctcatctc cgacctcacc tccctgctcc 240  
tccactcccc cgccagcgcc ggccgcggtg gctccggacc cgtcttctcc tccctctccc 300  
tttccatccc cactcccaaa cccaagccga accccagtcc cacatcagca ggcgcccgga 360  
ccccgctggc gcgcgcggcc atcggg

(2) INFORMATION FOR SEQ ID NO:2227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..128  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:

Ser	Pro	Ser	Leu	Cys	Gln	Ser	Gly	Gln	Leu	Ala	Ser	Pro	Val	Pro	Thr	
1			5						10					15		
Pro	Ile	Pro	Ser	His	Leu	Lys	Thr	Ala	Ser	Asn	Pro	Arg	Arg	Arg	Thr	
			20					25					30			
Ala	Arg	Leu	Ser	Arg	Xaa	Xaa	Ala	Ala	Gln	Leu	Arg	Ser	Pro	Pro		
			35				40				45					
Arg	Ala	Ser	Arg	Asn	Gly	Pro	Ile	Pro	Asp	Pro	Asp	Pro	Val	Pro	Gly	
			50			55				60						
Arg	Pro	Arg	Leu	Pro	Val	Pro	His	Leu	Arg	Pro	His	Leu	Pro	Ala	Pro	
			65			70				75				80		
Pro	Leu	Pro	Arg	Gln	Arg	Arg	Arg	Trp	Leu	Arg	Thr	Arg	Leu	Leu		
			85				90				95					
Leu	Leu	Leu	Pro	Phe	His	Pro	His	Ser	Gln	Thr	Gln	Ala	Glu	Pro	Gln	
			100				105					110				
Ser	His	Ile	Ser	Ser	Ala	Ala	Asp	Pro	Ala	Gly	Ala	Arg	Gly	His	Arg	
			115				120					125				

(2) INFORMATION FOR SEQ ID NO:2228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..90  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:

Met	Pro	Pro	Pro	Asn	Ser	Ala	Pro	Arg	Leu	Ala	Leu	Pro	Ala	Met	Ala	
1				5					10					15		

Arg	Ser	Gln	Thr	Gln	Thr	Gln	Ser	Gln	Gly	Asp	Leu	Asp	Phe	Pro	Ser	
			20						25				30			
Leu	Ile	Ser	Asp	Leu	Thr	Ser	Leu	Leu	Leu	His	Ser	Pro	Ala	Ser	Ala	
			35					40				45				
Gly	Ala	Gly	Gly	Ser	Gly	Pro	Val	Phe	Ser	Ser	Ser	Ser	Leu	Ser	Ile	
			50				55					60				
Pro	Thr	Pro	Lys	Pro	Lys	Pro	Asn	Pro	Ser	Pro	Thr	Ser	Ala	Ala	Pro	
					70					75					80	
Pro	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Ile	Gly							
					85				90							

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

Met	Ala	Arg	Ser	Gln	Thr	Gln	Thr	Gln	Ser	Gln	Gly	Asp	Leu	Asp	Phe	
				5					10				15			
Pro	Ser	Leu	Ile	Ser	Asp	Leu	Thr	Ser	Leu	Leu	Leu	His	Ser	Pro	Ala	
				20				25				30				
Ser	Ala	Gly	Ala	Gly	Gly	Ser	Gly	Pro	Val	Phe	Ser	Ser	Ser	Ser	Leu	
				35			40					45				
Ser	Ile	Pro	Thr	Pro	Lys	Pro	Lys	Pro	Asn	Pro	Ser	Pro	Thr	Ser	Ala	
				50			55				60					
Ala	Pro	Pro	Thr	Pro	Leu	Ala	Arg	Ala	Ala	Ile	Gly					
				65		70				75						

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1502713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

ttgatgatga	ggagaggccc	tatttaccta	agcacattct	ctacaggcaa	aaggaaacgt	60
tcagtgatgg	tggtgggtat	agttggatcg	atggattgaa	ggaccatgcc	agccaacatg	120
tctcogatgc	catgatgatg	aatgtgtgct	ttgtttacc	agagaacaca	cccacaacaa	180
aagaagggtg	ctactacaga	atgatattcg	agaaattctt	tcccaagcct	gcagcaaggt	240
caactgttcc	tgagggttcc	agtgtggcct	gcagcactgc	caaaagtgtt	gaatgggatg	300
catctgtgtc	caagaacctt	gatccttctg	ggcgtgctgc	tttgggtgtt	cacgatgctg	360
cgtatgaaga	cactgcaggg	gaaactctg	cctctgctga	tctctgtctc	gacaaggggc	420
ttcgtccagc	tattggcgaa	asstagggac	accggttgct	tcaggccacag	ctgtctaacc	480
ttatgtttat	c					

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

Asp Asp Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln  
1 5 10 15  
Lys Glu Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu  
20 25 30  
Lys Asp His Ala Ser Gln His Val Ser Asp Ser Met Met Asn Ala  
35 40 45  
Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys Glu Gly Tyr Tyr  
50 55 60  
Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro Ala Ala Arg Ser  
65 70 75 80  
Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr Ala Lys Ala Val  
85 90 95  
Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro Ser Gly Arg Ala  
100 105 110  
Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr Ala Gly Glu Thr  
115 120 125  
Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu Arg Pro Ala Ile  
130 135 140  
Gly Glu Xaa  
145

(2) INFORMATION FOR SEQ ID NO:2232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1502715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr  
1 5 10 15  
Lys Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys  
20 25 30  
Pro Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser  
35 40 45  
Thr Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp  
50 55 60  
Pro Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp  
65 70 75 80  
Thr Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly  
85 90 95  
Leu Arg Pro Ala Ile Gly Glu Xaa  
100

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1502716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:  
Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys  
1 5 10 15  
Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro  
20 25 30  
Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr  
35 40 45  
Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro  
50 55 60  
Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr  
65 70 75 80  
Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu  
85 90 95  
Arg Pro Ala Ile Gly Glu Xaa  
100

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..384  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

atcatctaca	cgcccgaggc	gccgacaacc	acttgccgac	catgagcacg	ggcacggacg	60
ccgtccggtc	gccgtggssc	cgcggaassc	ccgcccatca	acaagtacgc	cttcgcctgc	120
gccctgctcg	ctcccatgaa	ctccgtctct	ctcgctatg	acatctcggt	gatgagcgcg	180
ggcgassgtg	ttcatgaagg	aggacctcaa	gatcacggac	acgctagatc	gagatcctcg	240
cgccgcgtcat	caacatctac	tcgctcttcg	gmccctcgcc	cgcggcgcyc	acctccgamt	300
ggytcggccg	ccgtacacac	atggtgctgg	cgccgcccat	cttcttcacg	ggcgcgctcc	360
tcattgggct	cgcccgggac	tacg				

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..83  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

Met Asn Ser Val Leu Leu Gly Tyr Asp Ile Ser Val Met Ser Gly Ala  
1 5 10 15  
Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly His Ala Arg Ser  
20 25 30  
Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser Ser Xaa Pro Ser  
35 40 45  
Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Thr Pro Trp Cys  
50 55 60  
Trp Arg Pro Pro Ser Ser Ser Arg Ala Arg Ser Ser Trp Ala Ser Pro  
65 70 75 80  
Gly Thr Thr

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..71  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502719  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:  
Met Ser Gly Ala Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly  
1 5 10 15  
His Ala Arg Ser Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser  
20 25 30  
Ser Xaa Pro Ser Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala  
35 40 45  
Thr Pro Trp Cys Trp Arg Pro Pro Ser Ser Ser Arg Ala Arg Ser Ser  
50 55 60  
Trp Ala Ser Pro Gly Thr Thr  
65 70

(2) INFORMATION FOR SEQ ID NO:2237:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 63 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..63  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502720  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:  
Met Lys Glu Asp Leu Lys Ile Thr Asp Thr Leu Asp Arg Asp Pro Arg  
1 5 10 15  
Arg Arg His Gln His Leu Leu Ala Leu Arg Xaa Pro Arg Arg Gly Xaa  
20 25 30  
His Leu Arg Xaa Xaa Arg Pro Pro Leu His His Gly Ala Gly Gly Arg  
35 40 45  
His Leu Leu His Gly Arg Ala Pro His Gly Pro Arg Pro Gly Leu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2238:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 484 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..484  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502721  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:  
tatgcaatca gagagaacat tgagaaggat attgagaggg aaagggcggag aaaggacaaac 60  
cctgaggcga tggaggaaga tgaagtggat gagatcgccg agatcaggcg cctcactctc 120  
gaggagtcga tgaagtatgc tcggcgtagt gtcagtgatg ctgatatccg caagataccag 180  
gcgtttgccc agactttgca gcagtcgccg ggggttgcca gtgagttccg ctctcgggat 240  
cagccggcga casstgggtgc tgctgctgca sscgatccgt ttgctctgc ggggtgctgcg 300  
gctgatgacg acgatctata cagctagttg ggttgctcaa tatcagtcgcc gtcactcactc 360  
tgtttaaac tgatcatac aaacacgcac gtcagtcacat gatatttatt tgcggtacat 420  
ttggacgtcg ctgagatgat gcaactctcg ccttcgggta ccttttcctg ccatattctc 480  
catg

(2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 108 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..108  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502722  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:  
Tyr Ala Ile Arg Glu Asn Ile Glu Lys Asp Ile Glu Arg Glu Arg Arg  
1           5           10           15  
Arg Lys Asp Asn Pro Glu Ala Met Glu Glu Asp Glu Val Asp Glu Ile  
20           25           30  
Ala Glu Ile Arg Ala Pro His Phe Glu Glu Ser Met Lys Tyr Ala Arg  
35           40           45  
Arg Ser Val Ser Asp Ala Asp Ile Arg Lys Tyr Gln Ala Phe Ala Gln  
50           55           60  
Thr Leu Gln Gln Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Ser Asp  
65           70           75           80  
Gln Pro Ala Thr Xaa Gly Ala Ala Ala Xaa Asp Pro Phe Ala Ser  
85           90           95  
Ala Gly Ala Ala Ala Asp Asp Asp Asp Leu Tyr Ser  
100           105  
(2) INFORMATION FOR SEQ ID NO:2240:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 85 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..85  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502723  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:  
Met Glu Glu Asp Glu Val Asp Glu Ile Ala Glu Ile Arg Ala Pro His  
1           5           10           15  
Phe Glu Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser Asp Ala Asp  
20           25           30  
Ile Arg Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln Ser Arg Gly  
35           40           45  
Phe Gly Ser Glu Phe Arg Phe Ser Asp Gln Pro Ala Thr Xaa Gly Ala  
50           55           60  
Ala Ala Ala Xaa Asp Pro Phe Ala Ser Ala Gly Ala Ala Ala Asp Asp  
65           70           75           80  
Asp Asp Leu Tyr Ser  
85  
(2) INFORMATION FOR SEQ ID NO:2241:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 76 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..76  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502724  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

Met Leu Gly Val Val Ser Val Met Leu Ile Ser Ala Ser Thr Arg Arg  
1 5 10 15  
Leu Pro Arg Leu Cys Ser Ser Pro Gly Gly Leu Ala Val Ser Ser Ala  
20 25 30  
Ser Arg Ile Ser Arg Arg Xaa Xaa Val Leu Leu Leu Xaa Xaa Ile Arg  
35 40 45  
Leu Leu Leu Arg Val Leu Arg Leu Met Thr Thr Ile Tyr Thr Ala Ser  
50 55 60  
Trp Val Ala Gln Tyr Gln Ser Arg His Ser Ser Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

gaagcgagcc aaccagcca tggagaagcg gatcgatcgg cagcgggtcc tcctggcgca 60  
ctctctcccc tccccctcgg ccgcctcctc gcagcctcag cttgcggcgt cggcgtgcgc 120  
ggcgggggac agcgcgccct accagaggtc ctctctcttc ggggacgatg tcgtcgtcgt 180  
cgctgcctac aggacgcgca tatgcaagcg caagcgagga ggcttcaagg acacctacc 240  
agaggacctc ctactgttg ttctcaagcg tttctggac aacactagaa tcaatccagc 300  
tgacatcgg

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Lys Arg Ala Asn Pro Ala Met Glu Lys Ala Ile Asp Arg Gln Arg Val  
1 5 10 15  
Leu Leu Ala His Leu Leu Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro  
20 25 30  
Gln Leu Ala Ala Ser Ala Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln  
35 40 45  
Arg Ser Ser Ser Phe Gly Asp Asp Val Val Val Val Ala Ala Tyr Arg  
50 55 60  
Thr Pro Ile Cys Lys Ala Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro  
65 70 75 80  
Glu Asp Leu Leu Thr Val Val Leu Lys Ala Val Leu Asp Asn Thr Arg  
85 90 95  
Ile Asn Pro Ala Asp Ile  
100

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

Ser	Glu	Pro	Thr	Gln	Pro	Trp	Arg	Arg	Arg	Ser	Ile	Gly	Ser	Gly	Ser
1			5					10						15	
Ser	Trp	Arg	Thr	Ser	Ser	Pro	Pro	Pro	Pro	Pro	Pro	Arg	Ser	Leu	
			20				25					30			
Ser	Leu	Arg	Arg	Arg	Arg	Ala	Arg	Pro	Gly	Thr	Ala	Pro	Pro	Thr	Arg
			35				40				45				
Gly	Pro	Pro	Ser	Gly	Thr	Met	Ser	Ser	Ser	Ser	Ser	Leu	Pro	Thr	Gly
			50			55					60				
Arg	Arg	Tyr	Ala	Arg	Pro	Ser	Glu	Glu	Ala	Ser	Arg	Thr	Pro	Thr	Gln
65					70					75					80
Arg	Thr	Ser	Ser	Leu	Leu	Phe	Ser	Arg	Leu	Phe	Trp	Thr	Thr	Leu	Glu
				85					90					95	
Ser	Ile	Gln	Leu	Thr	Ser										
				100											

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..96  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

Met	Glu	Lys	Ala	Ile	Asp	Arg	Gln	Arg	Val	Leu	Leu	Ala	His	Leu	Leu
1			5					10					15		
Pro	Ser	Pro	Ser	Ala	Ala	Ser	Ser	Gln	Pro	Gln	Leu	Ala	Ala	Ser	Ala
			20				25					30			
Cys	Ala	Ala	Gly	Asp	Ser	Ala	Ala	Tyr	Gln	Arg	Ser	Ser	Ser	Phe	Gly
			35				40				45				
Asp	Asp	Val	Val	Val	Val	Ala	Ala	Tyr	Arg	Thr	Pro	Ile	Cys	Lys	Ala
			50			55					60				
Lys	Arg	Gly	Gly	Phe	Lys	Asp	Thr	Tyr	Pro	Glu	Asp	Leu	Leu	Thr	Val
65					70					75					80
Val	Leu	Lys	Ala	Val	Leu	Asp	Asn	Thr	Arg	Ile	Asn	Pro	Ala	Asp	Ile
				85				90						95	

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..496  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

gagaatcgag	cagagccacc	gattcgtcct	gagcactttc	cacattccag	ttccactccg	60
ctctcgctgc	cggtcgccgt	ctccgagact	ccgacagtcc	gaccgcaaga	aggatgagtg	120
aagaggataa	gactgtctgt	ctctgtgagc	agccgaagag	ggcccttaag	ctcaatgaaa	180
ggatctcttc	ttctctgtcc	aggaggtccg	tagctgtcta	tccattggcat	gatcttgaga	240

tcggtctctga tgcctctgct gttttcaatg ttgtaagtac cagcattacc ttagaacctgt 300  
ttgatgtggtt atagtgtcgg tgctgtggtgg acttaggttg tctggaacca tctacgggaa 360  
ggtgtgttag atcacaaagg gaagcaaaagt taaatatgag cttgacaaga aaactggact 420  
gattaaagtt gatcgagtc tgttactcat cagttgtata ccctcacaat tatggtttcg 480  
ttccaaagga ctcttt

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met Ser Glu Glu Asp Lys Thr Ala Ala Ser Ala Glu Gln Pro Lys Arg  
1 5 10 15  
Ala Pro Lys Leu Asn Glu Arg Ile Leu Ser Ser Leu Ser Arg Arg Ser  
20 25 30  
Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Asp Ala Pro  
35 40 45  
Ala Val Phe Asn Val Val Ser Thr Ser Ile Thr Leu Glu Pro Phe Asp  
50 55 60  
Val Leu Tyr Val Arg Cys Cys Gly Asp Leu Gly Cys Leu Glu Pro Ser  
65 70 75 80  
Thr Gly Arg Leu Leu Arg Ser Gln Arg Glu Ala Lys Leu Asn Met Ser  
85 90 95  
Leu Thr Arg Lys Leu Asp  
100

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

acatcaatcc attcctttc ctctccgcct ccacttccat gggcaagggtt cggtcctttct 60  
tctcgcgctc ccgcagcgccg aagcgcggca gscggagagc caggctcgct ctgcgcgcac 120  
tcctccggcg ccagcgcgcc ccgctccccg tccccactcc cgaggaggtc achgtcgctcg 180  
tcgtcaacca caaccagggg acgagacgga gcgcgtgttc cgcaagttcg acgcgaacgg 240  
cgacgggcag atttcgcggt ccgagc

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

Thr Ser Ile His Ser Leu Ser Ser Pro Ala Pro Leu Pro Trp Ala Arg

1 5 10 15  
Phe Gly Pro Ser Ser Arg Ala Pro Ala Ala Ser Ala Ala Xaa Arg  
20 25 30  
Arg Ala Gly Ser Ser Ser Pro His Ser Ser Ala Ala Ser Ala Pro Pro  
35 40 45  
Ser Pro Ser Pro Leu Pro Arg Arg Ser Xaa Ser Ser Ser Thr Thr  
50 55 60  
Thr Arg Gly Arg Asp Gly Ala Arg Val Pro Gln Val Arg Arg Glu Arg  
65 70 75 80  
Arg Arg Ala Asp Leu Ala Val Arg  
85

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

His Gln Ser Ile Pro Phe Pro Leu Pro Leu His Phe His Gly Gln Gly  
1 5 10 15  
Ser Val Leu Leu Leu Ala Leu Pro Gln Arg Gln Ala Arg Gln Xaa Gly  
20 25 30  
Glu Gln Ala Arg Pro Arg Arg Thr Pro Pro Arg Pro Ala Arg Arg Arg  
35 40 45  
Pro Arg Pro His Ser Arg Gly Gly His Xaa Arg Arg Arg Gln Pro Gln  
50 55 60  
Pro Gly Asp Glu Thr Glu Arg Val Phe Arg Lys Phe Asp Ala Asn Gly  
65 70 75 80  
Asp Gly Gln Ile Ser Arg Ser Glu  
85

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Ile Asn Pro Phe Pro Phe Leu Ser Arg Ser Thr Ser Met Gly Lys Val  
1 5 10 15  
Arg Ser Phe Phe Ser Arg Ser Arg Ser Gly Lys Arg Gly Xaa Pro Glu  
20 25 30  
Ser Arg Leu Val Leu Ala Ala Leu Leu Arg Gly Gln Arg Ala Ala Val  
35 40 45  
Pro Val Pro Thr Pro Glu Glu Val Xaa Val Val Val Val Asn His Asn  
50 55 60  
Gln Gly Thr Arg Arg Ser Ala Cys Ser Ala Ser Ser Thr Arg Thr Ala  
65 70 75 80  
Thr Gly Arg Ser Arg Gly Pro Ser  
85

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

Met Leu Cys Asp Ser Arg Arg Gly Val Ala Leu Val Ala Leu Leu Val  
1 5 10 15  
Gly Thr Asn Asn Asn Leu Gly Asn Ile Thr Asn Lys Gly Ser Val Arg  
20 25 30  
Lys Gly Phe Glu Glu Ile Asn Phe Phe Leu Phe  
35 40

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

agatcagatg gcagacaaaa taaggatcac ggaaktgcag agatatccaa tccaagcaca 60  
tcggagggtgc tcattgaaga gagaagatcc ttgggtccgg aaaaaggagac gagatcctgt 120  
ctctgggcagc gcaggagggg aggaagttaa acctgcgtcc cctggcacgt gtgggtcgcc 180  
ctgccccccc ccgcaagaag cgcgcccccc gcsttggtat ataagcgcgc mssaccggcc 240  
caaggctggg caagacggcg ggtcgctcgg gtcgacaggg gagtccaaag ttcatagttg 300  
cagcgtcggt ggagcagtg ccggggcgct gggggcgccg acgcgcacgt cctcgcgggt 360  
gacgacagct ccgtcgaccg cgccatcatc gccgccatac tccggagctc ccggtttcgt 420  
gtgactcggg tggaagtg gaagaggccc ctggaaactg taggcacgga gccgaacg

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

Arg Ser Asp Gly Arg Gln Asn Lys Asp His Gly Xaa Ala Glu Ile Ser  
1 5 10 15  
Asn Pro Ser Thr Ser Glu Val Leu Ile Glu Arg Arg Ser Leu Gly  
20 25 30  
Pro Glu Lys Glu Thr Arg Ser Cys Pro Gly Gln Arg Arg Arg Gly Gly  
35 40 45  
Val Asn Thr Cys Val Pro Trp His Val Trp Val Ala Leu Pro Arg Pro  
50 55 60  
Ala Arg Ser Ala Pro Pro Xaa Xaa Val Tyr Lys Arg Xaa Xaa Pro Ala  
65 70 75 80

Gln Gly Trp Ala Arg Arg Arg Val Val Gly Val Asp Arg Gly Val Gln  
85 90 95  
Ala Ser Asp Gly Gln Arg Arg Trp Ser Ser Gly Arg Gly Arg Gly Gly  
100 105 110  
Ala Asp Ala His Val Leu Ala Val Asp Asp Ser Ser Val Asp Arg Ala  
115 120 125  
Ile Ile Ala Ala Ile Leu Arg Ser Ser Arg Phe Arg Val Thr Ala Val  
130 135 140  
Glu Ser Gly Lys Arg Ala Leu Glu Leu Gly Thr Glu Pro Asn  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1502765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Asp Gln Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro  
1 5 10 15  
Ile Gln Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val  
20 25 30  
Arg Lys Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu  
35 40 45  
Leu Ile Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro  
50 55 60  
Gln Glu Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro  
65 70 75 80  
Lys Ala Gly Gln Asp Gly Gly Ser Ser Glu Ser Thr Gly Glu Ser Lys  
85 90 95  
Leu Gln Met Ala Ser Val Gly Gly Ala Val Ala Gly Gly Val Gly Ala  
100 105 110  
Pro Thr Arg Thr Ser Ser Arg Trp Thr Thr Ala Pro Ser Thr Ala Pro  
115 120 125  
Ser Ser Pro Pro Tyr Ser Gly Ala Pro Gly Phe Val  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1502766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro Ile Gln  
1 5 10 15  
Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val Arg Lys  
20 25 30  
Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu Leu Ile  
35 40 45  
Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro Gln Glu  
50 55 60  
Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro Lys Ala

65					70						75					80
Gly	Gln	Asp	Gly	Gly	Ser	Ser	Glu	Ser	Thr	Gly	Glu	Ser	Lys	Leu	Gln	
				85						90				95		
Met	Ala	Ser	Val	Gly	Gly	Ala	Val	Ala	Gly	Gly	Val	Gly	Ala	Pro	Thr	
			100						105				110			
Arg	Thr	Ser	Ser	Arg	Trp	Thr	Thr	Ala	Pro	Ser	Thr	Ala	Pro	Ser	Ser	
			115				120					125				
Pro	Pro	Tyr	Ser	Gly	Ala	Pro	Gly	Phe	Val							
	130					135										

(2) INFORMATION FOR SEQ ID NO:2260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..459
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2260:

atcgaccccg	tctccccggt	ctgactccgc	cckcgccgc	dctcccgac	gccccagggc	60
ttcatctccg	ccgccgtgc	cgccgcctcg	ctccgatcga	ccccgaaac	tccggaacc	120
gtgggcttcg	cgagatggat	ctcaaggata	gcctctccaa	atttaagcaa	cagcaggaga	180
gatgccagtc	atcactggcg	agcatagctg	cttcgacctc	aaagccaaag	cacagggcc	240
aaaccagcga	tgctcccaac	gtcccagcaa	gaccatcaca	acctattaa	ttttcaaatg	300
atacagaaa	gctgcagcac	atcaattcga	ttaggaaatc	tcctgttgg	gcacagatca	360
agcttgatc	cgaactctt	tacaagacaa	gacaagcttt	tactgcagag	cagantaaat	420
gaagcaactt	atgttgatat	tcattgtaat	aaagctgtc			

(2) INFORMATION FOR SEQ ID NO:2261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2261:

Arg	Thr	Arg	Leu	Pro	Val	Leu	Thr	Pro	Pro	Xaa	Pro	Xaa	Leu	Pro	His
1			5					10					15		
Ala	Pro	Arg	Leu	His	Leu	Arg	Arg	Arg	Arg	Arg	Ile	Ala	Pro	Ile	
			20					25			30				
Asp	Pro	Arg	Asn	Ser	Gly	Asn	Arg	Gly	Leu	Arg	Glu	Met	Asp	Leu	Lys
			35				40					45			
Asp	Ser	Leu	Ser	Lys	Phe	Lys	Gln	Gln	Gln	Glu	Arg	Cys	Gln	Ser	Ser
	50					55				60					
Leu	Ala	Ser	Ile	Ala	Ala	Ser	Thr	Ser	Lys	Pro	Lys	His	Arg	Ala	Gln
65					70					75				80	
Pro	Ala	His	Ala	Pro	Asn	Val	Pro	Ala	Arg	Pro	Ser	Gln	Pro	Ile	Lys
			85					90				95			
Phe	Ser	Asn	Asp	Thr	Glu	Arg	Leu	Gln	His	Ile	Asn	Ser	Ile	Arg	Lys
			100					105				110			
Ser	Pro	Val	Gly	Ala	Gln	Ile	Lys	Leu	Val	Ile	Glu	Leu	Leu	Tyr	Lys
			115				120				125				
Thr	Arg	Gln	Ala	Phe	Thr	Ala	Glu	Gln	Xaa	Lys					
	130					135									

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..95  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

Met	Asp	Leu	Lys	Asp	Ser	Leu	Ser	Lys	Phe	Lys	Gln	Gln	Glu	Arg
1				5				10					15	
Cys	Gln	Ser	Ser	Leu	Ala	Ser	Ile	Ala	Ala	Ser	Thr	Ser	Lys	Pro
				20				25					30	
His	Arg	Ala	Gln	Pro	Ala	His	Ala	Pro	Asn	Val	Pro	Ala	Arg	Pro
				35				40					45	
Gln	Pro	Ile	Lys	Phe	Ser	Asn	Asp	Thr	Glu	Arg	Leu	Gln	His	Ile
				50				55					60	
Ser	Ile	Arg	Lys	Ser	Pro	Val	Gly	Ala	Gln	Ile	Lys	Leu	Val	Ile
				65				70					75	
Leu	Leu	Tyr	Lys	Thr	Arg	Gln	Ala	Phe	Thr	Ala	Glu	Gln	Xaa	Lys
				85				90					95	

(2) INFORMATION FOR SEQ ID NO:2263:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..70  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

Met	Leu	Pro	Thr	Ser	Gln	Gln	Asp	His	His	Asn	Leu	Leu	Ser	Phe	Gln
1				5				10					15		
Met	Ile	Gln	Lys	Gly	Cys	Ser	Thr	Ser	Ile	Arg	Leu	Gly	Asn	Leu	Leu
				20				25					30		
Leu	Glu	His	Arg	Ser	Ser	Leu	Ser	Asn	Phe	Phe	Thr	Arg	Gln	Asp	
				35				40					45		
Lys	Leu	Leu	Leu	Gln	Ser	Arg	Xaa	Asn	Glu	Ala	Thr	Tyr	Val	Asp	Ile
				50				55					60		
His	Gly	Asn	Lys	Ala	Val										
65				70											

(2) INFORMATION FOR SEQ ID NO:2264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 486 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..486  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

gtgggacgag	acaaagtcca	cagctgatga	gctgcagact	ctgacaaaaca	acctatgcta	60
cacgtacgct	agggtcaccc	gctccgtgtc	aattgtgcc	cggcatact	atgctcatct	120
ggcagctctc	cgagctcgct	tctacatgga	gccagatacc	tctgacagtg	gctcaatggc	180
cagtggtgcc	cgtggccctc	caccagtgtc	ggcacssagc	atgagaggag	cggggagtgt	240
tgcggtcagg	cccctacctg	ctctcaagga	aaacgtgaag	cgtgtcatgt	tttactgctg	300

agatgctgag ctaccttcac caagaaaata tcctgacttg ttccatgtac cgcgactgtt 360  
tcggtgatac tatctgacac cgaatttatg cattaagtct tccagtgttc tggagatttt 420  
aagtaacgcc tgtttttatt cgtgagttgt aacgctgcag ttcgaggagc ttcagtgtctg 480  
tatgat

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

Trp	Asp	Glu	Asn	Lys	Phe	Thr	Ala	Asp	Glu	Leu	Gln	Thr	Leu	Thr	Asn
1			5					10			15				
Asn	Leu	Cys	Tyr	Thr	Tyr	Ala	Arg	Cys	Thr	Arg	Ser	Val	Ser	Ile	Val
			20				25					30			
Pro	Pro	Ala	Tyr	Tyr	Ala	His	Leu	Ala	Ala	Phe	Arg	Ala	Arg	Phe	Tyr
			35				40				45				
Met	Glu	Pro	Asp	Thr	Ser	Asp	Ser	Gly	Ser	Met	Ala	Ser	Gly	Ala	Arg
			50			55					60				
Gly	Pro	Pro	Pro	Gly	Ala	Ala	Xaa	Ser	Met	Arg	Gly	Ala	Gly	Ser	Val
			65			70				75				80	
Ala	Val	Arg	Pro	Leu	Pro	Ala	Leu	Lys	Glu	Asn	Val	Lys	Arg	Val	Met
				85					90					95	
Phe	Tyr	Cys													

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Met	Glu	Pro	Asp	Thr	Ser	Asp	Ser	Gly	Ser	Met	Ala	Ser	Gly	Ala	Arg
1			5					10					15		
Gly	Pro	Pro	Pro	Gly	Ala	Ala	Xaa	Ser	Met	Arg	Gly	Ala	Gly	Ser	Val
			20				25					30			
Ala	Val	Arg	Pro	Leu	Pro	Ala	Leu	Lys	Glu	Asn	Val	Lys	Arg	Val	Met
			35				40					45			
Phe	Tyr	Cys													
			50												

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:  
atcagyaaya acttcaggct tggagaaaga agaaaggcat agcagcggcg agcggcatgg 60  
gcaccakccc cgctatccct gcgacgatgc tcttcgtcgc tcttcttgtn nctgtctgct 120  
tc

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

Ser Xaa Xaa Thr Ser Gly Leu Glu Lys Glu Glu Arg His Ser Ser Gly  
1 5 10 15  
Gln Arg His Gly His Xaa Pro Arg His Pro Cys Asp Asp Ala Leu Arg  
20 25 30  
Arg Ser Ser Cys Xaa Cys Leu Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Gln Xaa Xaa Leu Gln Ala Trp Arg Lys Lys Lys Gly Ile Ala Ala Gly  
1 5 10 15  
Ser Gly Met Gly Thr Xaa Pro Val Ile Pro Ala Thr Met Leu Phe Val  
20 25 30  
Ala Leu Leu Xaa Xaa Val Cys Phe  
35 40

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

acccttactas saccagacggg tatcgtttcaa ggtccccata ctgctacaga agacgcaggt 60  
ssaccttctg tttcgcacata ctaccgccgg cacaggtaca gatctgtctc caagtcatcc 120  
agtctcatctc c

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

Thr Leu Leu Xaa Ala Asp Gly Ile Val Gln Gly Pro His Thr Ala Thr  
1 5 10 15  
Glu Asp Ala Gly Xaa Pro Ser Val Ser Pro Tyr Tyr Arg Arg His Arg  
20 25 30  
Tyr Arg Ser Val Ser Lys Ser Ser Ser Ser Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

Pro Tyr Xaa Xaa Gln Thr Val Ser Phe Lys Val Pro Ile Leu Leu Gln  
1 5 10 15  
Lys Thr Gln Xaa Xaa Leu Leu Phe Arg His Thr Thr Ala Gly Thr Gly  
20 25 30  
Thr Asp Leu Ser Pro Ser His Pro Val His Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

Leu Thr Xaa Ser Arg Arg Tyr Arg Ser Arg Ser Pro Tyr Cys Tyr Arg  
1 5 10 15  
Arg Arg Arg Xaa Thr Phe Cys Phe Ala Ile Leu Pro Pro Ala Gln Val  
20 25 30  
Gln Ile Cys Leu Gln Val Ile Gln Phe Ile Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1502805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

agattcccttt ccctttccgt tagcaggata gagagggaga ggagcagaag atagcagagg

gccagagggc cagaaggcag tcgcggacag gaggaagagg aagaagaagc ggcavsgcca 120  
ggatgccgtg cctgaacgtg tcgaccaacg tgaacctgga ggggggtggac acctcccgcca 180  
tcctcgccga agcctccaag tcgctcgcca acatcatcgg caagcccgag gcctacagtga 240  
tggtgtttct caagggttcg gtgcctatgg catttggagg taccacaggag ccagcagctt 300  
acggtagact ggtttccatc ggaggcctga accctgatgt gaacaagaag cttagtgctg 360  
gcctcgcttc tatectggag tcaaaagtgt ctgttcccaa gtcacgcttc tacctcaagt 420  
tctatgactc gaaggctcat cctgcacaag aaaatgtcca atgtttgcat gct

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1502806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Met Pro Cys Leu Asn Val Ser Thr Asn Val Asn Leu Glu Gly Val Asp  
1 5 10 15  
Thr Ser Ala Ile Leu Ala Glu Ala Ser Lys Ser Val Ala Asn Ile Ile  
20 25 30  
Gly Lys Pro Glu Ala Tyr Val Met Val Val Leu Lys Gly Ser Val Pro  
35 40 45  
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val  
50 55 60  
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly  
65 70 75 80  
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe  
85 90 95  
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala  
100 105 110  
Gln Cys Leu His Ala  
115

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1502807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

Met Val Val Leu Lys Gly Ser Val Pro Met Ala Phe Gly Gly Thr Gln  
1 5 10 15  
Glu Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Pro  
20 25 30  
Asp Val Asn Lys Lys Leu Ser Ala Gly Ile Ala Ser Ile Leu Glu Ser  
35 40 45  
Lys Leu Ser Val Pro Lys Ser Arg Phe Tyr Leu Lys Phe Tyr Asp Ser  
50 55 60  
Lys Ala His Pro Ala Gln Glu Asn Ala Gln Cys Leu His Ala  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502808  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:  
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val  
1 5 10 15  
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly  
20 25 30  
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe  
35 40 45  
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala  
50 55 60  
Gln Cys Leu His Ala  
65

(2) INFORMATION FOR SEQ ID NO:2278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..410  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:

agactgtctg ccagtggacg cgaggggagcg cctccgcctc agatccaacc cccaccgatg 60  
cgagctccgg cgatgtcccg ctggggccgcg gcgssctcg cggggctcct cgccgctcac 120  
cgcccgccgc gttttacctt cccggcgctgg cgccaacga cttccataag aaagatccac 180  
ttttggtgaa ggtgaatnag ctgacatcca cgaagacgca acttccctac tcatattact 240  
ctcttccttt ctgtaaacca aacacgatag ttgacagtgc agagaatctt ggagaagttc 300  
tgcgtggtga tcgcattgag aactctcctt atgtggtcag tactagattt ctgcttgtaa 360  
catattcagc attgtaattt gtaatgtacc aaatcactta gtcgtcatgc

(2) INFORMATION FOR SEQ ID NO:2279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..62  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:

Arg Leu Ser Ala Ser Gly Arg Glu Gly Ala Pro Pro Pro Gln Ile Gln  
1 5 10 15  
Pro Pro Pro Met Arg Ala Pro Ala Met Leu Arg Trp Ala Ala Ala Xaa  
20 25 30  
Leu Ala Gly Leu Leu Ala Ala His Arg Pro Pro Arg Phe Thr Tyr Pro  
35 40 45  
Ala Trp Arg Pro Thr Thr Ser Ile Arg Lys Ile His Phe Trp  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..124  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502811  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:  
Thr Val Cys Gln Trp Thr Arg Gly Ser Ala Ser Ala Ser Asp Pro Thr  
1 5 10 15  
Pro Thr Asp Ala Ser Ser Gly Asp Ala Pro Leu Gly Arg Gly Xaa Xaa  
20 25 30  
Arg Gly Ala Pro Arg Arg Ser Pro Ala Ala Ala Phe Tyr Leu Pro Gly  
35 40 45  
Val Ala Pro Asn Asp Phe His Lys Lys Asp Pro Leu Leu Val Lys Val  
50 55 60  
Asn Lys Leu Thr Ser Thr Lys Thr Gln Leu Pro Tyr Ser Tyr Tyr Ser  
65 70 75 80  
Leu Pro Phe Cys Lys Pro Asn Thr Ile Val Asp Ser Ala Glu Asn Leu  
85 90 95  
Gly Glu Val Leu Arg Gly Asp Arg Ile Glu Asn Ser Pro Tyr Val Val  
100 105 110  
Ser Thr Arg Leu Leu Leu Val Thr Tyr Ser Ala Leu  
115 120  
(2) INFORMATION FOR SEQ ID NO:2281:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..443  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502820  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:  
aacatcctaa tcgaaaaacg gaagtttcgg cggcgssgcg tgctcgtgat ctcaaccctaa 60  
ggcgtgcctc cgctccggtc acccgtcgct ccacgcaacc atgtcggagg ggaagaccag 120  
ggagaccaag gaggagaacg tcacccttgg acccactgtc cgtgaaggag agtatgtctt 180  
tggtgtcgct cacatctttg catccttcaa tgacaccttc attcatatca ctgattttgtc 240  
tgggagggaa actctgggttc ggatcacccg ttgcatgaag gtgaaggctg accgtgacga 300  
gtcgtcacct tacgctgcta tgcttgctgc tcaagacgtc gcacagcgct gcaaggagct 360  
tggcattact gcactgcaca ttaagcttcg gcgcaccgga gcaacaagac caagaccct 420  
ggacctgggtg cccagttctg cct  
(2) INFORMATION FOR SEQ ID NO:2282:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..91  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502821  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:  
His Pro Asn Arg Lys Thr Glu Val Ser Ala Ala Xaa Arg Ala Arg Asp  
1 5 10 15  
Leu Asn Pro Arg Arg Ala Ser Ala Pro Val Thr Arg Arg Ser Thr Gln  
20 25 30  
Pro Cys Arg Gly Gly Arg Pro Gly Ser Pro Arg Arg Arg Thr Ser Pro

35 40 45  
Leu Asp Pro Leu Ser Val Lys Glu Ser Met Ser Leu Val Ser Leu Thr  
50 55 60  
Ser Leu His Pro Ser Met Thr Pro Ser Phe Ile Ser Leu Ile Cys Leu  
65 70 75 80  
Gly Gly Lys Leu Trp Phe Gly Ser Pro Val Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1502822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu  
1 5 10 15  
Gly Pro Thr Val Arg Glu Gly Glu Tyr Val Phe Gly Val Ala His Ile  
20 25 30  
Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly  
35 40 45  
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp  
50 55 60  
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val  
65 70 75 80  
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu  
85 90 95  
Arg Ala Thr Gly Ala Thr Arg Pro Arg Pro Leu Asp Leu Val Pro Ser  
100 105 110  
Leu Pro

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

ttaactcgag aggaggtgaa gcatcccgga atggagatcc tgatgctttg gcaacaatga 60  
acgcaactgc agaagctctt gaagcaaaaag awaagcaaaa gccatcgctt gaattgtctg 120  
gaaagcttgc tgaggagacc aacagagttg caggtgtaaa tctattatat tcagaacccc 180  
cagaggctcg aaagtccagag attagatgga ggctctatgt atttaaagat ggtgaaccac 240  
tgaatgaacc acctgatgtt catcggtatga cctgctacct ttttgaaga gaaakgaaag 300  
ttgcagatgt cccacacagat catccctcct gcagcaagca acatgcagtt cttcaataca 360  
gacttgtgga gaaggagcaa ctatagtgga tactgacgaa gagaataagg ccttawctga 420  
tgatcttga tagtacaat gg

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1502835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

```
Asn Ser Arg Gly Gly Glu Ala Ser Arg Asn Gly Asp Pro Asp Ala Leu
1      5      10      15
Ala Thr Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln
20      25      30
Lys Pro Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg
35      40      45
Val Ala Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys
50      55      60
Ser Glu Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu
65      70      75      80
Asn Glu Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg
85      90      95
Glu Xaa Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys
100     105     110
Gln His Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp
115     120     125
Gly Ile Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser
130     135     140
Thr Asn
145
```

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

```
Met Asn Ala Thr Ala Glu Ala Leu Glu Ala Lys Xaa Lys Gln Lys Pro
1      5      10      15
Ser Phe Glu Leu Ser Gly Lys Leu Ala Glu Glu Thr Asn Arg Val Ala
20      25      30
Gly Val Asn Leu Leu Tyr Ser Glu Pro Pro Glu Ala Arg Lys Ser Glu
35      40      45
Ile Arg Trp Arg Leu Tyr Val Phe Lys Asp Gly Glu Pro Leu Asn Glu
50      55      60
Pro Leu Tyr Val His Arg Met Thr Cys Tyr Leu Phe Gly Arg Glu Xaa
65      70      75      80
Lys Val Ala Asp Val Pro Thr Asp His Pro Ser Cys Ser Lys Gln His
85      90      95
Ala Val Leu Gln Tyr Arg Leu Val Glu Lys Glu Gln Leu Asp Gly Ile
100     105     110
Leu Thr Lys Arg Ile Arg Pro Xaa Leu Met Asp Leu Asp Ser Thr Asn
115     120     125
```

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..461  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502844  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:  
tacgacctgc tcgggatctc agcggatggg agccccgatg atgttcgggc gtcctacagg 60  
cggctgcgcg taaagtacca cccagacgtg tccccctcgg cgccgcggcc gagaacacgc 120  
gccgtctcat cgagggtcag gaggcctacg agacgctctc cgaccccaag cgccgctcca 180  
gctacgaccg tgcaactgcc cgcggsstct gccgctcgcc ttctccgggc gccgttccca 240  
atccccacc gcctactacc accaccagga gcagggagag agatctgggt ggagaaggct 300  
ctgggaggac cagatcgcat agctgaagag gaggagcggt gcgaaggatt cagaagagaa 360  
cctgtcgtgg ggcgctcgca tgcggagaag gcccaggcgc tcacagcgna gtactgtcga 420  
(2) INFORMATION FOR SEQ ID NO:2288:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 137 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..137  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502845  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:  
Tyr Asp Leu Leu Gly Ile Ser Ala Asp Gly Ser Pro Asp Asp Val Arg  
1 5 10 15  
Ala Ser Tyr Arg Arg Leu Ala Leu Lys Tyr His Pro Asp Val Ser Pro  
20 25 30  
Pro Ala Pro Arg Pro Arg Thr Arg Ala Ala Ser Ser Arg Cys Arg Arg  
35 40 45  
Pro Thr Arg Arg Ser Pro Thr Gln Ala Ala Ala Pro Ala Thr Thr Val  
50 55 60  
His Ser Pro Ala Xaa Ser Ala Ala Arg Leu Leu Arg Ala Pro Phe Pro  
65 70 75 80  
Ile Pro Pro Arg Leu Leu Pro Pro Pro Gly Ala Gly Arg Glu Ile Trp  
85 90 95  
Val Glu Lys Val Leu Gly Gly Pro Asp Arg Arg Ala Glu Glu Glu Glu  
100 105 110  
Arg Gly Glu Gly Phe Arg Arg Glu Pro Val Val Gly Arg Ser His Ala  
115 120 125  
Glu Lys Gly Arg Gly Val Thr Ala Xaa  
130 135  
(2) INFORMATION FOR SEQ ID NO:2289:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 503 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..503  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502850  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:  
atgcgtgcac gcggtgctag ctaggctacct tgcggccaag agcgaggcgg accactacaa 60  
gcgggagatg agaaggkagc aggaggagat catcgccgct ccagacacgg aggcckctga 120  
gattggagat atcatgtcac ggtatgggct cgagcccgag agtacggccc tgtcgtcgcc 180  
gggctcaggc ggaaccctca agcttkgcta gacttcatgr tgaggttcga gctgggactg 240

gagagacggg atcccagaag ggcctctgcag acgccttcac gatcgcaactg tcctacgtgg 300  
tcggcggggct ggtccctctc ctgccctacg tgctcgtctc cgccgcgcag gatgccatgc 360  
tcacatccgt cggagtcacg ctggccgcgc tgcttttctt cggctacgtc aagggccgct 420  
tcacggggga accgkccgtt cgccagtgcc gtccagacccg ctgtcattgg agcgcctcgct 480  
tcggcggggg cgtacssgga tgg

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Cys Val His Gly Val Leu Ala Arg Tyr Leu Ala Ala Lys Ser Glu Ala  
1 5 10 15  
Asp His Tyr Lys Arg Glu Met Arg Arg Xaa Gln Glu Glu Ile Ala  
20 25 30  
Val Pro Asp Thr Glu Ala Xaa Glu Ile Gly Asp Ile Met Ser Arg Tyr  
35 40 45  
Gly Leu Glu Pro Gln Ser Thr Ala Leu Ser Ser Pro Gly Ser Gly Gly  
50 55 60  
Thr Leu Lys Leu Xaa  
65

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Gly Ser Ser Arg Val Arg Pro Cys Arg Arg Arg Ala Gln Ala  
1 5 10 15  
Glu Pro Ser Ser Xaa Ala Arg Leu His Xaa Glu Val Arg Ala Gly Thr  
20 25 30  
Gly Glu Thr Gly Ser Gln Lys Gly Ser Ala Asp Ala Phe Thr Ile Ala  
35 40 45  
Leu Ser Tyr Val Val Gly Gly Leu Val Pro Leu Leu Pro Tyr Val Leu  
50 55 60  
Val Ser Ala Ala Gln Asp Ala Met Leu Thr Ser Val Gly Val Thr Leu  
65 70 75 80  
Ala Ala Leu Leu Phe Phe Gly Tyr Val Lys Gly Arg Phe Thr Gly Glu  
85 90 95  
Pro Xaa Val Arg Gln Cys Arg Pro Asp Arg Cys His Trp Ser Ala Arg  
100 105 110  
Phe Gly Gly Gly Val Xaa Gly Trp  
115 120

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..95  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502853  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:  
Met Xaa Arg Phe Glu Leu Gly Leu Glu Arg Pro Asp Pro Arg Arg Ala  
1                  5                  10                  15  
Leu Gln Thr Pro Ser Arg Ser His Cys Pro Thr Trp Ser Ala Gly Trp  
                  20                  25                  30  
Ser Leu Ser Cys Pro Thr Cys Ser Ser Pro Pro Arg Arg Met Pro Cys  
                  35                  40                  45  
Ser His Pro Ser Glu Ser Arg Trp Pro Arg Cys Phe Ser Ser Ala Thr  
                  50                  55                  60  
Ser Arg Ala Ala Ser Arg Gly Asn Xaa Pro Phe Ala Ser Ala Val Gln  
65                  70                  75                  80  
Thr Ala Val Ile Gly Ala Leu Ala Ser Ala Ala Tyr Xaa Asp  
                  85                  90                  95

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..475  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502860  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

atcccaaaagc acaagagcac gcactgcagc accacttcct gcgctgtgctc tcatacacaca 60  
ccgtagtact aacactccat cgccacaatg gctcccaagg ttgcgtctct ccttgccttc 120  
agcctcctct tcgctgcgcg cgcgcatggc tgcgaacctt actgtcccg ccagtcgtc 180  
ccaacgccgc ccgtcgtgcc gtgcgcacagc cacggggcgt gcssatcgac gcaataaagc 240  
tcaaggtgtg cgccaacgtg ctggacctcg tcaaggtcgg cctaccccag cagcagcaat 300  
gttgcccgct gctggagggg ctggtggacc tcgacgcgcg actgtgcctc tgaccgcgca 360  
tcaagggtaa cgtcctcggc atccacctca acgtgcccct tagcctcaac ctcctcctca 420  
acaattgcgg caagatttgc ccaaaagact ttacttgccc caactaatgt agctg

(2) INFORMATION FOR SEQ ID NO:2294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..122  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502861  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

Ser Gln Ser Thr Arg Ala Arg Thr Ala Ala Pro Leu Pro Ala Leu Leu  
1                  5                  10                  15  
Leu Ile Thr His Arg Ser Thr Asn Thr Pro Ser Pro Gln Trp Leu Pro  
                  20                  25                  30  
Arg Leu Arg Ser Ser Leu Pro Ser Ala Ser Ser Ser Leu Pro Pro Arg  
                  35                  40                  45  
Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Pro  
                  50                  55                  60  
Ser Cys Arg Arg Thr Ala Thr Gly Ala Xaa Xaa Arg Arg Thr Lys Ala  
65                  70                  75                  80  
Gln Gly Val Arg Gln Arg Ala Gly Pro Arg Gln Gly Arg Pro Thr Pro

85 90 95  
Ala Arg Ala Met Leu Pro Ala Ala Gly Gly Ala Gly Gly Pro Arg Arg  
100 105 110  
Arg Thr Val Pro Leu His Arg His Gln Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

Pro Lys Ala Gln Glu His Ala Leu Gln His His Phe Leu Arg Cys Cys  
1 5 10 15  
Ser Ser His Thr Val Val Leu Thr Leu His Arg His Asn Gly Ser Gln  
20 25 30  
Gly Cys Ala Leu Pro Cys Pro Gln Pro Pro Leu Arg Cys Arg Arg Ala  
35 40 45  
Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro Asn Ala Ala Arg  
50 55 60  
Arg Ala Val Ala Gln Pro Arg Ala Leu Xaa Ile Asp Ala Leu Lys Leu  
65 70 75 80  
Lys Val Cys Ala Asn Val Leu Asp Leu Val Lys Val Gly Leu Pro Gln  
85 90 95  
His Glu Gln Cys Cys Pro Leu Leu Glu Gly Leu Val Asp Leu Asp Ala  
100 105 110  
Ala Leu Cys Leu Cys Thr Ala Ile Lys Ala Asn Val Leu Gly Ile His  
115 120 125  
Leu Asn Val Pro Leu Ser Leu Asn Leu Ile Leu Asn Asn Cys Gly Lys  
130 135 140  
Ile Cys Pro Lys Asp Phe Thr Cys Pro Asn  
145 150

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

caacttctcta agacgagttg tggtagcccg aattatgcag cacctgaggt catatctggt 60  
aaactatatg ctgttcctga agttgacgtc tggagctgtg gagttattot ttatgtctct 120  
ctttgtggca ctctcccaatt tgacgatgag aatattccaa accttttcaa gaaaataaag 180  
ggtggaatat atacccttcc tagtcaattg tcaccctcag cgaggggactt gattccccaga 240  
atgctgggtg ttgatccaat gaaaaggatt acaatacgtg aaatccgtga acatgtgttg 300  
ttcaagatcc gacttccgag ctatttggtg gtgc

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..111  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502897  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:  
His Phe Leu Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu  
1          5          10          15  
Val Ile Ser Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser  
          20          25          30  
Cys Gly Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp  
          35          40          45  
Asp Glu Asn Ile Pro Asn Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr  
50          55          60  
Thr Leu Pro Ser His Leu Ser Pro Ser Ala Arg Asp Leu Ile Pro Arg  
65          70          75          80  
Met Leu Val Val Asp Pro Met Lys Arg Ile Thr Ile Arg Glu Ile Arg  
          85          90          95  
Glu His Val Trp Phe Lys Ile Arg Leu Pro Arg Tyr Leu Ala Val  
          100         105         110

(2) INFORMATION FOR SEQ ID NO:2298:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:  
Thr Phe Leu Arg Val Val Val Ala Arg Ile Met Gln His Leu Arg  
1          5          10          15  
Ser Tyr Leu Val Asn Tyr Met Leu Val Leu Lys Leu Thr Ser Gly Ala  
          20          25          30  
Val Glu Leu Phe Phe Met Leu Phe Phe Val Ala Leu Ser His Leu Thr  
          35          40          45  
Met Arg Ile Phe Gln Thr Phe Ser Arg Lys  
50          55

(2) INFORMATION FOR SEQ ID NO:2299:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 315 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..315  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:

atcagtcctg tccaccagca ccgcnaccac actcgccgac cgnaaatgaa ccacggcggc 60  
ggcgggaggga gcagcagccg gctccgggac cggctggccc ggatgttccg ccgagcgcg 120  
ctgtcccgct ccacctgcaa caccggccgcc gccgcatact cctgtctctc ctgcctctcc 180  
gcgtccacgg ccaagcctcc gccctccgct gtggctgcgg cggcctccgc gtgtctctcc 240  
agccgcgcgc tgctgcgcgc cgtcgtcgac ggggactcgt cgttcctcgc ctccctcgcg 300  
cgcgacctcg ccgctc

(2) INFORMATION FOR SEQ ID NO:2300:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 105 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..105  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502903  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:  
Ile Ser Pro Val His Gln His Arg Xaa His Thr Arg Arg Pro Xaa Met  
1 5 10 15  
Asn His Gly Gly Gly Arg Ser Ser Ser Arg Leu Arg Asp Arg Leu  
20 25 30  
Ala Arg Met Phe Arg Pro Ser Ala Leu Arg Ser Thr Cys Asn Thr  
35 40 45  
Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Pro Ala Ser Thr Ala  
50 55 60  
Lys Pro Pro Pro Pro Val Ala Ala Ala Ser Ala Cys Ser Ser  
65 70 75 80  
Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe Leu  
85 90 95  
Ala Ser Ser Arg Arg Asp Leu Ala Val  
100 105  
(2) INFORMATION FOR SEQ ID NO:2301:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 104 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..104  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502904  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:  
Gln Ser Cys Pro Pro Ala Pro Xaa Pro His Ser Pro Thr Xaa Asn Glu  
1 5 10 15  
Pro Arg Arg Arg Arg Glu Glu Gln Gln Pro Ala Pro Gly Pro Ala Gly  
20 25 30  
Pro Asp Val Pro Pro Glu Arg Ala Ala Pro Leu His Leu Gln His Gly  
35 40 45  
Arg Arg Arg Ile Leu Leu Leu Leu Val Ser Arg Val His Gly Gln  
50 55 60  
Ala Ser Ala Ser Ala Cys Gly Cys Gly Gly Leu Arg Val Leu Leu Gln  
65 70 75 80  
Pro Arg Ala Ala Arg Arg Arg Arg Arg Gly Leu Val Val Pro Arg  
85 90 95  
Leu Leu Ala Ala Arg Pro Arg Arg  
100  
(2) INFORMATION FOR SEQ ID NO:2302:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 90 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..90  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1502905  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met Asn His Gly Gly Gly Arg Ser Ser Arg Leu Arg Asp Arg  
1 5 10 15  
Leu Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn  
20 25 30  
Thr Ala Ala Ala Ser Ser Cys Ser Ser Ser Ser Pro Ala Ser Thr  
35 40 45  
Ala Lys Pro Pro Pro Pro Val Ala Ala Ala Ser Ala Cys Ser  
50 55 60  
Ser Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe  
65 70 75 80  
Leu Ala Ser Ser Arg Arg Asp Leu Ala Val  
85 90

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

aaaaccatt gtgtgccgc cgtcgacgca gcctccgtcc tccccgcgat ccgaatcacg 60  
cacgccaaag tccccacct gtcatggcca cctccacgca cggcgcgcg accagcggcg 120  
ctcctctcca tcccaaagga aggcgagcgc atcatcgcg ccacgssaccg ccccgacggc 180  
acgctccgca aggccatccg catccgcgcg gggtacgtgc cccaggaggga ggctcgccatc 240  
taccagtcga agggcgccct aatgaggaag tcaggggccg acgtgccgcc ggggtacgac 300  
ccggcgcyta gtggccgacg ccaaaccccc ccccccc

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Lys Thr His Cys Val Pro Ala Val Asp Ala Ala Ser Val Leu Pro Arg  
1 5 10 15  
Ile Arg Ile Thr His Ala Asn Val Pro Pro Leu Ser Trp Pro Pro Pro  
20 25 30  
Ala Thr Ala Arg Arg Pro Ala Ala Leu Leu Ser Ile Pro Lys Glu Gly  
35 40 45  
Glu Arg Ile Ile Ala Pro Thr Xaa Arg Pro Asp Gly Thr Leu Arg Lys  
50 55 60  
Ala Ile Arg Ile Arg Ala Gly Tyr Val Pro Gln Glu Glu Val Ala Ile  
65 70 75 80  
Tyr Gln Ser Lys Gly Ala Leu Met Arg Lys Ser Gly Pro Asp Val Pro  
85 90 95  
Pro Gly Tyr Asp Pro Ala Xaa Ser Gly Arg Arg Gln Thr Pro Pro Pro  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..86  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502939  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:  
Lys Pro Ile Val Cys Pro Pro Ser Thr Gln Pro Pro Ser Ser Pro Ala  
1 5 10 15  
Ser Glu Ser Arg Thr Pro Thr Ser His Pro Cys His Gly His Leu Gln  
20 25 30  
Arg Arg Arg Gly Asp Gln Arg Arg Ser Ser Pro Ser Pro Arg Lys Ala  
35 40 45  
Ser Ala Ser Ser Arg Pro Xaa Xaa Ala Pro Thr Ala Arg Ser Ala Arg  
50 55 60  
Pro Ser Ala Ser Ala Pro Val Thr Cys Pro Arg Arg Arg Ser Pro Ser  
65 70 75 80  
Thr Ser Pro Arg Ala Pro  
85

(2) INFORMATION FOR SEQ ID NO:2306:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 102 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..102  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502940  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:  
Asn Pro Leu Cys Ala Arg Arg Arg Arg Ser Leu Arg Pro Pro Pro His  
1 5 10 15  
Pro Asn His Ala Arg Gln Arg Pro Thr Pro Val Met Ala Thr Ser Ser  
20 25 30  
Asp Gly Ala Ala Thr Ser Gly Ala Pro Leu His Pro Gln Gly Arg Arg  
35 40 45  
Ala His His Arg Ala His Xaa Pro Pro Arg Arg His Ala Pro Gln Gly  
50 55 60  
His Pro His Pro Arg Arg Leu Arg Ala Pro Gly Gly Gly Arg His Leu  
65 70 75 80  
Pro Val Gln Gly Arg Pro Asn Glu Glu Val Arg Ala Arg Arg Ala Ala  
85 90 95  
Gly Val Arg Pro Gly Xaa  
100

(2) INFORMATION FOR SEQ ID NO:2307:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 443 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..443  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502981  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:  
aatcggtcaa tcacgtctac ttgcttcgcag acgattctcc agggatacgt cccatctgct 60  
gcgaccaggg cgatggggga ggaggagacc cgcgcaggcg acctcccga gccgtgcctg 120

gcgacgacca tcgcgtccac ctgcgcgcgc gacgcctgcc gctgcgcgcgc cgtctccccc 180  
gccttcgcgcg ccgcgcgcga ctccgaactac gtctggggccc gcttcgtccc ggaggatacac 240  
cgccgcgcga tcgcctcgca tctgcattgcc gccgggcgggg accgtggggcc gaggaaggac 300  
gcgtaccttg cgctctcgca cggcgggcgcc ggcggcgctcc ccgtcgacgt cgacgtcgas 360  
gccttggtgc agdgtgtggc tggaccaggc cagcgssgccc aagtgtctacg cgctgtcgcc 420  
gaggaggctc agcctgccgt ggg

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

Asn Arg Ser Ile Thr Ser Thr Cys Leu Gln Thr Ile Leu Gln Gly Tyr  
1 5 10 15  
Val Pro Ser Ala Ala Thr Arg Ala Met Gly Glu Glu Glu Thr Arg Ala  
20 25 30  
Gly Asp Leu Pro Glu Pro Cys Leu Ala His Ala Ile Ala Leu Thr Ser  
35 40 45  
Pro Arg Asp Ala Cys Arg Cys Ala Ala Val Ser Pro Ala Phe Arg Ala  
50 55 60  
Ala Ala Asp Ser Asp Tyr Val Trp Gly Arg Phe Val Pro Glu Asp His  
65 70 75 80  
Arg Arg Ala Ile Ala Leu His Leu His Ala Ala Gly Arg Asp Arg Gly  
85 90 95  
Pro Arg Lys Asp Ala Tyr Leu Ala Leu Cys Asp Gly Gly Gly Gly Gly  
100 105 110  
Val Pro Val Asp Val Asp Val Xaa Ala Leu Val Gln Ala Val Ala Gly  
115 120 125  
Pro Gly Gln Xaa Xaa Gln Val Leu Arg Ala Val Gly Glu Glu Ala Gln  
130 135 140  
Pro Ala Val  
145

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Ile Gly Gln Ser Arg Leu Leu Ala Cys Arg Arg Phe Ser Arg Asp Thr  
1 5 10 15  
Ser His Leu Leu Arg Pro Gly Arg Trp Gly Arg Arg Arg Pro Ala Gln  
20 25 30  
Ala Thr Ser Arg Ser Arg Ala Trp Arg Thr Pro Ser Arg Ser Pro Arg  
35 40 45  
Arg Ala Thr Pro Ala Ala Ala Pro Pro Ser Pro Pro Ser Ala Pro  
50 55 60  
Pro Pro Thr Pro Thr Thr Ser Gly Ala Ala Ser Ser Arg Arg Ile Thr  
65 70 75 80  
Ala Ala Pro Ser Pro Cys Ile Cys Met Pro Pro Ala Gly Thr Val Gly

[illegible]

(2) INFORMATION FOR SEQ ID NO:2310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1502984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1502985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aaacggaaac | ggggggcagt | ggtgagttgg | gacttgggag | ccgcagctgt | cggggtgac  | 60  |
| cagtcgccct | cgacgcggcc | gaacgcggcc | gcgcggcagc | ctctctctac | cgggacssgg | 120 |
| nagtgacctt | ccactccgac | agccggcggt | gtccgactgt | gaagccatgt | cggaaatcat | 180 |
| cgtctccggc | gcgcgcggcc | cgccgcgggg | ckcgccctcg | ttctctaac  | tggccgtggt | 240 |
| ctccaaactg | ccgctctgtg | ccgcggtgct | cgccctcgcc | atcgcgcagt | ccatcaaggt | 300 |
| ctctaccacc | tgtataaagg | agaacagggt | gacqac     |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2312

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..111  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502986  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:  
Thr Glu Thr Gly Ala Val Gly Glu Leu Gly Leu Gly Ser Arg Arg Cys  
1 5 10 15  
Arg Gly Asp Pro Val Ala Ala Asp Ala Glu Arg Ala Arg Ala Arg  
20 25 30  
Ala Ser Leu Tyr Ala Asp Xaa Xaa Gly Pro Phe His Ser Gln Ser Arg  
35 40 45  
Ala Cys Pro Ile Val Ser Pro Trp Arg Asn Pro Ser Ser Pro Ala Pro  
50 55 60  
Pro Pro Arg Arg Arg Xaa Arg Pro Arg Ser Pro Thr Trp Pro Cys Ser  
65 70 75 80  
Pro Thr Ala Arg Ser Ser Pro Arg Cys Ser Pro Ser Pro Ser Arg Ser  
85 90 95  
Pro Ser Arg Ser Ser Pro Pro Gly Ile Arg Arg Thr Gly Gly Thr  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..56  
(D) OTHER INFORMATION: / Ceres Seq. ID 1502987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:

Met Ala Glu Ser Ile Val Ser Gly Ala Ala Pro Pro Pro Gly Xaa  
1 5 10 15  
Pro Ser Phe Ser Tyr Leu Ala Val Phe Ser Asn Cys Pro Leu Val Ala  
20 25 30  
Ala Val Leu Ala Phe Ala Ile Ala Gln Ser Ile Lys Val Leu Thr Thr  
35 40 45  
Trp Tyr Lys Glu Asn Arg Trp Asp  
50 55

(2) INFORMATION FOR SEQ ID NO:2314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..505  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:

gaaggacttc cggtgcgcgc tcaagcaggt gctcgacctg ttccaggaca actaccccgga 60  
gctcgctcgcg agaaacatct tgatcaacgt gccgttctgg tactacgcgt tcagaccct 120  
gttctaccgcg ttcttgacgc agaggacgaa gagcaagttc gtctgtgctc gccctgccaa 180  
ggtcacccgag accctctcca agtacattcc gatcgaggcc atcccggtga agtacggcgg 240  
cctgaagcgc gacggcgaca ccgagttctc cgcgagcgac ggcgaggtcg cggaggtcac 300

cgtcaaggga agctccacgg agaccatcga gatcgaagcc actgaggctg atgccacgct 360  
gacatgggac ctgacgggtc tgggggtggga ggtgaactac aaggaggagt tctgtccggc 420  
ggacgagggc tcctacacca tcatcgtcag gaagggcaag aagatggcgt ccggcgagga 480  
kgcggctccg aactcgttcc gcacc

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

Glu Gly Leu Pro Arg Arg Gln Ala Gly Ala Arg Pro Val Pro Gly  
1 5 10 15  
Gln Leu Pro Arg Ala Arg Arg Glu Lys His Leu Asp Gln Arg Ala Val  
20 25 30  
Leu Val Leu Arg Val Gln His Pro Val Leu Pro Val Pro Asp Ala Glu  
35 40 45  
Asp Glu Glu Gln Val Arg Arg Cys Ser Pro Val Gln Gly His Arg Asp  
50 55 60  
Pro Pro Gln Val His Ser Asp Arg Gly His Pro Gly Glu Val Arg Arg  
65 70 75 80  
Pro Glu Ala Arg Arg Arg His Arg Val Leu Arg Gly Arg Arg Arg Gly  
85 90 95  
Arg Gly Gly His Arg Gln Gly Lys Leu His Gly Asp His Arg Asp Arg  
100 105 110  
Ser His

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Lys Asp Phe Arg Val Ala Val Lys Gln Val Leu Asp Leu Phe Gln Asp  
1 5 10 15  
Asn Tyr Pro Glu Leu Val Ala Arg Asn Ile Leu Ile Asn Val Pro Phe  
20 25 30  
Trp Tyr Tyr Ala Phe Ser Thr Leu Phe Tyr Pro Phe Leu Thr Gln Arg  
35 40 45  
Thr Lys Ser Lys Phe Val Val Ala Arg Pro Ser Lys Val Thr Glu Thr  
50 55 60  
Leu Leu Lys Tyr Ile Pro Ile Glu Ala Ile Pro Val Lys Tyr Gly Gly  
65 70 75 80  
Leu Lys Arg Asp Gly Asp Thr Glu Phe Ser Ala Asp Asp Gly Glu Val  
85 90 95  
Ala Glu Val Thr Val Lys Gly Ser Ser Thr Glu Thr Ile Glu Ile Glu  
100 105 110  
Ala Thr Glu Ala Asp Ala Thr Leu Thr Trp Asp Leu Thr Val Leu Gly  
115 120 125  
Trp Glu Val Asn Tyr Lys Glu Glu Phe Val Pro Ala Asp Glu Gly Ser

130 135 140  
Tyr Thr Ile Ile Val Arg Lys Gly Lys Lys Met Ala Ser Gly Glu Xaa  
145 150 155 160  
Ala Val Arg Asn Ser Phe Arg Thr

- 165  
(2) INFORMATION FOR SEQ ID NO:2317:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 495 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..495  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503010  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:  
gtcgggtccat agcatcgatt cactccgcgc gcgccgctgt ctctcgtctg tcgcccgcttt 60  
cctcgtattat ctctccatgg cgcccgctca tcccccgctg catccgcgcg ctcccccggt 120  
aggggtgccgg cgacctctcc gcggcassaag cggcgcgacg gctgggtgcc cctgcgccat 180  
atgcctcgaa gccttcaaaag acgaggccta cctcgacact tgcttccatt ccttttgcta 240  
caagtgtata tgcaggtggg taaggatagt agcgagcaag cagcgagaac ctttgtcttc 300  
agtttagatgt ccactttgta agactgagaa tctatccgtc atacatgctt ttgatggcga 360  
atcatttgag cgggtgtaca taaatcagga acytaggaag aggcgttctt tcagatgcac 420  
acgagttggt gtcacaattc tataacatga aagagaccac aagcaacatt tctagggtgc 480  
agcaatactg ggagc

- (2) INFORMATION FOR SEQ ID NO:2318:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503011  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:  
Ser Val His Ser Ile Asp Ser Leu Arg Ala Arg Cys Leu Leu Val  
1 5 10 15  
Val Ala Ala Phe Leu Asp Tyr Leu Ser Met Ala Ala Ala His Pro Pro  
20 25 30  
Leu His Pro Pro Pro Pro Val Gly Cys Arg Arg Pro Ser Arg Gly  
35 40 45  
Xaa Ser Gly Ala Thr Ala Gly Cys Pro Cys Pro Ile Cys Leu Glu Ala  
50 55 60  
Phe Lys Asp Glu Ala Tyr Leu Asp Thr Cys Phe His Ser Phe Cys Tyr  
65 70 75 80  
Lys Cys Ile Cys Gln Trp Val Arg Ile Val Ala Ser Lys His Ala Glu  
85 90 95  
Pro Leu Ser Ser Val Arg Cys Pro Leu Cys Lys Thr Glu Asn Leu Ser  
100 105 110  
Val Ile His Ala Phe Asp Gly Glu Ser Phe Glu Arg Trp Tyr Ile Asn  
115 120 125  
Gln Glu Xaa Arg Lys Arg Arg Ser Phe Arg Cys Thr Arg Val Gly Val  
130 135 140  
Thr Ile Leu  
145

- (2) INFORMATION FOR SEQ ID NO:2319:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..122  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503012  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:  
Met Ala Ala Ala His Pro Pro Leu His Pro Pro Pro Val Gly  
1 5 10 15  
Cys Arg Arg Pro Ser Arg Gly Xaa Ser Gly Ala Thr Ala Gly Cys Pro  
20 25 30  
Cys Pro Ile Cys Leu Glu Ala Phe Lys Asp Glu Ala Tyr Leu Asp Thr  
35 40 45  
Cys Phe His Ser Phe Cys Tyr Lys Cys Ile Cys Gln Trp Val Arg Ile  
50 55 60  
Val Ala Ser Lys His Ala Glu Pro Leu Ser Ser Val Arg Cys Pro Leu  
65 70 75 80  
Cys Lys Thr Glu Asn Leu Ser Val Ile His Ala Phe Asp Gly Glu Ser  
85 90 95  
Phe Glu Arg Trp Tyr Ile Asn Gln Glu Xaa Arg Lys Arg Arg Ser Phe  
100 105 110  
Arg Cys Thr Arg Val Gly Val Thr Ile Leu  
115 120  
(2) INFORMATION FOR SEQ ID NO:2320:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 436 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..436  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503042  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:  
cttttttcgg aggaggcgga ccaggtaagc agcagcagga accctagcac cgccgcatcc 60  
gcagccatgg gtatcgacct cgttgccggt gggaggaaca agaagaccaa ggcacacgcs 120  
cgaagtcctga cgatgtttat ctcaagctccc ttgtcaagct ctaccggttc ttggtcagga 180  
ggaccaagag caacttcaat gctgtcattc tcaagaggct ctccatgagc aaaaccaatc 240  
gcccaccaat ctccatgcgc cgcttctgca agttcatgga aggaagaggag aagaacattg 300  
ctgtgattgt tggcacagtc acagatgaca agaggatcca agaggttcca gcaatgaagg 360  
gaagctcgat gactacatga agttcttctg ttgtcttctc gcttagatgt ttatttgtga 420  
ctgctagggg cgatgt  
(2) INFORMATION FOR SEQ ID NO:2321:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 75 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..75  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503043  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:  
Leu Phe Ser Glu Glu Ala Asp Gln Val Ser Ser Ser Arg Asn Pro Ser  
1 5 10 15  
Thr Ala Ala Ser Ala Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg  
20 25 30

Asn Lys Lys Thr Lys Arg Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser  
35 40 45  
Ser Ser Leu Ser Ser Ser Thr Val Ser Trp Ser Gly Gly Pro Arg Ala  
50 55 60  
Thr Ser Met Leu Ser Phe Ser Arg Gly Ser Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg  
1 5 10 15  
Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser Ser Ser Leu Ser Ser Ser  
20 25 30  
Thr Val Ser Trp Ser Gly Gly Pro Arg Ala Thr Ser Met Leu Ser Phe  
35 40 45  
Ser Arg Gly Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys  
1 5 10 15  
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val  
20 25 30  
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Gly Ser Ser  
35 40 45  
Met Thr Thr  
50

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

aggacaggtt gcatttgcac ctgagttcct gatcgttgta ttccagtttc ttccgtgagt 60  
tttgtgggat ccgcagggaag aaggatgtcg tgctgcggag gcaactgcgg gtgcgcgcgc 120  
ggggcassagg ccggcgccgca gtgcctgcgg cagctgaacc gcctcctggs stgcgcgcgc 180

tacctgtgtgc cgggcgcgcc ggacccccagc gcggactgct gcagcgc

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Cys | Cys | Gly | Gly | Asn | Cys | Gly | Cys | Gly | Ala | Gly | Xaa | Xaa | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Gly | Gly | Gln | Cys | Leu | Pro | Gln | Leu | Asn | Arg | Leu | Leu | Xaa | Cys | Arg | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Val | Pro | Gly | Ala | Pro | Asp | Pro | Ser | Ala | Asp | Cys | Cys | Ser |     |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1503064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| aattctcccc  | gcctccccct  | cgcaccctcc  | gactaccgcc | gcctcctggs | scasstctcc | 60  |
| tccgcgggcc  | tcttcgagcg  | cgctggcccc  | acccccaggg | tacagctcgc | cctgatggcc | 120 |
| gtctctttct  | acgcggcgct  | ctacctctgc  | ctcgccctgc | ccassgcctc | ggcgsacatg | 180 |
| ctcgctgggg  | ggctcatcgg  | cttcgtctgg  | atccagtcgc | gctggatggg | ccacgactcg | 240 |
| ggccaccacc  | gcatacgcgg  | ccatcccgctc | ctggaccgcg | tcgtgcaggt | gctctccgga | 300 |
| aaactgcctca | ctggcctcag  | catcgccctgg | tggaaatgca | accacaacac | gcaccacatc | 360 |
| gcctgcaaca  | gcctggacca  | tgaccgggac  | ctccagcaca | tgccgctctt | cgtgtgtctc | 420 |
| cccaagctgt  | tcggcaacat  | atggctctac  | tkctaccagg | ggaccctggc | cttcgacggc | 480 |
| gcctcgaaat  | tcctcatcatg | ctaccagcac  | tg         |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1503065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Pro | Arg | Leu | Pro | Leu | Arg | Pro | Ser | Asp | Tyr | Arg | Arg | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Xaa | Xaa | Xaa | Ser | Ser | Ala | Gly | Leu | Phe | Glu | Arg | Val | Gly | Pro | Thr | Pro |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Val | Gln | Leu | Ala | Leu | Met | Ala | Val | Leu | Phe | Tyr | Ala | Ala | Leu | Tyr |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Leu | Val | Leu | Ala | Cys | Ala | Xaa | Ala | Ser | Xaa | Xaa | Met | Leu | Ala | Gly | Gly |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Leu | Ile | Gly | Phe | Val | Trp | Ile | Gln | Ser | Gly | Trp | Met | Gly | His | Asp | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|--|--|--|--|
| 65  | 70  |     |     |     |     |     |     |     |     |     | 75  |     |     |     |     | 80 |  |  |  |  |
| Gly | His | His | Arg | Ile | Thr | Gly | His | Pro | Leu | Leu | Asp | Arg | Val | Val | Gln |    |  |  |  |  |
| Val | Leu | Ser | Gly | Asn | Cys | Leu | Thr | Gly | Leu | Ser | Ile | Ala | Trp | Trp | Lys |    |  |  |  |  |
| Cys | Asn | His | Asn | Thr | His | His | Ile | Ala | Cys | Asn | Ser | Leu | Asp | His | Asp |    |  |  |  |  |
| Pro | Asp | Leu | Gln | His | Met | Pro | Leu | Phe | Ala | Val | Ser | Pro | Lys | Leu | Phe |    |  |  |  |  |
| Gly | Asn | Ile | Trp | Ser | Tyr | Xaa | Tyr | Gln | Arg | Thr | Leu | Ala | Phe | Asp | Ala |    |  |  |  |  |
| Ala | Ser | Lys | Phe | Leu | Ile | Ser | Tyr | Gln | His |     |     |     |     |     |     |    |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..126  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

1 Phe Ser Pro Pro Pro Pro Pro Thr Leu Arg Leu Pro Pro Pro Xaa  
 5 10 15  
 Xaa Xaa Leu Leu Arg Gly Pro Leu Arg Ala Arg Arg Pro His Pro Gln  
 20 25 30  
 Gly Thr Ala Arg Pro Asp Gly Arg Pro Leu Leu Arg Gly Ala Leu Pro  
 35 40 45  
 Arg Pro Arg Leu Arg Xaa Xaa Leu Gly Xaa His Ala Arg Trp Gly Ala  
 50 55 60  
 His Arg Leu Arg Leu Asp Pro Val Arg Leu Asp Gly Pro Arg Leu Gly  
 65 70 75 80  
 Pro Pro Pro His His Gly Pro Ser Ala Pro Gly Pro Arg Arg Ala Gly  
 85 90 95  
 Ala Leu Arg Lys Leu Pro His Trp Pro Gln His Arg Leu Val Glu Met  
 100 105 110  
 Gln Pro Gln His Ala Pro His Arg Leu Gln Gln Pro Gly Pro  
 115 120 125

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..132  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Leu | Phe | Tyr | Ala | Ala | Leu | Tyr | Leu | Val | Leu | Ala | Cys | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Xaa | Ala | Ser | Xaa | Xaa | Met | Leu | Ala | Gly | Gly | Leu | Ile | Gly | Phe | Val | Trp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Ser | Gly | Trp | Met | Gly | His | Asp | Ser | Gly | His | His | Arg | Ile | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Gly | His | Pro | Leu | Leu | Asp | Arg | Val | Val | Gln | Val | Leu | Val | Ser | Gly | Asn |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Leu Thr Gly Leu Ser Ile Ala Trp Trp Lys Cys Asn His Asn Thr His  
65 70 75 80  
His Ile Ala Cys Asn Ser Leu Asp His Asp Pro Asp Leu Gln His Met  
85 90 95  
Pro Leu Phe Ala Val Ser Pro Lys Leu Phe Gly Asn Ile Trp Ser Tyr  
100 105 110  
Xaa Tyr Gln Arg Thr Leu Ala Phe Asp Ala Ala Ser Lys Phe Leu Ile  
115 120 125  
Ser Tyr Gln His  
130

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| catgaagaaa | agaaaggcgg | tatccagacc | tcaagccctg | ctctgaagga | ggagctgcgc | 60  |
| aagaggctga | gcgttgctga | agatgatgag | gatttaagct | gggatatcga | ggatgacgat | 120 |
| gacaatgcct | gaataccatt | ggtgatatgg | aagtgtcagt | tgkatttcta | cattttgcac | 180 |
| cttcattac  | tcgtgcaagt | tactgtgatt | tggccaatwa | gattggctat | cattatgcta | 240 |
| tggacacggt | tgatactgt  | aaactctcca | gtttgatgat | atcaagtggc | aatgggctaa | 300 |
| gcgcc      |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Glu | Glu | Lys | Lys | Gly | Gly | Ile | Gln | Thr | Ser | Ser | Pro | Ala | Leu | Lys |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Glu | Glu | Leu | Arg | Lys | Arg | Leu | Ser | Val | Ala | Glu | Asp | Asp | Glu | Asp | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Trp | Asp | Ile | Glu | Asp | Asp | Asp | Asn | Ala |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Val | Ser | Val | Xaa | Phe | Leu | His | Phe | Ala | Pro | Ser | Ile | Thr | Arg |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Ala | Ser | Tyr | Cys | Asp | Leu | Ala | Asn | Xaa | Ile | Gly | Tyr | Pro | Tyr | Ala | Met |

Asp Thr Phe Val Tyr Cys Lys Leu Ser Ser Leu Met Ile Ser Ser Gly  
          35                    40                    45  
Asn Trp Leu Ser Ala  
       50

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..414  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

| Table 2.3.3.1 |            |            |            |            |            |     |
|---------------|------------|------------|------------|------------|------------|-----|
| ctccacacga    | aacaaagcga | gagagagaga | gaaccccagc | gggcaaacgc | ctccctcccc | 60  |
| atgctccacg    | cgcgcacgac | cggccatccg | ggtagctcca | gacctctctc | aatggcggtc | 120 |
| aaggtctacg    | tcgtgtttta | cgccacctac | gggcaagctg | caacgcttgc | taggaagagc | 180 |
| atgaagaaagc   | ccgctctcag | tgaagagcgt | gagctcaaac | tatggcaggt | ccccgagatc | 240 |
| ctgtccgagc    | aggtgctcgt | caaatgaggg | cgcccccaca | aagaccgacg | cgcggtgatc | 300 |
| accccgcaga    | gcgtgcggag | gccgacggcg | tcctcttcgg | gttccccaac | cggttcggca | 360 |
| tgatggcgag    | gcagatgaag | gccttctctc | acgcgcagcg | cgggctgtgg | cgccg      |     |

(2) INFORMATION FOR SEQ ID NO:2334

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

|     |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1   | file | Pro | Arg | Lys | Gln | Ala | Gln | Arg | Glu | Arg | Glu | Pro | Gln | Arg | Ala | Asn |
| 15  |      |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ser  | Leu | Pro | Leu | Pro | Pro | Gly | Pro | Arg | Ser | Gly | His | Pro | Gly | Ser |     |
|     |      |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Arg  | Pro | Ser | Pro | Met | Ala | Val | Lys | Val | Tyr | Val | Val | Phe | Tyr | Ser |     |
|     |      | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Tyr  | Gly | His | Val | Ala | Lys | Leu | Ala | Glu | Glu | Met | Lys | Lys | Gly | Ala |     |
|     | 50   |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Ser  | Val | Glu | Gly | Val | Glu | Val | Lys | Val | Trp | Gln | Val | Pro | Glu | Ile |     |
|     |      |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| 65  |      |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Ser  | Glu | Glu | Val | Leu | Gly | Lys | Met | Gly | Ala | Pro | Pro | Lys | Thr | Asp |     |
|     |      |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Pro  | Val | Ile | Thr | Pro | Gln | Ser | Trp | Arg | Arg | Pro | Thr | Ala | Ser | Ser |     |
|     |      | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Gly  | Ser | Pro | Arg | Gly | Ser | Ala |     |     |     |     |     |     |     |     |     |
|     |      | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Lys | Val | Tyr | Val | Val | Phe | Tyr | Ser | Thr | Tyr | Gly | His | Val |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Lys | Leu | Ala | Glu | Glu | Met | Lys | Lys | Gly | Ala | Ala | Ser | Val | Glu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Glu | Val | Lys | Val | Trp | Gln | Val | Pro | Glu | Ile | Leu | Ser | Glu | Glu | Val |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Gly | Lys | Met | Gly | Ala | Pro | Pro | Lys | Thr | Asp | Ala | Pro | Val | Ile | Thr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Pro | Gln | Ser | Trp | Arg | Arg | Pro | Thr | Ala | Ser | Ser | Gly | Ser | Pro | Arg |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Ser | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Pro | Gly | Asp | Ser | Val | Arg | Gly | Gly | Ala | Arg | Gln | Asp | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Ala | Thr | Gln | Asp | Arg | Arg | Ala | Gly | His | His | Pro | Ala | Gly | Leu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Asp | Gly | Val | Leu | Phe | Gly | Phe | Pro | Thr | Arg | Phe | Gly | Met | Met |
|     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ala | Gln | Met | Lys | Ala | Phe | Phe | Asp | Ala | Thr | Gly | Gly | Leu | Trp | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| gtkattgggt | tgtcgcttg   | gttcttccct | gccggaagat  | acctttcgtt | cggtgtgcgc | 60  |
| aactcgccat | tcttgggagg  | tcttggtcgg | gaccggtgct  | gatggaggag | aggtacgagg | 120 |
| cgctgaagga | gctgggggccc | ggcaacttcg | gcgtggcgag  | gctggtcagg | gacaacggga | 180 |
| ccaaggagct | ggtagccgctc | aagtacatcg | agaggggcaa  | gaagattgat | gagaacgtgc | 240 |
| agagggagat | catcaatcac  | caatcgctcc | ggcacccata  | catcgtacgg | ttcaaggagg | 300 |
| tttgtctaac | acccacacat  | cttgctattg | tcattggaata | tgctgctggt | ggagagctat | 360 |
| ttgagaaaaa | ctgctcagca  | ggcgcatcca | gtgaagatgw  | ktccaggat  | ttcttccaac | 420 |
| agctgataac | aggggttcag  | ctactgccat | ttcatggaaa  | tttgtcaccg | tgatctttaa | 480 |
| acttkagaac | acctctcttg  | atgggagtc  |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1503109

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

Xaa Trp Val Gly Arg Leu Val Leu Pro Cys Arg Lys Ile Pro Phe Val  
1 5 10 15  
Arg Cys Arg Gln Leu Ala Ile Leu Gly Arg Ser Trp Ser Gly Pro Val  
20 25 30  
Leu Met Glu Glu Arg Tyr Glu Ala Leu Lys Glu Leu Gly Ala Gly Asn  
35 40 45  
Phe Gly Val Ala Arg Leu Val Arg Asp Lys Arg Thr Lys Glu Leu Val  
50 55 60  
Ala Val Lys Tyr Ile Glu Arg Gly Lys Lys Ile Asp Glu Asn Val Gln  
65 70 75 80  
Arg Glu Ile Ile Asn His Gln Ser Leu Arg His Pro Asn Ile Val Arg  
85 90 95  
Phe Lys Glu Val Cys Leu Thr Pro Thr His Leu Ala Ile Val Met Glu  
100 105 110  
Tyr Ala Ala Gly Gly Glu Leu Phe Glu Lys Ile Cys Ser Ala Gly Arg  
115 120 125  
Phe Ser Glu Asp Xaa Ser Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly  
130 135 140  
Val Gln Leu Leu Pro Phe Tyr Gly Asn Leu Ser Pro  
145 150 155

- (2) INFORMATION FOR SEQ ID NO:2339:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503110

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

Met Glu Glu Arg Tyr Glu Ala Leu Lys Glu Leu Gly Ala Gly Asn Phe  
1 5 10 15  
Gly Val Ala Arg Leu Val Arg Asp Lys Arg Thr Lys Glu Leu Val Ala  
20 25 30  
Val Lys Tyr Ile Glu Arg Gly Lys Lys Ile Asp Glu Asn Val Gln Arg  
35 40 45  
Glu Ile Ile Asn His Gln Ser Leu Arg His Pro Asn Ile Val Arg Phe  
50 55 60  
Lys Glu Val Cys Leu Thr Pro Thr His Leu Ala Ile Val Met Glu Tyr  
65 70 75 80  
Ala Ala Gly Gly Glu Leu Phe Glu Lys Ile Cys Ser Ala Gly Arg Phe  
85 90 95  
Ser Glu Asp Xaa Ser Arg Tyr Phe Phe Gln Gln Leu Ile Ser Gly Val  
100 105 110  
Gln Leu Leu Pro Phe Tyr Gly Asn Leu Ser Pro  
115 120

- (2) INFORMATION FOR SEQ ID NO:2340:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..263  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| accagccggt | gttgggttca | gcttgatcc  | ccactctgtc | gcacagcgctc | gcccgtcgcc | 60  |
| gctgagatcc | taggaagaaa | tggagctctc | tcgcaagctc | ttcacggccg  | tcctcctcgt | 120 |
| catgctgctg | ctgctgtccg | cagaggtcgg | gccggtggcg | gtggcggagg  | cgcggacgtg | 180 |
| ccagtcgcag | agccacaggt | tccggggccc | ctgcctccgc | cggccaact   | gcgccaactg | 240 |
| ctgcaggacc | gaggggttcc | ccg        |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2341:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Arg | Cys | Trp | Phe | Gln | Leu | Val | Phe | Pro | Leu | Cys | Arg | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Val | Ala | Ala | Glu | Ile | Leu | Gly | Arg | Asn | Gly | Ala | Leu | Ser | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Leu | His | Gly | Arg | Pro | Pro | Arg | His | Ala | Ala | Ala | Val | Arg | Arg |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Arg | Ala | Gly | Gly | Gly | Gly | Gly | Gly | Ala | Asp | Val | Pro | Val | Ala | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     | 60  |     |     |     |     |     |
| Pro | Gln | Val | Pro | Gly | Pro | Leu | Pro | Pro | Pro | Val | Gln | Leu | Arg | Gln | Arg |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Gln | Asp | Arg | Gly | Val | Pro |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2342:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 61 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..61  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ser | Arg | Lys | Leu | Phe | Thr | Ala | Val | Leu | Leu | Val | Met | Leu |
| 1   |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Leu | Leu | Ser | Ala | Glu | Val | Gly | Pro | Val | Ala | Val | Ala | Glu | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Cys | Gln | Ser | Gln | Ser | His | Arg | Phe | Arg | Gly | Pro | Cys | Leu | Arg | Arg |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asn | Cys | Ala | Asn | Val | Cys | Arg | Thr | Glu | Gly | Phe | Pro |     |     |     |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     | 60  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2343:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 47 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..47  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503135  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:  
Met Leu Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu  
1 5 10 15  
Ala Arg Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu  
20 25 30  
Arg Arg Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro  
35 40 45  
(2) INFORMATION FOR SEQ ID NO:2344:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 342 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..342  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503136  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:  
tccaccaccg cttaccaccg cctccaccg ccaccaccac catggcctct ccttcccctt 60  
cttcccgcgc cgcgcctcgc ggccgcgcgc tgccgcgcgc gtgctggacg accgacgaga 120  
ccctcgcgct cgcgssggtc ctacaccgcg ccgcctcgcg cgtcggccgg gacgacctga 180  
cctccaccga ctgggcgcgc gtagccgcgcg cgccccgtcc aagaccgccca gcagtgcgcg 240  
cacaagatcg agaagctccg ccgacgcctc cggtccaacc gccgacgccc atgcccgctt 300  
cctcgacgcc atggatctcc tcgacgcgcc ttccccgcc ct  
(2) INFORMATION FOR SEQ ID NO:2345:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..113  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503137  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:  
Pro Pro Pro Leu His His Pro Leu Gln Ala His His His His Gly Leu  
1 5 10 15  
Ser Phe Pro Phe Phe Pro Arg Pro Arg Leu Arg Pro Pro Arg Ala Ala  
20 25 30  
Ala Val Leu Asp Asp Arg Arg Asp Pro Arg Ala Arg Xaa Gly Pro Thr  
35 40 45  
Pro Arg Pro Pro Arg Arg Arg Pro Gly Ala Pro Asp Leu His Arg Leu  
50 55 60  
Gly Arg Arg Ser Arg Gly Ala Pro Ser Lys Thr Ala Ser Ser Ala Ala  
65 70 75 80  
Thr Arg Ser Arg Ser Ser Ala Asp Ala Ser Gly Pro Thr Ala Asp Ala  
85 90 95  
His Ala Arg Phe Leu Asp Ala Met Asp Leu Leu Asp Gly Pro Phe Pro  
100 105 110  
Ala

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..113  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503138  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:  
His His Arg Phe Thr Ile Pro Ser Arg Pro Thr Thr Thr Met Ala Ser  
1                  5                  10                  15  
Pro Ser Pro Ser Pro Ala Arg Ala Ser Gly Arg Arg Val Pro Pro  
                  20                  25                  30  
Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Ala Xaa Val Leu His  
                  35                  40                  45  
Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser Thr Asp Trp  
50                  55                  60  
Ala Ala Val Ala Ala Ala Pro Arg Pro Arg Pro Pro Ala Val Pro Pro  
65                  70                  75                  80  
Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro Pro Thr Pro  
                  85                  90                  95  
Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala Leu Ser Pro  
                  100                  105                  110  
Pro

(2) INFORMATION FOR SEQ ID NO:2347:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 100 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..100  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503139  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:  
Met Ala Ser Pro Ser Pro Ser Ser Pro Ala Arg Ala Ser Gly Arg Arg  
1                  5                  10                  15  
Val Pro Pro Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Ala Xaa  
                  20                  25                  30  
Val Leu His Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser  
35                  40                  45  
Thr Asp Trp Ala Ala Val Ala Ala Pro Arg Pro Arg Pro Pro Ala  
50                  55                  60  
Val Pro Pro Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro  
65                  70                  75                  80  
Pro Thr Pro Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala  
                  85                  90                  95  
Leu Ser Pro Pro  
                  100

(2) INFORMATION FOR SEQ ID NO:2348:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 536 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1503144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:

|            |            |            |            |             |             |     |
|------------|------------|------------|------------|-------------|-------------|-----|
| attacacacc | agcctcttga | tgcaggtttt | agtgcattt  | tggaaatcatg | caaggkccctc | 60  |
| agkgcggttt | agcttttcag | tcccttccac | gcacagctga | tttaaatatct | tcgggggcaca | 120 |
| cgctgacagt | cttgagatgc | tctcgattgc | cttcgcgcgg | aacagtgaat  | tgggctccca  | 180 |
| ttacattcta | tccgggtgc  | agagcttgaa | gaagctagag | atttaggaatc | gcccaatttgg | 240 |
| tgacaagccc | ttgctggcaa | acgctgccaa | ctcggaagca | atgcgactccc | tttgatgtct  | 300 |
| gacgtgctca | atgaccttgc | ggcacttcgg | cagcttgcgc | ccaagaatgcc | cgcgtcttagt | 360 |
| ctggagagtc | tgaattatgc | tgcagagaga | ttccoccttg | actctctaac  | agatgagac   | 420 |
| ctgtttgaga | cgtttgatgt | ctacccggca | atttcaggct | caaktgccca  | cacacacagct | 480 |
| tctgtccaca | ttctctaaag | ggcagctgtg | gtctcaaaag | gtactatgga  | agctac      |     |

(2) INFORMATION FOR SEQ ID NO:2349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.,123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | His | Thr | Ser | Leu | Leu | Met | Gln | Val | Leu | Val | Pro | Leu | Trp | Asn | His |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Arg | Xaa | Ser | Xaa | Gly | Phe | Leu | Phe | Gln | Val | Leu | Leu | Thr | Asp | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Phe | Lys | Ser | Ile | Gly | Ala | His | Ala | Asp | Arg | Leu | Glu | Met | Leu | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Phe | Ala | Gly | Asn | Ser | Asp | Leu | Gly | Leu | His | Tyr | Ile | Leu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Cys | Lys | Ser | Leu | Lys | Lys | Leu | Glu | Ile | Arg | Asp | Cys | Pro | Phe | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Lys | Pro | Leu | Leu | Ala | Asn | Ala | Ala | Lys | Leu | Glu | Thr | Met | Arg | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Trp | Met | Ser | Thr | Cys | Ser | Met | Thr | Leu | Gly | Ala | Cys | Gly | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ala | Arg | Cys | Pro | Val | Leu | Val | Trp | Arg | Ser |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1503146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Val | Leu | Val | Pro | Leu | Trp | Asn | His | Ala | Arg | Xaa | Ser | Xaa | Gly |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Phe | Leu | Phe | Gln | Val | Leu | Leu | Thr | Asp | Ser | Val | Phe | Lys | Ser | Ile | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | His | Ala | Asp | Arg | Leu | Glu | Met | Leu | Ser | Ile | Ala | Phe | Ala | Gly | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ser | Asp | Leu | Gly | Leu | His | Tyr | Ile | Leu | Ser | Gly | Cys | Lys | Ser | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Lys Leu Glu Ile Arg Asp Cys Pro Phe Gly Asp Lys Pro Leu Leu Ala  
65 70 75 80  
Asn Ala Ala Lys Leu Glu Thr Met Arg Ser Leu Trp Met Ser Thr Cys  
85 90 95  
Ser Met Thr Leu Gly Ala Cys Gly Ser Leu Arg Ala Arg Cys Pro Val  
100 105 110  
Leu Val Trp Arg Ser  
115

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

Met Leu Ser Ile Ala Phe Ala Gly Asn Ser Asp Leu Gly Leu His Tyr  
1 5 10 15  
Ile Leu Ser Gly Cys Lys Ser Leu Lys Lys Leu Glu Ile Arg Asp Cys  
20 25 30  
Pro Phe Gly Asp Lys Pro Leu Leu Ala Asn Ala Ala Lys Leu Glu Thr  
35 40 45  
Met Arg Ser Leu Trp Met Ser Thr Cys Ser Met Thr Leu Gly Ala Cys  
50 55 60  
Gly Ser Leu Arg Ala Arg Cys Pro Val Leu Val Trp Arg Ser  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

atcaatgcgc gggtcaggct ctggaagcca atggtggagg agatgtacgt ggaggagatg 60  
aaggccgagg gcaggacggc gggggccagc agcaggtagg cgtcgcgkcg ccaacaaccc 120  
taaccctagc agcgcggcgc acgcctccga ggcggcgtaga ggacg

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr  
1 5 10 15  
Val Glu Glu Met Lys Ala Glu Gly Arg Thr Ala Gly Ala Ser Ser Arg  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..54  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..453  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| ctctcagcgcg | gctccagcaca | atccggcaat | cccgctcccc  | caagctcgctg | ctgcgcgcgct | 120 |
| ctctcccgccg | ctccgcgcgat | gagctctccc | ctctcgctccg | ccgctgcgcg  | cgatctccgcg | 160 |
| ctgcagctggc | agcattggtct | ccctctcgta | gtctccctccc | gcactccgc   | cgatctccgc  | 200 |
| ggcgacgctgc | cgcttgcctg  | ttctgcgcgc | ggggcgcttc  | accggtgcac  | cgctgcgctg  | 240 |
| ccctggcgctc | ttctccgcgc  | tcgcgcgcgc | gtccgcgcgc  | ctctccctcg  | gcgctcgaga  | 280 |
| ctcaagcttt  | gaktactgct  | gtgttgatt  | catgccccgt  | gaaggatagt  | tgcgactgcg  | 320 |
| ctcgtggagca | cgcttctcaa  | acttaaacag | ctccgcgata  | aaaggaaagc  | actgctgcgt  | 420 |
| gggctttacca | cacagctgct  | gaagcatggg | aagc        |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Gly | Ser | Ser | Gln | Ser | Gly | Asn | Pro | Ala | Pro | Pro | Ala | Arg |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Ser | Pro | Ala | Leu | Leu | Arg | Pro | Pro | Pro | Trp | Xaa | Leu | Pro | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Val | Ala | Gly | Asp | Leu | Arg | Leu | Asp | Leu | Glu | His | Gly | Phe | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Tyr | Val | Pro | Pro | Arg | Thr | Pro | Pro | Leu | Pro | Arg | Gly | Gln | Ala | Pro |

50                      55                      60  
Phe Val Val Leu Ala Arg Gly Ala Val His Gly Cys Ile Gly Arg Leu  
65                      70                      75                      80  
Pro Arg Val Leu Leu Arg Pro Arg Ala Arg Leu Glu Ser Pro Leu Pro  
85                      90                      95  
Arg Arg

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..115

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

Ser Pro Ala Ala Pro Ala Asn Pro Ala Ile Pro Leu Pro Gln Leu Ala  
1                      5                      10                      15  
Ala Arg Pro Leu Ser Ser Ala Leu Arg His Xaa Ala Phe Pro Ser Ala  
20                      25                      30  
Ser Pro Ser Pro Ala Ile Ser Ala Ser Thr Trp Ser Met Ala Ser Leu  
35                      40                      45  
Arg Thr Ser Leu Pro Ala Leu Arg Pro Ser Pro Ala Gly Arg Leu Arg  
50                      55                      60  
Ser Ser Phe Ser Pro Ala Gly Arg Ser Thr Ala Ala Ser Val Gly Cys  
65                      70                      75                      80  
Leu Gly Ser Phe Ser Gly Leu Ala Pro Val Ser Asn Leu Leu Ser Leu  
85                      90                      95  
Gly Ala Glu Asn Ser Ser Phe Xaa His Arg Leu Phe Gly Leu Met Pro  
100                      105                      110  
Val Glu Gly  
115

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..109

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

Leu Gln Arg Leu Gln Pro Ile Arg Gln Ser Arg Ser Pro Ser Ser Leu  
1                      5                      10                      15  
Leu Ala Arg Ser Pro Pro Pro Ser Ala Met Xaa Pro Ser Pro Pro Pro  
20                      25                      30  
Pro Arg Arg Arg Arg Ser Pro Pro Arg Pro Gly Ala Trp Leu Pro Ser  
35                      40                      45  
Val Arg Pro Ser Pro His Ser Ala Pro Pro Pro Arg Ala Gly Ser Val  
50                      55                      60  
Arg Arg Ser Arg Pro Arg Gly Gly Pro Arg Leu His Arg Ser Ala Ala  
65                      70                      75                      80  
Ser Gly Pro Ser Pro Ala Ser Arg Pro Ser Arg Ile Ser Ser Pro Ser  
85                      90                      95  
Ala Leu Arg Thr Gln Ala Leu Xaa Ile Gly Cys Leu Asp  
100                      105

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| aaaggatgca  | ctgggtccag  | tccaacctcc  | ctgagctgtg | atgggaatcg | cattccctct | 60  |
| ataattccta  | taaatagggg  | ccctcccgct  | cccatcacaa | tcacccatca | ctcgtatat  | 120 |
| tccattccca  | agtccecgct  | cttggtattcc | cgacgacgag | ctcggagctt | cttcttccct | 180 |
| gctcgggtgct | cgccgcaaca  | gctgccgcca  | tgtctgcgcg | gaaccagctc | gccgctctgg | 240 |
| tcagcaacat  | gtacgccacg  | ggtttgcttg  | acgatcagtt | ccacgagctc | cagctsttcc | 300 |
| aggacccccg  | cgccccctgac | tttcgtctcc  | gaggtcgtea | cgctcttctg | tcaggacggc | 360 |
| gagcgggatca | tcgaagagct  | ggccaaactg  | ctggagaagc | ccaacgtgga | ttttgacagg | 420 |
| gttgacgcct  | ytgtgcatca  | gctcaaggga  | agcag      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Lys | Gly | Cys | Thr | Gly | Ser | Ser | Ser | Thr | Ser | Leu | Ser | Cys | Asp | Gly | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Arg | Ile | Pro | Ser | Ile | Ile | Pro | Ile | Asn | Arg | Gly | Pro | Pro | Ala | Pro | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Ile | Thr | His | His | Ser | Leu | Tyr | Ser | His | Ser | Lys | Ser | Pro | Leu | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Ser | Arg | Arg | Arg | Ala | Arg | Ser | Phe | Phe | Phe | Pro | Ala | Arg | Cys | Ser |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Gln | Gln | Leu | Pro | Pro | Cys | Leu | Pro | Arg | Thr | Ser | Ser | Pro | Leu | Trp |  |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Ala | Thr | Cys | Thr | Pro | Arg | Val | Cys | Leu | Thr | Ile | Ser | Ser | Ser | Ser |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Ser | Xaa | Ser | Arg | Thr | Pro | Ala | Pro | Leu | Thr | Phe | Val | Ser | Glu | Val |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Val | Thr | Leu | Phe | Cys | Gln | Asp | Gly | Glu | Arg | Ile | Ile | Glu | Glu | Leu | Ala |  |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Lys | Leu | Leu | Glu | Lys | Pro | Asn | Val | Asp | Phe | Asp | Arg | Val | Asp | Ala | Xaa |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Val | His | Gln | Leu | Lys | Gly | Ser |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 145 |     | 150 |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1503170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

|             |             |            |            |             |            |     |
|-------------|-------------|------------|------------|-------------|------------|-----|
| ctatggactt  | cggtgaaggt  | ttgcctcgct | cacagcatgc | tgattgcatc  | ctgggtattg | 60  |
| tggacaaaatt | ctctaaatat  | ggccacttcc | ttccactcag | tcattccctat | actgctcact | 120 |
| cggttgctca  | cagcttcttg  | ttcaatgttt | acaagatcca | tggtctttct  | tcagttatta | 180 |
| tttcggatcg  | tgacctagtg  | ttcaccagcc | agttttggca | acaacccgtt  | cgctctgcgg | 240 |
| gcattgagct  | taagccgagt  | tcttcttacc | atccccaaac | cgacggacag  | accgaacaag | 300 |
| tcaatcaatg  | cttggaaaaca | tatctgcgct | gcttcgcaaa | tgtctgcccc  | acgaaatgga | 360 |
| aagagtgggt  | gcctgtgggc  | gagtagtggt | acaacaccag | ctccactct   | gcactggggc | 420 |
| gtgcaccatt  | tgaggttctt  | tatggccgcc | aaccctgtac | c           |            |     |

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Val | Glu | Gly | Leu | Pro | Arg | Ser | Gln | His | Ala | Asp | Cys | Ile |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Leu | Val | Ile | Val | Asp | Lys | Phe | Ser | Lys | Tyr | Gly | His | Phe | Leu | Pro | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | His | Pro | Tyr | Thr | Ala | His | Ser | Val | Ala | His | Ser | Phe | Leu | Phe | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | Tyr | Lys | Ile | His | Gly | Leu | Ser | Ser | Val | Ile | Ile | Ser | Asp | Arg | Asp |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Leu | Val | Phe | Thr | Ser | Gln | Phe | Trp | Gln | Gln | Pro | Phe | Arg | Leu | Ala | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | Leu | Lys | Pro | Ser | Ser | Ser | Tyr | His | Pro | Gln | Thr | Asp | Gly | Gln |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Thr | Glu | Gln | Val | Asn | Gln | Cys | Leu | Glu | Thr | Tyr | Leu | Arg | Cys | Phe | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Val | Cys | Pro | Thr | Lys | Trp | Lys | Glu | Trp | Leu | Pro | Val | Gly | Glu | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Tyr | Asn | Thr | Ser | Leu | His | Ser | Ala | Leu | Gly | Arg | Ala | Pro | Phe | Glu |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Val | Leu | Tyr | Gly | Arg | Gln | Pro | Arg | Thr |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Val | Glu | Gly | Leu | Pro | Arg | Ser | Gln | His | Ala | Asp | Cys | Ile |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |     |
| Leu | Val | Ile | Val | Asp | Lys | Phe | Ser | Lys | Tyr | Gly | His | Phe | Leu | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ser | His | Pro | Tyr | Thr | Ala | His | Ser | Val | Ala | His | Ser | Phe | Leu | Phe | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Val Tyr Lys Ile His Gly Leu Ser Ser Val Ile Ile Ser Asp Arg Asp  
50 55 60  
Leu Val Phe Thr Ser Gln Phe Trp Gln Gln Pro Phe Arg Leu Ala Gly  
65 70 75 80  
Ile Glu Leu Lys Pro Ser Ser Ser Tyr His Pro Gln Thr Asp Gly Gln  
85 90 95  
Thr Glu Gln Val Asn Gln Cys Leu Glu Thr Tyr Leu Arg Cys Phe Ala  
100 105 110  
Asn Val Cys Pro Thr Lys Trp Lys Glu Trp Leu Pro Val Gly Glu Tyr  
115 120 125  
Trp Tyr Asn Thr Ser Leu His Ser Ala Leu Gly Arg Ala Pro Phe Glu  
130 135 140  
Val Leu Tyr Gly Arg Gln Pro Arg Thr  
145 150

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| acacttcgat | cagtgtcgcc  | aacaagtgc  | tagacgatga | gcagaggagc  | tgagaagaag  | 60  |
| aattggccgc | cgctctgcgtc | ttcttctctc | tcctctcttt | caccgcagctc | gtcgtnngggt | 120 |
| cgccagcagg | tcctatggcgg | ggttctaccg | ctaccgcgtc | tcacatcgca  | ctctccgcaw  | 180 |
| kgacagaacc | cagccgcgcg  | cagcaccagc | tgacccgaca | caacaacaag  | gcgacaagag  | 240 |
| cagcagcaag | aagaagagga  | ggagtatcag | catcgccgcg | agcatcacgt  | gcgcgggctc  | 300 |
| catctgcagt | accaaggaga  | gtcgggtcat | gagccgggac | cgccgcggcg  | cctccagcag  | 360 |
| gtcgctcagg | gcaccctacg  | tcgacgtcga | cgtcaacgac | gcctctgcgc  | ccgcatctc   | 420 |
| cgccacgtcg | tccttcaact  | cggagaccac | cgtggc     |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Arg | Gly | Ala | Glu | Lys | Lys | Asn | Trp | Pro | Pro | Ser | Arg | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Ser | Ser | Ser | Ser | Ser | Pro | Thr | Ser | Ser | Xaa | Gly | Arg | Gln | Gln | Val |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Gly | Gly | Val | Leu | Pro | Leu | Pro | Val | Leu | His | Ser | His | Leu | Arg | Xaa |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Xaa | Gln | Asn | Pro | Ala | Ala | Ser | Thr | Ser | Cys | Thr | Asp | Thr | Thr | Thr | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Arg | Gln | Glu | Gln | Gln | Gln | Glu | Glu | Glu | Glu | Tyr | Gln | His | Arg |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Pro | Glu | His | His | Val | Arg | Gly | Leu | His | Leu | Gln | Tyr | Gln | Gly | Glu | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | His | Glu | Pro | Gly | Pro | Pro | Arg | Arg | Leu | Gln | Gln | Val | Ala | Gln | Gly |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Thr | Leu | Arg | Arg | Arg | Arg | Arg | Gln | Arg | Arg | Leu | Cys | Arg | Arg | His | Leu |

115 120 125  
Arg His Val Val Leu Gln Leu Gly Asp His Arg Gly  
130 135 140  
(2) INFORMATION FOR SEQ ID NO:2366:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..107  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503193  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:  
Met Ala Gly Phe Tyr Arg Tyr Pro Ser Ser Thr Arg Thr Ser Gly Xaa  
1 5 10 15  
Asp Arg Thr Gln Pro Pro Ala Pro Ala Ala Pro Thr Gln Gln  
20 25 30  
Gly Asp Lys Ser Ser Ser Lys Lys Lys Arg Arg Ser Ile Ser Ile Gly  
35 40 45  
Arg Ser Ile Thr Cys Ala Gly Ser Ile Cys Ser Thr Lys Glu Ser Ser  
50 55 60  
Val Met Ser Arg Asp Arg Arg Gly Ala Ser Ser Arg Ser Leu Arg Ala  
65 70 75 80  
Pro Tyr Val Asp Val Asn Asp Ala Ser Ala Ala Ala Ile Ser  
85 90 95  
Ala Thr Ser Ser Phe Asn Ser Glu Thr Thr Val  
100 105  
(2) INFORMATION FOR SEQ ID NO:2367:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 512 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..512  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503200  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:  
atgcatgctg aaactgtggc aaattggaac cacttattca gttggtgttt tgc aaattca 60  
gatttgggtg aattactgac tctcaactgc cctgctgaca gagcaatggt gotgctgatg 120  
tacc aaattg agttgagact gctcaattgg gcttggcgag acgagtggtg ctccaactcg 180  
tgtctacttc gattacacag tgttgttcat agcagcctag ccaatgttta taaatcctgg 240  
ttgataacag tgattcaccc aaacactcca attggccaag atcatttttg gcataacgtg 300  
gatagggtgt tgggtgtgtg aattaaggat agatgctgtg caagattggc aaagctagtgt 360  
ttatctgcta cactgacaca agattctggc aagctttctc aacttgaatt gcaccatcca 420  
ttgtgttgta atactcagtc aagcggcttg aggacaagcc ggatttcaag cggtggggaa 480  
tatcagcata tcactcttct ctaagtcaaa ag  
(2) INFORMATION FOR SEQ ID NO:2368:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..170  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Met His Ala Glu Thr Val Ala Asn Trp Asn His Leu Phe Ser Trp Cys  
1 5 10 15  
Phe Ala Asn Ser Asp Leu Gly Glu Leu Thr Leu Asn Cys Pro Ala  
20 25 30  
Asp Arg Ala Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu  
35 40 45  
Asn Trp Ala Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg  
50 55 60  
Leu His Ser Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp  
65 70 75 80  
Leu Ile Thr Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe  
85 90 95  
Trp His Asn Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys  
100 105 110  
Cys Ala Arg Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp  
115 120 125  
Ser Gly Lys Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn  
130 135 140  
Thr Gln Ser Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu  
145 150 155 160  
Tyr Gln His Ile Ile Phe Ser Ser Ser Gln  
165 170

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1503202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

Met His Ala Glu Thr Val Ala Asn Trp Asn His Leu Phe Ser Trp Cys  
1 5 10 15  
Phe Ala Asn Ser Asp Leu Gly Glu Leu Leu Thr Leu Asn Cys Pro Ala  
20 25 30  
Asp Arg Ala Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu  
35 40 45  
Asn Trp Ala Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg  
50 55 60  
Leu His Ser Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp  
65 70 75 80  
Leu Ile Thr Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe  
85 90 95  
Trp His Asn Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys  
100 105 110  
Cys Ala Arg Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp  
115 120 125  
Ser Gly Lys Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn  
130 135 140  
Thr Gln Ser Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu  
145 150 155 160  
Tyr Gln His Ile Ile Phe Ser Ser Ser Gln  
165 170

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503203  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:  
Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu Asn Trp Ala  
1 5 10 15  
Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg Leu His Ser  
20 25 30  
Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp Leu Ile Thr  
35 40 45  
Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe Trp His Asn  
50 55 60  
Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys Cys Ala Arg  
65 70 75 80  
Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp Ser Gly Lys  
85 90 95  
Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn Thr Gln Ser  
100 105 110  
Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu Tyr Gln His  
115 120 125  
Ile Ile Phe Ser Ser Ser Gln  
130 135

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..345  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:  
tctccgcgca ctccacccca ctgcgcgcgc ccgctgccac cgcgcttgc tgcgcgagcc 60  
gccatggggg cgtacaagta cgtatcggaa ctatggagga ggaagcagtc ggacgtgatg 120  
cgcgctacgc cgcgcgcgcgc gcgcgcgtga gggactgatg tgtgggccca tctcgcttc 180  
ggcgcgagta tcttatctat ctatagtatc gtgttaccgt tcgctcttgt caccgtgtta 240  
gtgtccgttc tacctttgga ttagggtgtg gtaccctgt gtccctttt ggttgctccc 300  
gctatgaaac gagacgagag aagaatgagc aaggtttttg ttcgc

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

Ser Pro Arg Thr Pro Pro His Ser Pro Pro Leu Pro Pro Pro Leu  
1 5 10 15  
Ala Ala Ala Ala Ala Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp  
20 25 30  
Arg Arg Lys Gln Ser Asp Val Met Ala Ala Thr Ala Ala Ala Ala

35 40 45  
Ala Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile  
50 55 60  
Leu Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu  
65 70 75 80  
Val Ser Val Leu Pro Leu Asp  
85

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..51

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Ser Ala His Ser Thr Pro Leu Ala Ala Ala Thr Ala Ala Cys  
1 5 10 15  
Cys Arg Ser Arg His Gly Gly Val Gln Val Arg Ile Gly Thr Met Glu  
20 25 30  
Glu Glu Ala Val Gly Arg Asp Gly Gly Tyr Gly Gly Gly Gly  
35 40 45  
Trp Arg Asp  
50

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..66

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp Arg Arg Lys Gln Ser  
1 5 10 15  
Asp Val Met Ala Ala Thr Ala Ala Ala Ala Gly Gly Thr Asp  
20 25 30  
Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu Ser Ile Tyr Ser  
35 40 45  
Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val Ser Val Leu Pro  
50 55 60  
Leu Asp  
65

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..400

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

cccggttaaaa tcacgacgcg gtggtgactg gtgagtcac agtccacact ccccaactcca 60  
ttttctacca teacactgac acgttcatag ctagctagtc ttcagctagt aacgtacgac 120  
ggactaatct cgatctggga gcgaggagga ggacgacgat aatgaagatg agctccgtgc 180  
cgcggcgass cgggtgatgg tgggtggtgt gctgctctct gcggcgggcg cgactgtgac 240  
ggggcaggcg cttgtgcggg gcgtgatgat ctteggcgac tcggtggttg acgcaggcaa 300  
caacaaccgg ctacgcacgc tggtgcgcg cgacttcccg ccctacggcc gcgacttccc 360  
gcgacgacac gcgcccacgg gntnnctgc aacggcaagc

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..68

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

Met Val Val Val Val Leu Leu Ser Ala Ala Ala Thr Val Thr Gly  
1 5 10 15  
Gln Ala Leu Val Pro Gly Val Met Ile Phe Gly Asp Ser Val Val Asp  
20 25 30  
Ala Gly Asn Asn Asn Arg Leu Ala Thr Leu Val Arg Ala Asp Phe Pro  
35 40 45  
Pro Tyr Gly Arg Asp Phe Pro Ala Thr His Ala Pro Thr Xaa Xaa Pro  
50 55 60  
Ala Thr Ala Ser  
65

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..45

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

Met Ile Phe Gly Asp Ser Val Val Asp Ala Gly Asn Asn Asn Arg Leu  
1 5 10 15  
Ala Thr Leu Val Arg Ala Asp Phe Pro Pro Tyr Gly Arg Asp Phe Pro  
20 25 30  
Ala Thr His Ala Pro Thr Xaa Xaa Pro Ala Thr Ala Ser  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..463

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

ctctttctcc ccagtagcaa cgaccggcg tctctcgccn ccgcactaaa cctactcca 60  
tgtaccacagg tctgcgtcgg gcccccggc gatgagaacc cgtcagttcc aaagatgggt 120

cgtcgtggat tgaatgaaca kgacttaagc aaactggatg tgacgaagct tcacccctgt 180  
tcacctgaag ttatctcaag ccaagcaaca atcaatatgg gtaccattgg ccatgtggct 240  
kcatggaaag tccactgttg ttaaaagtat atctggtggt cagactgttc ggttcaagaa 300  
tgagctggaa cgtaacatta ctataaagct gggttacgct aatgcaaaaa tctacaaatg 360  
tgaggatgac agatgtccgc gaccaatgtg ctacaaggcc tatggaaagc gaaaaakaag 420  
tagccctcta tgtgatgtgc ctggatttga aaacactaga atg

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

Leu Phe Leu Pro Ser Ser Asn Asp Arg Ala Ser Ser Ala Xaa Ala Leu  
1 5 10 15  
Asn Pro Thr Pro Cys Thr Gln Val Cys Val Gly Pro Pro Gly Asp Glu  
20 25 30  
Asn Pro Ser Val Pro Lys Met Ala Arg Arg Gly Leu Met Glu Xaa Asp  
35 40 45  
Leu Ser Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu Val  
50 55 60  
Ile Ser Arg Gln Ala Thr Ile Asn Met Gly Thr Ile Gly His Val Ala  
65 70 75 80  
Xaa Trp Lys Val His Cys Cys  
85

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1503277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

Met Ala Arg Arg Gly Leu Met Glu Xaa Asp Leu Ser Lys Leu Asp Val  
1 5 10 15  
Thr Lys Leu His Pro Leu Ser Pro Glu Val Ile Ser Arg Gln Ala Thr  
20 25 30  
Ile Asn Met Gly Thr Ile Gly His Val Ala Xaa Trp Lys Val His Cys  
35 40 45  
Cys

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1503278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:  
Met Trp Xaa His Gly Lys Ser Thr Val Val Lys Ala Ile Ser Gly Val  
1 5 10 15  
Gln Thr Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys  
20 25 30  
Leu Gly Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Arg Cys  
35 40 45  
Pro Arg Pro Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Xaa Asp Ser  
50 55 60  
Pro Leu Cys Asp Val Pro Gly Phe Glu Asn Thr Arg Met  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

|            |            |            |             |            |            |     |
|------------|------------|------------|-------------|------------|------------|-----|
| ttgttgatga | tttagtgcaa | tctgggggaa | ctcttagaga  | atgccagaad | agttctagct | 60  |
| ttgcatggcg | ctgcaaaagt | cagtgtctat | gtgactcatg  | ctgtgtttcc | taagcagtca | 120 |
| tatgaacggt | tcatggcgct | tagttctgct | gggccagggtg | acagatttgc | ttacttctgg | 180 |
| atcacggact | catgccacca | cacagtaaaa | gctattgggc  | aaagacctcc | atttgaggtt | 240 |
| ctagacctcg | ctggctcaat | tcgagatgct | cttcagatat  | gagcgtacac | tggtagatgc | 300 |
| ctaggggctt | ggattgttga | tgcccaccag | attgaaaactt | gtactatgag | gtggaatgct | 360 |
| cccgcttttc | ctaaatgtaa | gagttgggtt | ccagttctcg  | gaaaagcaaa | taatgtgtag | 420 |
| taagttaaag | tacctgaagg | ttccataaac | agccctgtgg  | ctt        |            |     |

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

Val Asp Asp Leu Val Gln Ser Gly Gly Thr Leu Arg Glu Cys Gln Xaa  
1 5 10 15  
Ser Ser Ser Phe Ala Trp Arg Cys Lys Ser Gln Cys Leu Cys Asp Ser  
20 25 30  
Cys Cys Val Ser  
35

(2) INFORMATION FOR SEQ ID NO:2384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Met Leu Cys Phe Leu Ser Ser His Met Asn Val Ser Trp Arg Leu Val  
1 5 10 15  
Leu Leu Gly Gln Val Thr Asp Leu Leu Thr Ser Gly Ser Arg Thr His  
20 25 30  
Ala His Thr Gln  
35

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

Met Ala Ser Ser Ser Ala Gly Pro Gly Asp Arg Phe Ala Tyr Phe Trp  
1 5 10 15  
Ile Thr Asp Ser Cys Pro His Thr Val Lys Ala Ile Gly Gln Arg Pro  
20 25 30  
Pro Phe Glu Val Leu Ser Leu Ala Gly Ser Ile Ala Asp Ala Leu Gln  
35 40 45  
Ile

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

cacagggtgc tgaagtgtgata gagaaagctc cagatggcac tccagctggt ggtggccttg 60  
tttatgttgt tgttcatgaa gcccaagatc ttgaggggaa gcaccataca aacccataatg 120  
caaaaataat ttcaaaagcc gaggagaaga aaactaaggt catcaagaag aatagggatc 180  
caagatggga ggatgagttt gagtctcgtgt gtgaggagcc tcctgtgaat gataaactgc 240  
atgttggaat cataagtaaa gcccgaagc agggctgata catggcaagg aaactttggg 300  
ctatattgat attagccttg cagacgtgat cagcaacaag cggattaatg aaaagtacca 360  
tctcatagac tcgaaaaaatg gtcagatcca gatcgagttg cagtggaaga ctctctagac 420  
aggaagwgwc cagaatgcct tgaatgttct ctattcagtt tgcgtatatc tgtgattgag 480  
gattgaggtc atgtagataa tttctttt

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

Gln Gly Ala Asp Val Ile Glu Lys Ala Pro Asp Gly Thr Pro Ala Gly  
1 5 10 15

Gly Gly Leu Leu Tyr Val Val Val His Glu Ala Gln Asp Leu Glu Gly  
20 25 30  
Lys His His Thr Asn Pro Tyr Ala Lys Ile Ile Phe Lys Gly Glu Glu  
35 40 45  
Lys Lys Thr Lys Val Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp  
50 55 60  
Glu Phe Glu Phe Val Cys Glu Glu Pro Pro Val Asn Asp Lys Leu His  
65 70 75 80  
Val Glu Val Ile Ser Lys Ala Pro Lys Gln Gly  
85 90

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tacatcgtga | tattaagtct | agcaacatct | tgcttgatgg | cagtttcgag | gcccggtgat | 60  |
| cagactttgg | acttgcaaaq | cttttagagg | atgaagaatc | acatattact | acaatagtgt | 120 |
| caggaacatt | tggtaccctt | gcaccagagt | atatgcaatt | tgccagagca | ccgagaagac | 180 |
| tgatgtctac | agttttgggg | ttttgttact | cgaaataact | agtggaagac | ggcctactga | 240 |
| tgcatccttc | attgagaagg | gactaaacat | tggtggatgg | ttaaattttc | ttgctagtga | 300 |
| gaaccggggg | aggggaattg | tcgacctgaa | ctgtgaagga | gtgcagactg | agaccttaga | 360 |
| tgccctgtgc | tctcttgcca | agcaatgtgt | tagctcctcg | ccagagagag | gccgacaatg | 420 |
| gcaggggtgg | tacatatgct | gggagtcgga | tgtaattaca | ccgtgcacct | gcgacttcta | 480 |
| tg         |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| His Arg Asp Ile Lys Ser Ser Asn Ile Leu Leu Asp Gly Ser Phe Glu |  |
| 1 5 10 15                                                       |  |
| Ala Arg Val Ser Asp Phe Gly Leu Ala Lys Leu Leu Glu Asp Glu Glu |  |
| 20 25 30                                                        |  |
| Ser His Ile Thr Thr Ile Val Ala Gly Thr Phe Gly Tyr Leu Ala Pro |  |
| 35 40 45                                                        |  |
| Glu Tyr Met Gln Phe Gly Arg Ala Pro Arg Arg Leu Met Ser Thr Val |  |
| 50 55 60                                                        |  |
| Leu Gly Phe Trp Tyr Ser Lys Tyr Ser Val Glu Ser Gly Leu Leu Met |  |
| 65 70 75 80                                                     |  |
| His Pro Ser Leu Arg Arg Asp                                     |  |
| 85                                                              |  |

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..448

(D) OTHER INFORMATION: / Ceres Seq. ID 1503305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

|             |             |            |             |             |             |     |
|-------------|-------------|------------|-------------|-------------|-------------|-----|
| aagcagcaac  | atatcaagct  | cagagcctca | gagcgccass  | caagtctttgc | ggtcgccaag  | 60  |
| agcaacgcga  | caagatgggtg | aagctcgcat | tcggaagcgt  | cggcgactcc  | ttcagcgctca | 120 |
| ccctccatcaa | ggcctacgtn  | gcggaagtta | tcgccaccct  | cctctctcgtc | ttcgccggcg  | 180 |
| tggtttccgc  | catcgctctc  | gggcaactga | cgaatggcgg  | cgcgctggac  | cctgcgggac  | 240 |
| tggtggcgat  | cgcggtggcg  | cacgcgctgg | ccctctctcgt | ggcgctctcc  | gtggccgcga  | 300 |
| acacctccgc  | cgccaccctg  | aaccccgccg | tgacgttcgg  | cctggccctg  | ggcgccacat  | 360 |
| tcaccgtcct  | caccggcctc  | ttctactggg | tgggccccag  | tgctggggcg  | gtccgtggcg  | 420 |
| tgctggctc   | ctcaggttcg  | tgacccac   |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ser | Asn | Ile | Ser | Ser | Ser | Glu | Pro | Gln | Ser | Ala | Xaa | Gln | Val | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Ser | Arg | Arg | Ala | Thr | Gln | Gln | Asp | Gly | Ala | Arg | Ile | Arg | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Leu | Leu | Gln | Arg | His | Leu | His | Gln | Gly | Leu | Arg | Xaa | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Val | His | Arg | His | Pro | Pro | Leu | Arg | Leu | Arg | Arg | Gly | Phe | Arg | His |     |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Leu | Arg | Ala | Thr | Asp | Glu | Trp | Arg | Arg | Ala | Gly | Pro | Cys | Gly | Thr |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Gly | Gly | Asp | Arg | Gly | Gly | Ala | Arg | Ala | Gly | Pro | Leu | Arg | Gly | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Gly | Arg | Glu | His | Leu | Arg | Arg | Pro | Pro | Glu | Pro | Arg | Arg | Asp | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Pro | Gly | Arg | Gly | Arg | His | Ile | His | Arg | Pro | His | Arg | Pro | Leu | Leu |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Leu | Gly | Gly | Pro | Ser | Cys | Trp | Ala | Arg | Pro | Trp | Arg | Ala | Trp | Leu | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Phe | Val | Thr | His |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1503307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Thr | Tyr | Gln | Ala | Gln | Ser | Leu | Arg | Ala | Pro | Xaa | Lys | Ser | Cys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Arg | Glu | Glu | Gln | Arg | Asn | Lys | Met | Val | Lys | Leu | Ala | Phe | Gly | Ser |

20 25 30  
Val Gly Asp Ser Phe Ser Val Thr Ser Ile Lys Ala Tyr Xaa Ala Glu  
35 40 45  
Phe Ile Ala Thr Leu Leu Phe Val Phe Ala Gly Val Gly Ser Ala Ile  
50 55 60  
Ala Phe Gly Gln Leu Thr Asn Gly Gly Ala Leu Asp Pro Ala Gly Leu  
65 70 75 80  
Val Ala Ile Ala Val Ala His Ala Leu Ala Leu Phe Val Gly Val Ser  
85 90 95  
Val Ala Ala Asn Thr Ser Gly Gly His Leu Asn Pro Ala Val Thr Phe  
100 105 110  
Gly Leu Ala Val Gly Gly Thr Phe Thr Val Leu Thr Gly Leu Phe Tyr  
115 120 125  
Trp Val Gly Pro Ala Ala Gly Arg Val Arg Gly Val Pro Gly Ser Ser  
130 135 140  
Gly Ser  
145

(2) INFORMATION FOR SEQ ID NO:2393:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1503308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

Met Val Lys Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Val Thr  
1 5 10 15  
Ser Ile Lys Ala Tyr Xaa Ala Glu Phe Ile Ala Thr Leu Leu Phe Val  
20 25 30  
Phe Ala Gly Val Gly Ser Ala Ile Ala Phe Gly Gln Leu Thr Asn Gly  
35 40 45  
Gly Ala Leu Asp Pro Ala Gly Leu Val Ala Ile Ala Val Ala His Ala  
50 55 60  
Leu Ala Leu Phe Val Gly Val Ser Val Ala Ala Asn Thr Ser Gly Gly  
65 70 75 80  
His Leu Asn Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly Thr Phe  
85 90 95  
Thr Val Leu Thr Gly Leu Phe Tyr Trp Val Gly Pro Ala Ala Gly Arg  
100 105 110  
Val Arg Gly Val Pro Gly Ser Ser Gly Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:2394:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 464 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1503322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

gtggcctcgt ctcttccccc acttcggcct cggcagttcc gacttcgcgc tcgccggccgcg 60  
agcctcgtcc cgccttcgat ctgcgacttc ggcgccttcg cgcctgcgatt tcttagcagc 120  
tcctcggcgc ctccaccacc cccctgcgcgc gcgagatgga gctcaagccc ggcattgctgcg 180  
cgctcgtcac cggcggcgcc tcggcgatcg ggaaagcact ttgtattgct tttgcaagga 240

ggggttttatt tgtgactgtc gttgatttct cagaggaaaa tggaagagaa gttgctacat 300  
tagttcaaaa agaaaatagc aaatttcacg gagatcttag aattccatct tcaatatttg 360  
ttaagtgtga tgttagtaat cgagataatc ttgctgcttg ttttgagaag catgtacaga 420  
catacaatgg actagatatc tgcatacaat gtgctggaat tgct

(2) INFORMATION FOR SEQ ID NO:2395:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..87  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

Trp Pro Arg Leu Leu Pro His Phe Gly Leu Gly Ser Ser Asp Phe Arg  
1 5 10 15  
Val Pro Ala Gly Ala Ser Ser Arg Phe Ala Ser Arg Thr Ser Arg Leu  
20 25 30  
Arg Arg Cys Asp Ser Leu Ala Ala Pro Arg Pro Leu His Pro Pro Leu  
35 40 45  
Arg Arg Arg Asp Gly Ala Gln Ala Arg His Val Gly Ala Arg His Arg  
50 55 60  
Arg Arg Leu Arg His Arg Glu Ser Thr Leu Tyr Cys Phe Cys Lys Glu  
65 70 75 80  
Gly Phe Ile Cys Asp Cys Arg  
85

(2) INFORMATION FOR SEQ ID NO:2396:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..103  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

Met Glu Leu Lys Pro Gly Met Ser Ala Leu Val Thr Gly Gly Ala Ser  
1 5 10 15  
Gly Ile Gly Lys Ala Leu Cys Ile Ala Phe Ala Arg Arg Gly Leu Phe  
20 25 30  
Val Thr Val Val Asp Phe Ser Glu Glu Asn Gly Arg Gly Val Ala Thr  
35 40 45  
Leu Val Gln Lys Glu Asn Ser Lys Phe His Gly Asp Leu Arg Ile Pro  
50 55 60  
Ser Ser Ile Phe Val Lys Cys Asp Val Ser Asn Ala Asp Asn Leu Ala  
65 70 75 80  
Ala Cys Phe Glu Lys His Val Gln Thr Tyr Asn Gly Leu Asp Ile Cys  
85 90 95  
Ile Asn Cys Ala Gly Ile Ala  
100

(2) INFORMATION FOR SEQ ID NO:2397:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1503325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Leu | Val | Thr | Gly | Gly | Ala | Ser | Gly | Ile | Gly | Lys | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Cys | Ile | Ala | Phe | Ala | Arg | Arg | Gly | Leu | Phe | Val | Thr | Val | Val | Asp | Phe |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Glu | Glu | Asn | Gly | Arg | Glu | Val | Ala | Thr | Leu | Val | Gln | Lys | Glu | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Phe | His | Gly | Asp | Leu | Arg | Ile | Pro | Ser | Ser | Ile | Phe | Val | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Cys | Asp | Val | Ser | Asn | Ala | Asp | Asn | Leu | Ala | Ala | Cys | Phe | Glu | Lys | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Gln | Thr | Tyr | Asn | Gly | Leu | Asp | Ile | Cys | Ile | Asn | Cys | Ala | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1503330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

|            |             |             |             |            |            |     |
|------------|-------------|-------------|-------------|------------|------------|-----|
| tgtagagagt | ttcaggtgct  | cagcaacaag  | gataggatct  | gatggtgagg | tcgcatttgt | 60  |
| ctgaggcatt | ggggacatgc  | actcgtctga  | agaaacttga  | tcttagggac | aacttggttg | 120 |
| gtgttgatgc | aggggttagct | ctcagcgaaa  | cccttcctctg | actacctgat | ctgtgtgagc | 180 |
| tttatctcag | tgatctcaat  | cttgagaaca  | agggtactat  | agcaattgca | aaagccctca | 240 |
| aacagtcagc | actgcagttg  | gaggtccttg  | aaattgctgg  | aaatgaaata | aatgccaaag | 300 |
| cagccccaga | tttggtcgaa  | tgctctagcag | taatgcagtc  | actcaagaag | ctgaccttgg | 360 |
| ctgaaaatga | actgaaggac  | aatggtgctg  | tgataattgc  | aaaatcattg | gaagatggcc | 420 |
| actcagatct | caaggaaact  | gatgtgagca  | cgaacatgct  | gcagagggtt | ggagctcggg | 480 |
| gctttacgc  |             |             |             |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Ser | His | Leu | Ser | Glu | Ala | Leu | Gly | Thr | Cys | Thr | Arg | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Lys | Lys | Leu | Asp | Leu | Arg | Asp | Asn | Leu | Phe | Gly | Val | Asp | Ala | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ala | Leu | Ser | Glu | Thr | Leu | Pro | Lys | Leu | Pro | Asp | Leu | Val | Glu | Leu | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Asp | Leu | Asn | Leu | Glu | Asn | Lys | Gly | Thr | Ile | Ala | Ile | Ala | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Lys | Gln | Ser | Ala | Leu | Gln | Leu | Glu | Val | Leu | Glu | Ile | Ala | Gly |

65 70 75 80  
Asn Glu Ile Asn Ala Lys Ala Ala Pro Asp Leu Ala Glu Cys Leu Ala  
85 90 95  
Val Met Gln Ser Leu Lys Lys Leu Thr Leu Ala Glu Asn Glu Leu Lys  
100 105 110  
Asp Asn Gly Ala Val Ile Ile Ala Lys Ser Leu Glu Asp Gly His Ser  
115 120 125  
Asp Leu Lys Glu Leu Asp Val Ser Thr Asn Met Leu Gln Arg Val Gly  
130 135 140  
Ala Arg Cys Phe Thr  
145

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 1503332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| tctcttcttc | caatcattgg | tggttggtgct | ctagctgctg | tcacagagct | gaactttaat | 60  |
| atggttggat | ttaggggtgc | catgatatacc | aaccttgc   | ttgtttccg  | caacatcttc | 120 |
| tcgaagagg  | catgaagggg | aagtcctgca  | gtggcatgaa | ttaactacgt | tgccgtgcaa | 180 |
| ttagtccct  | ggtcatactg | actccatttg  | ctatagctat | ggaaggccct | caaatgtggg | 240 |
| ctgtggttg  | gcaaaaggct | cttcgagaag  | ttggacccaa | tggtgtctg  | tggtgtgctg | 300 |
| cacagagcgt | gtctaccac  | ttatataacc  | aggtgtccca | catgtctctc | gacagattt  | 360 |
| ctccattgac | atccagcatt | ggcaatacaa  | tgaagcgat  | atcagtgatt | gtttcatcaa | 420 |
| tcattatctt | ccacactcct | gtccgcgt    |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1503333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Lys Gly Lys Ser Val Ser Gly Met Asn Tyr Tyr Ala Cys Leu Ser |  |
| 1 5 10 15                                                       |  |
| Ile Met Ser Leu Val Ile Leu Thr Pro Phe Ala Ile Ala Met Glu Gly |  |
| 20 25 30                                                        |  |
| Pro Gln Met Trp Ala Ala Gly Trp Gln Lys Ala Leu Ala Glu Val Gly |  |
| 35 40 45                                                        |  |
| Pro Asn Val Val Trp Trp Ile Ala Ala Gln Ser Val Phe Tyr His Leu |  |
| 50 55 60                                                        |  |
| Tyr Asn Gln Val Ser Tyr Met Ser Leu Asp Gln Ile Ser Pro Leu Thr |  |
| 65 70 75 80                                                     |  |
| Phe Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ser Ser |  |
| 85 90 95                                                        |  |
| Ile Ile Ile Phe His Thr Pro Val Arg Ala                         |  |
| 100 105                                                         |  |

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..98  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503334  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:  
Met Asn Tyr Tyr Ala Cys Leu Ser Ile Met Ser Leu Val Ile Leu Thr  
1 5 10 15  
Pro Phe Ala Ile Ala Met Glu Gly Pro Gln Met Trp Ala Ala Gly Trp  
20 25 30  
Gln Lys Ala Leu Ala Glu Val Gly Pro Asn Val Val Trp Trp Ile Ala  
35 40 45  
Ala Gln Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser  
50 55 60  
Leu Asp Gln Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys  
65 70 75 80  
Arg Ile Ser Val Ile Val Ser Ser Ile Ile Ile Phe His Thr Pro Val  
85 90 95  
Arg Ala

(2) INFORMATION FOR SEQ ID NO:2403:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 89 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..89  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503335  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:  
Met Ser Leu Val Ile Leu Thr Pro Phe Ala Ile Ala Met Glu Gly Pro  
1 5 10 15  
Gln Met Trp Ala Ala Gly Trp Gln Lys Ala Leu Ala Glu Val Gly Pro  
20 25 30  
Asn Val Val Trp Trp Ile Ala Ala Gln Ser Val Phe Tyr His Leu Tyr  
35 40 45  
Asn Gln Val Ser Tyr Met Ser Leu Asp Gln Ile Ser Pro Leu Thr Phe  
50 55 60  
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ser Ser Ile  
65 70 75 80  
Ile Ile Phe His Thr Pro Val Arg Ala  
85

(2) INFORMATION FOR SEQ ID NO:2404:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503336  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:  
aacacataga ggcgtgagga cgttggtcat cagtcacac ctatctaact agctagctag 60  
cttgaaacaag agcgtacgta gcaagaaaac agctccgctg cgagagaaaag ctaagggacc 120  
tagctagcta tcatgtcttg gacctaccgt gagaacgcgc tgttcgagcg scctctggcca 180

cctacgacgccc ggacacgccc aggcgggtggg agctcgtggc cgccgcgggtg ggc  
(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Trp | Thr | Tyr | Arg | Glu | Asn | Ala | Leu | Phe | Glu | Xaa | Leu | Trp | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Pro | Thr | Thr | Gly | Thr | Arg | Pro | Gly | Gly | Gly | Ser | Ser | Trp | Pro | Pro | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

Trp

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| actttccatt | gaggatggta | cagtattgaa | gtccttcagc | caccttctcc | atcgtaacaa | 60  |
| gaaggtagat | ttcattgaac | agttcaatga | aaagcttctg | gtcaagcagg | aaggggagaa | 120 |
| tcctcaaat  | cttgatgtaa | ggaaactcca | attgacagaa | gtgagcagaa | ctgagtttat | 180 |
| gactccatct | gcctttattt | tctgtatga  | gctgcaactg | tctctgacgt | tccggaatcg | 240 |
| atcagtagca | gtttggaact | tctgaggtga | actgggtcac | tcatttgaag | atcacctgtt | 300 |
| gtggcaccc  | gactgcaaca | caaacaacat | atacattaca | agtgatcaag | atcttattat | 360 |
| ttcatactgc | aagcgtgact | caactgattc | ctcttcagaa | gaaaatgctg | gctctataaa | 420 |
| cataagcagc | atactgacgg | gcaaatgctt | ggcaaaaata | aacctgtgaa | attcgcgac  |     |

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ile | Glu | Asp | Gly | Thr | Val | Leu | Lys | Ser | Phe | Ser | His | Leu | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| His | Arg | Asn | Lys | Lys | Val | Asp | Phe | Ile | Glu | Gln | Phe | Asn | Glu | Lys | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Leu | Val | Lys | Gln | Glu | Gly | Glu | Asn | Leu | Gln | Ile | Leu | Asp | Val | Arg | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Phe | Gln | Leu | Thr | Glu | Val | Ser | Arg | Thr | Glu | Phe | Met | Thr | Pro | Ser | Ala |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Phe | Leu | Tyr | Glu | Leu | Gln | Leu | Phe | Leu | Thr | Phe | Arg | Asn | Arg |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |     |

Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu Val Thr Ser Phe Glu  
85 90 95  
Asp His Leu Leu Trp His Pro Asp Cys Asn Thr Asn Asn Ile Tyr Ile  
100 105 110  
Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys Lys Ala Asp Ser Thr  
115 120 125  
Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile Asn Ile Ser Ser Ile  
130 135 140  
Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro Gly Asn Ser Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

Met Thr Pro Ser Ala Phe Ile Phe Leu Tyr Glu Leu Gln Leu Phe Leu  
1 5 10 15  
Thr Phe Arg Asn Arg Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu  
20 25 30  
Val Thr Ser Phe Glu Asp His Leu Leu Trp His Pro Asp Cys Asn Thr  
35 40 45  
Asn Asn Ile Tyr Ile Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys  
50 55 60  
Lys Ala Asp Ser Thr Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile  
65 70 75 80  
Asn Ile Ser Ser Ile Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro  
85 90 95  
Gly Asn Ser Arg  
100

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

agagttgttg attgcaggga aaccgccaat tggcaaggat gaagcttgtg accgccttcg 60  
ttgtgctgct cttttctctc ctcccgcact cgtccaccgc ggaggacttc gatctctctc 120  
accttgccca acagtgccgc ggctegtctc gcgacacgcg gcagggttgc tgcctcccg 180  
acggcgccgg caagccggab snctgttcgg catccacggg ctgtggccaa ctacgcccaak 240  
tgccgcgcc gccaccgc

(2) INFORMATION FOR SEQ ID NO:2410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..86  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503346  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:  
Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala Cys  
1 5 10 15  
Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val His  
20 25 30  
Arg Gly Gly Leu Arg Phe Leu Leu Pro Cys Pro Thr Val Ala Gly Leu  
35 40 45  
Val Leu Arg His Ala Ala Gly Leu Leu Leu Pro Gly Arg Arg Gly Gln  
50 55 60  
Ala Gly Xaa Arg Phe Gly Ile His Gly Leu Trp Pro Thr Thr Pro Xaa  
65 70 75 80  
Ala Ala Ala Ala Thr Thr  
85

(2) INFORMATION FOR SEQ ID NO:2411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Lys Leu Val Thr Ala Phe Val Val Leu Leu Phe Ser Leu Leu Pro  
1 5 10 15  
Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln  
20 25 30  
Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp  
35 40 45  
Gly Ala Gly Lys Pro Xaa Xaa Val Ser Ala Ser Thr Gly Cys Gly Gln  
50 55 60  
Leu Arg Gln Xaa Pro Arg Pro Pro Pro Pro  
65 70

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1503351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

aattctactaa aaaaactctc caactgcggc aattgccaac cgccagcacc agcgccgccg 60  
ccccgntccc cccgcggcgg cctcgagaaa ttggattggc tgggcgcgtg acccgccgcc 120  
gccgtccgcg agcagcagcg acccccctcg ccggccatga cctctgctca ttccaagc

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..36  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503352  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:  
Asn Leu Leu Lys Lys Leu Ser Asn Cys Gly Asn Cys Gln Pro Pro Ala  
1 5 10 15  
Pro Ala Pro Pro Pro Xaa Leu Pro Arg Arg Leu Gly Glu Leu Asp  
20 25 30  
Trp Leu Gly Ala  
35

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..58  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

Ser Thr Lys Lys Thr Leu Gln Leu Arg Gln Leu Pro Thr Ala Ser Thr  
1 5 10 15  
Ser Ala Ala Ala Pro Xaa Pro Pro Pro Ala Pro Arg Arg Ile Gly Leu  
20 25 30  
Ala Gly Arg Val Thr Arg Arg Arg Arg Pro Arg Ala Ala Ala Thr Pro  
35 40 45  
Leu Ala Gly His Asp Leu Cys Ser Phe Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..492  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

atacagaagt ggtagggttc ttccggcgct ctgctgcatc tgatcactgt cgtttgcgtg 60  
caacaaatgg atcagttcac catgaactga ttgacgcaga ccatggcaga ccaagaagtg 120  
cgatcaggtg ctgcagcagc acggcaaggg gaaggaccag ggactattac ataccaggtg 180  
ctgggcacgc caattcaatc cacacctcag cagatcaaag aggtttacag gaaactccag 240  
aagcaacace atccagacat cgccggctac aaggggccac actacacgct gctgctgaac 300  
gaggcgtaga aggttctgat gcgggatgtt tccagttcca ggcacgcaga tggaaggggc 360  
aggagtaggg tggggtcagg agccggttac accgtggacg gatacagttc ttgggaaggg 420  
cccgtagaaa gccaaagctct cttcgtggac gagaacaagt gcataggatg ccgggagtg 480  
gtgcaccatg cc

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

Thr Glu Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys  
1 5 10 15  
Arg Leu Leu Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg  
20 25 30  
His His Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Ser Thr Ala  
35 40 45  
Arg Gly Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn  
50 55 60  
Ser Ile His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu  
65 70 75 80  
Ala Thr Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala  
85 90 95  
Ala Ala Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe  
100 105 110  
Gln Ala Arg Arg Trp Lys Gly Gln Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1503356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys Arg Leu  
1 5 10 15  
Leu Thr Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg His His  
20 25 30  
Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Ser Thr Ala Arg Gly  
35 40 45  
Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn Ser Ile  
50 55 60  
His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu Ala Thr  
65 70 75 80  
Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala Ala Ala  
85 90 95  
Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe Gln Ala  
100 105 110  
Arg Arg Trp Lys Gly Gln Glu  
115

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met Ala Asp Gln Glu Val Arg Ser Gly Ala Ala Ala Arg Gln Gly  
1 5 10 15  
Glu Gly Pro Gly Thr Ile Thr Tyr Gln Val Leu Gly Ile Ala Ile Gln

|                                                                 |     |     |     |    |    |  |
|-----------------------------------------------------------------|-----|-----|-----|----|----|--|
|                                                                 | 20  |     | 25  |    | 30 |  |
| Ser Thr Pro Gln Gln Ile Lys Glu Ala Tyr Arg Lys Leu Gln Lys Gln | 35  | 40  | 45  |    |    |  |
| His His Pro Asp Ile Ala Gly Tyr Lys Gly His Asp Tyr Thr Leu Leu | 50  | 55  | 60  |    |    |  |
| Leu Asn Glu Ala Tyr Lys Val Leu Met Arg Asp Val Ser Ser Ser Arg | 65  | 70  | 75  | 80 |    |  |
| His Ala Asp Gly Arg Gly Arg Ser Arg Val Gly Ser Gly Ala Gly Tyr | 85  | 90  | 95  |    |    |  |
| Thr Val Asp Gly Tyr Ser Ser Trp Glu Gly Pro Val Arg Ser Gln Ala | 100 | 105 | 110 |    |    |  |
| Leu Phe Val Asp Glu Asn Lys Cys Ile Gly Cys Arg Glu Cys Val His | 115 | 120 | 125 |    |    |  |
| His Ala                                                         | 130 |     |     |    |    |  |

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

|                                                                      |     |
|----------------------------------------------------------------------|-----|
| acatgcaaaag tataaacacag accagatcaa acccaagttc aggcctccgc aatcattccag | 60  |
| caagccacta ttgagtgccg atccactctat catctccgc gatcttgaac caaatgactg    | 120 |
| tttcactata ttgcactcag atgagttgtg ggagcacctc agcaatcaaag aagccgttga   | 180 |
| gattgttcaac agccatcaac gtgctggaag cgcaagaaga ctattataag ccgctctaca   | 240 |
| agaagcagcg cgnaasstga gatgcgttac tcggtatctta caaagatcga taagaaagt    | 300 |
| cgcaggcatt tccatgatga cattactgtc atcgtcttat ttataaacta tgacctatta    | 360 |
| ttgaaagggt ctccgcagga caaccctctc ccatcatgatg tgccctagat tattgacagt   | 420 |
| gagctagttc acccactggt attcaagctc ctgcgtgcag cc                       |     |

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

|                                                                 |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|----|
| His Ala Lys Tyr Asn Thr Asp Gln Ile Lys Pro Lys Phe Arg Leu Pro | 1   | 5   | 10  | 15 |
| Glu Ser Phe Ser Lys Pro Leu Leu Ser Ala Asp Pro Ser Ile Ile Ser | 20  | 25  | 30  |    |
| Arg Asp Leu Glu Pro Asn Asp Cys Phe Ile Ile Phe Ala Ser Asp Gly | 35  | 40  | 45  |    |
| Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Glu Ile Val His Ser | 50  | 55  | 60  |    |
| His Gln Arg Ala Gly Ser Ala Arg Arg Leu Ile Lys Ala Ala Leu Gln | 65  | 70  | 75  | 80 |
| Glu Ala Ala Xaa Xaa Xaa Arg Cys Val Thr Arg Ile Leu Gln Arg Ser | 85  | 90  | 95  |    |
| Ile Arg Lys Phe Ala Gly Ile Ser Met Met Thr Leu Leu Ser Ser Ser | 100 | 105 | 110 |    |

Tyr Leu

(2) INFORMATION FOR SEQ ID NO:2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tttcggtgcc | gccaccagc  | cccttaacnc | tggttcctct | agccgtctcg | cgcagcacag | 60  |
| cttcatttc  | tcctccgacg | gggtgcggc  | tagctcaacc | atggcggaac | ccaaggccac | 120 |
| ctcggcggtc | accctccgca | ctckcaagtt | catgaccaac | cgggggcccn | tgctggcccg | 180 |
| cwaacaattt | gtgcttgagg | ttatccacc  | cgggcgcgcc | aacgtctcca | agcgaggatt | 240 |
| gaaggggaag | ggcttgccaa | gatgtacgag | gtgaaggacc | ccaacaccat | cttcgtcttc | 300 |
| aagttccgca | cccacttcgg | tgagggaag  | tcactggct  | tcgggc     |            |     |

(2) INFORMATION FOR SEQ ID NO:2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Arg | Ala | Ala | Thr | Gln | Pro | Leu | Asn | Xaa | Arg | Ser | Ser | Ser | Arg | Leu |     |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Gln | His | Ser | Leu | His | Phe | Ser | Ser | Ser | Asp | Gly | Gly | Ala | Ala | Ser | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Thr | Met | Ala | Asp | Ser | Lys | Ala | Thr | Ser | Ala | Val | Thr | Leu | Arg | Thr | Xaa |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Phe | Met | Thr | Asn | Arg | Gly | Pro | Xaa | Leu | Ala | Arg | Xaa | Gln | Phe | Val |     |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Leu | Glu | Val | Ile | His | Pro | Gly | Arg | Ala | Asn | Val | Ser | Lys | Ala | Glu | Leu |     |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Lys | Gly | Arg | Gly | Leu | Pro | Arg | Cys | Thr | Arg |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Val | Pro | Pro | Pro | Ser | Pro | Leu | Xaa | Leu | Val | Pro | Leu | Ala | Val | Ser |  |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |  |
| Arg | Ser | Thr | Ala | Ser | Ile | Ser | Pro | Pro | Thr | Ala | Val | Arg | Leu | Ala | Gln |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Pro | Trp | Arg | Thr | Pro | Arg | Pro | Pro | Arg | Arg | Ser | Pro | Ser | Ala | Leu | Xaa |  |

35 40 45  
Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asp | Ser | Lys | Ala | Thr | Ser | Ala | Val | Thr | Leu | Arg | Thr | Xaa | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |  |
| Phe | Met | Thr | Asn | Arg | Gly | Pro | Xaa | Leu | Ala | Arg | Xaa | Gln | Phe | Val | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Val | Ile | His | Pro | Gly | Arg | Ala | Asn | Val | Ser | Lys | Ala | Glu | Leu | Lys |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Gly | Arg | Gly | Leu | Pro | Arg | Cys | Thr | Arg |     |     |     |     |     |     |     |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

|            |             |            |             |             |             |     |
|------------|-------------|------------|-------------|-------------|-------------|-----|
| tatgaaaaat | caagatctcc  | tgggaggttc | tttgacctag  | tttatcatga  | aaatgccccgt | 60  |
| gttctactcc | atgatgagag  | catataccga | tttgaatgtt  | gctcgagtcc  | gacaagggtg  | 120 |
| tctattcagc | tgatgggaata | tggtcacgaa | aagccagaag  | tgactgcagt  | atcaattgaa  | 180 |
| ccaaattttt | cttcgtatct  | ttttagcgag | tacttgtgta  | gtacgcgaga  | caagaaatta  | 240 |
| tctgaaggcg | tctaccttgg  | aaggaataag | cggaatatatt | caaaataatga | tgaaccttca  | 300 |
| gattctttga | aggcaatgga  | tggtatcaat | gttgtaagt   | gtcttgaatg  | caagatatcc  | 360 |
| tgcaagacct | cgaaagtttc  | atatgtcctt | gatactgaag  | atttcttgtt  | ccggttcg    | 420 |
| aagagaagga | aaatttttgcg | gggcgggaat | gtgcccgacc  | gtttgcagat  | ttcatcaata  | 480 |
| tctgctg    |             |            |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1503423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Glu | Lys | Ser | Arg | Ser | Pro | Gly | Arg | Phe | Asp | Leu | Val | Tyr | His |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Asn | Ala | Arg | Val | Leu | Leu | His | Asp | Glu | Ser | Ile | Tyr | Arg | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Cys | Cys | Ser | Ser | Pro | Thr | Arg | Leu | Ser | Ile | Gln | Leu | Met | Glu | Tyr | Gly |

|                         |                         |                 |
|-------------------------|-------------------------|-----------------|
| 35                      | 40                      | 45              |
| His Glu Lys Pro Glu Val | Thr Ala Val Ser Ile Glu | Pro Asn Phe Ser |
| 50                      | 55                      | 60              |
| Ser Tyr Leu Phe Ser Glu | Tyr Leu Cys Ser Thr Pro | Asp Lys Lys Leu |
| 65                      | 70                      | 75              |
| Ser Glu Gly Val Tyr Leu | Gly Arg Asn Lys Arg Lys | Tyr Ser Asn Asn |
| 80                      | 85                      | 90              |
| Asp Glu Pro Ser Asp Ser | Leu Lys Ala Met Asp Gly | Ile Asn Val Val |
| 100                     | 105                     | 110             |
| Asn Gly Leu Glu Cys Lys | Ile Ser Cys Lys Thr Ser | Lys Val Ser Tyr |
| 115                     | 120                     | 125             |
| Val Leu Asp Thr Glu Asp | Phe Leu Phe Arg Leu Arg | Lys Arg Arg Lys |
| 130                     | 135                     | 140             |
| Ile Leu Arg Gly Gly Asn | Val Pro Asp Arg Leu Gln | Ile Ser Ser Ile |
| 145                     | 150                     | 155             |
| Ser Ala                 |                         | 160             |

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Glu Tyr Gly His Glu Lys Pro Glu Val Thr Ala Val Ser Ile Glu |     |
| 1                                                               | 5   |
| Pro Asn Phe Ser Ser Tyr Leu Phe Ser Glu Tyr Leu Cys Ser Thr Pro | 10  |
| 20                                                              | 25  |
| Asp Lys Lys Leu Ser Glu Gly Val Tyr Leu Gly Arg Asn Lys Arg Lys | 30  |
| 35                                                              | 40  |
| Tyr Ser Asn Asn Asp Glu Pro Ser Asp Ser Leu Lys Ala Met Asp Gly | 45  |
| 50                                                              | 55  |
| Ile Asn Val Val Asn Gly Leu Glu Cys Lys Ile Ser Cys Lys Thr Ser | 60  |
| 65                                                              | 70  |
| Lys Val Ser Tyr Val Leu Asp Thr Glu Asp Phe Leu Phe Arg Leu Arg | 75  |
| 80                                                              | 85  |
| Lys Arg Arg Lys Ile Leu Arg Gly Gly Asn Val Pro Asp Arg Leu Gln | 90  |
| 100                                                             | 105 |
| Ile Ser Ser Ile Ser Ala                                         | 110 |
| 115                                                             |     |

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| acacctactt cataagcctg gccttctccc cgacggccct catcggcctc aactccgacc  | 60  |
| tgaaagtgcc caagttttgag ttctgtgcga acgcgamscg tcgctgttcg attaccacca | 120 |
| gccagtgcac cagcagacca cagccacgtc agtcaaggtg ccggcggsca tctgtcgcac  | 180 |
| ctatgcgaag tcctaatcca gggcaaggaa ggacgcagag agcaaggcca aggcgaagac  | 240 |

agaggactct tccagtgcctt ctacttcgat gcagggtggac ggcgcttctg ctgctgggtgc 300  
tgctgcagag aagaaggccc cggagccaga gcctacgttc cagatcctga cgaaccgggc 360  
ccgggtcggt ccagcccagg agaagttcat aaagttctcg gaagacagca ggtacaagcc 420  
ggtgaaggct gccccctcg

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..41
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Thr Tyr Phe Ile Ser Leu Ala Phe Ser Pro Thr Ala Leu Ile Gly Leu  
1 5 10 15  
Asn Ser Asp Leu Lys Val Pro Lys Phe Glu Phe Leu Ser Asn Ala Xaa  
20 25 30  
Arg Arg Cys Ser Ile Thr Pro Ser Gln  
35 40

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

Met Pro Ser Pro Asn Pro Gly Gln Gly Arg Thr Gln Arg Ala Arg Pro  
1 5 10 15  
Arg Arg Lys Gln Arg Thr Leu Pro Val Leu Leu Leu Arg Cys Arg Trp  
20 25 30  
Thr Ala Leu Leu Leu Val Leu Leu Gln Arg Arg Arg Pro Arg Ser  
35 40 45  
Gln Ser Leu Arg Ser Arg Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

Met Gln Val Asp Gly Ala Ser Ala Ala Gly Ala Ala Glu Lys Lys  
1 5 10 15  
Ala Pro Glu Pro Glu Pro Thr Phe Gln Ile Leu Thr Asn Pro Ala Arg  
20 25 30  
Val Val Pro Ala Gln Glu Lys Phe Ile Lys Phe Leu Glu Asp Ser Arg  
35 40 45  
Tyr Lys Pro Val Lys Ala Ala Pro Ser

50 55

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

|            |             |             |            |            |            |     |
|------------|-------------|-------------|------------|------------|------------|-----|
| actggcggtg | aacagcgaga  | acctaaccag  | gacagcgaa  | acgactcgcc | taacctccgg | 60  |
| acagccacgt | ctttcccccac | ttctccggagc | aaccttcccg | atggcgacgc | gacctcccc  | 120 |
| ccagctgccc | ccgctgccac  | cgccaccacc  | tcgctctcg  | gtctccggcc | actgcgcccc | 180 |
| ttctctccgc | gccttcgctt  | ctggccagca  | ccagtgccgc | ccgcgcgct  | gtgcctttct | 240 |
| cgattgtctc | gggcccaggc  | tgctctccct  | tgcccgccat | acgctgtcga | gccgccgcgc | 300 |
| ggccctcgcc | gcctcctcca  | gagccccctc  | ctccatcccc | gcacggttg  | caagagaggc | 360 |
| tgtaagttt  | gcaggataga  | gcaaggatct  | tccttgccgt | ctgtctctgg | atgtcatgt  | 420 |
| ttttcgggg  | aagtgccttg  | gatggaagta  | acaactcggg | aggcaagaag | c          |     |

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Gly | Glu | Gln | Arg | Glu | Pro | Lys | Gln | Asp | Ser | Glu | His | Asp | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Asn | Leu | Arg | Thr | Ala | Thr | Ser | Phe | Pro | Thr | Leu | Arg | Thr | Asn | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asp | Gly | Asp | Ala | Thr | Ser | Pro | Pro | Ala | Ala | Pro | Ala | Ser | Thr | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Thr | Thr | Ser | Val | Ser | Arg | Leu | Arg | Pro | Leu | Arg | Pro | Phe | Leu | Pro | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Leu | Arg | Phe | Trp | Pro | Ala | Pro | Val | Ala | Ala | Ala | Pro | Xaa | Cys | Leu | Ser |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Arg | Leu | Leu | Trp | Ala | Gln | Ala | Val | Val | Pro | Cys | Pro | Ala | Tyr | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Pro | Pro | Pro | Gly | Pro | Arg | Arg | Pro | Pro | Gln | Ser | Pro | Leu | Leu | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Arg | Thr | Val | Gly | Lys | Arg | Gly | Cys | Gln | Val | Cys | Arg | Ile | Glu | Gln |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Ser | Ser | Leu | Pro | Phe | Cys | Ser | Gly | Cys | His | Cys | Phe | Ser | Gly | Glu |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Val | Leu | Gly | Met | Glu | Val | Thr | Thr | Arg | Glu | Ala | Arg | Ser |     |     |     |
|     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ala | Val | Asn | Ser | Glu | Asn | Leu | Asn | Arg | Thr | Ala | Asn | Thr | Thr | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Leu | Thr | Ser | Gly | Gln | Pro | Arg | Leu | Ser | Pro | Leu | Ser | Gly | Arg | Thr | Phe |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Pro | Met | Ala | Thr | Arg | Pro | Pro | Leu | Gln | Leu | Pro | Pro | Arg | Pro | Pro | Pro |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Pro | Pro | Pro | Ser | Arg | Val | Ser | Gly | His | Cys | Ala | Leu | Ser | Phe | Arg | Ala |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Ala | Ser | Gly | Gln | His | Gln | Trp | Arg | Pro | Arg | Xaa | Cys | Ala | Phe | Leu |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asp | Cys | Ser | Gly | Pro | Arg | Leu | Ser | Ser | Leu | Ala | Arg | His | Thr | Leu | Ser |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Ser | Arg | Arg | Arg | Ala | Leu | Ala | Ala | Leu | Leu | Arg | Ala | Pro | Ser | Ser | Ile |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Pro | Ala | Arg | Leu | Ala | Arg | Glu | Ala | Val | Lys | Phe | Ala | Gly |     |     |     |  |
|     | 115 |     |     |     | 120 |     |     |     |     |     |     | 125 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1503446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Arg | Pro | Pro | Leu | Gln | Leu | Pro | Pro | Arg | Pro | Pro | Pro | Pro |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Pro | Pro | Ser | Arg | Val | Ser | Gly | His | Cys | Ala | Leu | Ser | Phe | Arg | Ala | Phe |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ala | Ser | Gly | Gln | His | Gln | Trp | Arg | Pro | Arg | Xaa | Cys | Ala | Phe | Leu | Asp |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Cys | Ser | Gly | Pro | Arg | Leu | Ser | Ser | Leu | Ala | Arg | His | Thr | Leu | Ser | Ser |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Arg | Arg | Arg | Ala | Leu | Ala | Leu | Leu | Arg | Ala | Pro | Ser | Ser | Ile | Pro |     |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |  |
| Ala | Arg | Leu | Ala | Arg | Glu | Ala | Val | Lys | Phe | Ala | Gly |     |     |     |     |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1503476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| gaaactcact | cgccatcgcc  | gggcatcgcg | ggcatcgcac  | acaaacgcaa | cctgcagcca | 60  |
| tgccacagaa | gtctgcgcca  | ccgacggcgg | sggtcgctgt  | cgctctgtgt | ggcgtcgctt | 120 |
| tgctggccgc | cgccagacaac | tcggggtgcg | cgctcgggcct | gtgctgcagc | cggttcgggt | 180 |
| actcggggac | ggcgaggagac | tactcgggcg | ccgggtgcca  | gtcgggcccc | tcgcagctgc | 240 |
| cgagagacca | caacgcgtcc  | gtggccagca | tcgtgacgcc  | ggccttcttc | gacgcgtcc  | 300 |

tcgcgcaggc cgccgcctcg tgcgaggcca acggcttcta caccgcgcac gccttctctg 360  
ccgcgcgcgg ctactaccgc gcgttcggcc gcaccggcac cgtcgacgac tccaagcgcg 420  
agatgcgcgc cttcttcggc aacgc

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1503477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

Lys Leu Thr Arg His Arg Arg Ala Ser Arg Ala Ser His Thr Asn Ala  
1 5 10 15  
Thr Cys Ser His Gly Thr Glu Ala Arg Ala Thr Asp Gly Xaa Gly Arg  
20 25 30  
Arg Arg Pro Ala Gly Ala Arg Leu Val Gly Arg Arg Ala Glu Leu Arg  
35 40 45  
Val Arg Val Gly Pro Val Leu Gln Pro Val Arg Val Leu Arg Asp Gly  
50 55 60  
Arg Gly Leu Leu Arg Arg Arg Val Pro Val Gly Pro Leu Arg Arg Ala  
65 70 75 80  
Gly Asp Gln Gln Arg Val Arg Gly Gln His Arg Asp Ala Gly Leu Leu  
85 90 95  
Arg Arg Ala Pro Arg Ala Gly Arg Arg Leu Val Arg Gly Gln Arg Leu  
100 105 110  
Leu His Pro Arg Arg Leu Pro Arg Arg Arg Leu Leu Pro Gly Val  
115 120 125  
Arg Pro His Arg His Arg Arg Leu Gln Ala Arg Asp Arg Arg Leu  
130 135 140  
Leu Arg Gln Arg  
145

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1503478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Asn Ser Leu Ala Ile Ala Gly His Arg Gly His Arg Thr Gln Thr Gln  
1 5 10 15  
Pro Ala Ala Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val  
20 25 30  
Val Val Leu Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly  
35 40 45  
Cys Ala Ser Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly  
50 55 60  
Glu Asp Tyr Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro  
65 70 75 80  
Glu Thr Asn Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe  
85 90 95  
Asp Ala Leu Leu Ala Gln Ala Ala Ala Ser Cys Glu Ala Asn Gly Phe  
100 105 110

Tyr Thr Arg Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe  
115 120 125  
Gly Arg Thr Gly Thr Val Asp Ser Lys Arg Glu Ile Ala Ala Phe  
130 135 140  
Phe Gly Asn  
145

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1503479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val Val Val Leu  
1 5 10 15  
Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly Cys Ala Ser  
20 25 30  
Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly Glu Asp Tyr  
35 40 45  
Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro Glu Thr Asn  
50 55 60  
Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe Asp Ala Leu  
65 70 75 80  
Leu Ala Gln Ala Ala Ala Ser Cys Glu Ala Asn Gly Phe Tyr Thr Arg  
85 90 95  
Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe Gly Arg Thr  
100 105 110  
Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe Gly Asn  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1503480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

caaatgcaag agcagcaact gttaagtgt gaaaaacagt gtgccgagca cataatgctt 60  
gtggacttgg gaaggaatga tgttggcaag gtatccaaac caggatcagt gaaggtggag 120  
aagttgatga acattgagag atactcccat gttatgcaca tcagctcaac ggtagtgga 180  
cagttgggatg atcatctcca gaggttggat gccttgagag ctgccttgcc cggtggaaca 240  
gtcagtggtg caccaaaagt gaaggccatg gatgtgattg ataagttgga agttacgagg 300  
cgaggacacat atagtgggtg tctaggagga atatcgtttg atggtgacat gcaaatgaca 360  
ctttctctcc gcaccatcgt attctcaaca gcgccgagcc acaacacgat gtactcatat 420  
aaagacgcag ataggcgctg gggagtggtt cgctcatctt caggctggtg caggcattgt 480  
tgccgacagt agcccagatg acgaacaacg t

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..163  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503481  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:  
Gln Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu  
1 5 10 15  
His Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser  
20 25 30  
Lys Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr  
35 40 45  
Ser His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp  
50 55 60  
His Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr  
65 70 75 80  
Val Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu  
85 90 95  
Glu Val Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser  
100 105 110  
Phe Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe  
115 120 125  
Ser Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp  
130 135 140  
Arg Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys  
145 150 155 160  
Cys Arg Gln

(2) INFORMATION FOR SEQ ID NO:2442:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..162  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503482  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:  
Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu His  
1 5 10 15  
Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys  
20 25 30  
Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser  
35 40 45  
His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His  
50 55 60  
Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val  
65 70 75 80  
Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu  
85 90 95  
Val Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser Phe  
100 105 110  
Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser  
115 120 125  
Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg  
130 135 140  
Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys

145  
Arg Gln

150

155

160

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..145

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Val | Asp | Leu | Gly | Arg | Asn | Asp | Val | Gly | Lys | Val | Ser | Lys | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Ser | Val | Lys | Val | Glu | Lys | Leu | Met | Asn | Ile | Glu | Arg | Tyr | Ser | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Met | His | Ile | Ser | Ser | Thr | Val | Ser | Gly | Gln | Leu | Asp | Asp | His | Leu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gln | Ser | Trp | Asp | Ala | Leu | Arg | Ala | Ala | Leu | Pro | Val | Gly | Thr | Val | Ser |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Ala | Pro | Lys | Val | Lys | Ala | Met | Glu | Leu | Ile | Asp | Lys | Leu | Glu | Val |  |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |  |
| Thr | Arg | Arg | Gly | Pro | Tyr | Ser | Gly | Gly | Leu | Gly | Gly | Ile | Ser | Phe | Asp |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Gly | Asp | Met | Gln | Ile | Ala | Leu | Ser | Leu | Arg | Thr | Ile | Val | Phe | Ser | Thr |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ala | Pro | Ser | His | Asn | Thr | Met | Tyr | Ser | Tyr | Lys | Asp | Ala | Asp | Arg | Arg |  |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Arg | Gly | Val | Gly | Arg | Ser | Ser | Ser | Gly | Trp | Cys | Arg | His | Cys | Cys | Arg |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..515

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| aatcaacacc  | agaagctctc | gattccaccg | aggaagaaga | gaggaaatggc | gtccgaggag  | 60  |
| gagggaagtcg | tgatgcgctg | ccacaccaag | gccgacttcg | acgcccaaat  | ggccaaggcc  | 120 |
| aaggagggccg | gcaagctggt | gatcattgac | ttcacggcct | cctgggtgcg  | ccctgcccgt  | 180 |
| ttcatcgcg   | cactgttcgt | cgagcaacgc | aagaagtcca | ccagggctgt  | gttctctgaag | 240 |
| gtggacgttg  | acgagctgaa | ggaagttgcc | gcggcctacg | atgtcgaggc  | gatgccgacc  | 300 |
| ttccacttcg  | tcaagaaacg | ggtgacggtg | gagacggctg | tcggtgccag  | gaaggagaaac | 360 |
| ctctctggcc  | agatcgagaa | gcaactgcgc | gcggccgctg | ctgctgcgtc  | tgcgtagaga  | 420 |
| ggatggacca  | gcacgtacgt | ggcggtggtg | gtgggtctgt | cgtttcagtt  | tgggcttgct  | 480 |
| agcgctgtgg  | ctgggtggct | gattgtgaac | tggag      |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..138  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gln | His | Gln | Lys | Leu | Ser | Ile | Pro | Pro | Arg | Lys | Lys | Arg | Gly | Met |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |
| Ala | Ser | Glu | Glu | Glu | Gly | Val | Val | Ile | Ala | Cys | His | Thr | Lys | Ala | Asp |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     |     | 30  |     |     |
| Phe | Asp | Ala | His | Met | Ala | Lys | Ala | Lys | Glu | Ala | Gly | Lys | Leu | Val | Ile |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| Ile | Asp | Phe | Thr | Ala | Ser | Trp | Cys | Gly | Pro | Cys | Arg | Phe | Ile | Ala | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Val | Glu | His | Ala | Lys | Lys | Phe | Thr | Gln | Ala | Val | Phe | Leu | Lys |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Asp | Val | Asp | Glu | Leu | Lys | Glu | Val | Ala | Ala | Tyr | Asp | Val | Glu |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Met | Pro | Thr | Phe | His | Phe | Val | Lys | Asn | Gly | Val | Thr | Val | Glu | Thr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Val | Gly | Ala | Arg | Lys | Glu | Asn | Leu | Leu | Ala | Gln | Ile | Glu | Lys | His |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Cys | Ala | Ala | Ala | Val | Ser | Ala | Ala | Ser | Ala |     |     |     |     |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2446:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Glu | Glu | Gly | Val | Val | Ile | Ala | Cys | His | Thr | Lys | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Phe | Asp | Ala | His | Met | Ala | Lys | Ala | Lys | Glu | Ala | Gly | Lys | Leu |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Ile | Asp | Phe | Thr | Ala | Ser | Trp | Cys | Gly | Pro | Cys | Arg | Phe | Ile |
|     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Phe | Val | Glu | His | Ala | Lys | Lys | Phe | Thr | Gln | Ala | Val | Phe |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Val | Asp | Val | Asp | Glu | Leu | Lys | Glu | Val | Ala | Ala | Tyr | Asp | Val |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Ala | Met | Pro | Thr | Phe | His | Phe | Val | Lys | Asn | Gly | Val | Thr | Val |
|     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Val | Val | Gly | Ala | Arg | Lys | Glu | Asn | Leu | Leu | Ala | Gln | Ile | Glu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| His | Cys | Ala | Ala | Ala | Val | Ser | Ala | Ala | Ser | Ala |     |     |     |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2447:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr  
1 5 10 15  
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu  
20 25 30  
His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp  
35 40 45  
Glu Leu Lys Glu Val Ala Ala Tyr Asp Val Glu Ala Met Pro Thr  
50 55 60  
Phe His Phe Val Lys Asn Gly Val Thr Val Glu Thr Val Val Gly Ala  
65 70 75 80  
Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala  
85 90 95  
Val Ser Ala Ala Ser Ala  
100

(2) INFORMATION FOR SEQ ID NO:2448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1503492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

aacctctagc tgattgatct ctggtttacc actctttcct tccctccttc aattctaaat 60  
accacaaatc aaagtgtgctt tgcgatgggtg agcagcagca tggacacgac gaggacaaaa 120  
cgtgcgtcat ccattgctggc tectaaccct ggcaaggcca cgtacctcgc ctctggccac 180  
gccttcccg agcagntgtc atgcaggact acgtctgtcga cggtctcatg aagaacacca 240  
tcgtgtacgt gctggagaac atggtggagg acaccgcgcg gaggaggctg ctggctgccg 300  
acgacggtgg agaggactgc gagggtgggc tcatcctcdc gtctggggcg gggatcacgt 360  
tcgagggcac cctcgccagg aacttgcagg caaccgcgcg cgcttcagcc cagccctgat 420  
cacctcttgt tgggttgctt ttctgcttgc tctgcacctc tgctcccggtg tgattgctgc 480  
tttgagggag aatgctgagc atcaacattg ctcattgagca tc

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1503493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Ile Val Tyr  
1 5 10 15  
Val Leu Glu Asn Met Val Glu Asp Thr Arg Arg Arg Arg Leu Leu Ala  
20 25 30  
Ala Asp Asp Gly Gly Glu Asp Cys Glu Trp Gly Leu Ile Leu Xaa Phe  
35 40 45  
Gly Pro Gly Ile Thr Phe Glu Gly Ile Leu Ala Arg Asn Leu Gln Ala  
50 55 60  
Thr Ala Arg Ala Ser Ala Gln Pro  
65 70

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Thr | Ile | Val | Tyr | Val | Leu | Glu | Asn | Met | Val | Glu | Asp | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Arg | Arg | Arg | Leu | Leu | Ala | Ala | Asp | Gly | Gly | Glu | Asp | Cys | Glu |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Trp | Gly | Leu | Ile | Leu | Xaa | Phe | Gly | Pro | Gly | Ile | Thr | Phe | Glu | Gly | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Leu | Ala | Arg | Asn | Leu | Gln | Ala | Thr | Ala | Arg | Ala | Ser | Ala | Gln | Pro |     |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Glu | Asp | Thr | Arg | Arg | Arg | Arg | Leu | Leu | Ala | Ala | Asp | Asp | Gly |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Glu | Asp | Cys | Glu | Trp | Gly | Leu | Ile | Leu | Xaa | Phe | Gly | Pro | Gly | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Thr | Phe | Glu | Gly | Ile | Leu | Ala | Arg | Asn | Leu | Gln | Ala | Thr | Ala | Arg | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Ala | Gln | Pro |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atgtcgacac | tctacaccca | cctctctgtc | gagccacggg | tctccccact | agtgaacccg | 60  |
| ctttctcttc | cacgggtgac | ccctcccccc | cagcgcacgg | cctgcgaggg | tgcgacactg | 120 |
| cagcatgccc | gacgccatct | atctcttctt | cgcgtccacg | tagacctccc | ccgtgcctac | 180 |
| gcccatccct | ggtgcggcgg | cgtgcccccc | tcatgcggcc | aacatcgaca | tccttccctt | 240 |
| ctccacgtac | cggctgcaac | tgacggcatc | aaaccccttc | tcacgcccag | ttcatctgtc | 300 |
| tgtggcgccg | gcgcgccttc | tccccgcacg | ctggccttgc | gtcggacacg | tcctccgacg | 360 |
| ccagcgctcc | ctctctcaaa | gatgacgagt | gaggcgtcyc | ctccccacg  | tcacgcgagc | 420 |
| gcaasscagg | gaccataccc | acgcctccct | ccctctcggt | cgcggg     |            |     |

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 155 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..155  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503497  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Leu | Tyr | Thr | His | Pro | Pro | Val | Glu | Pro | Arg | Val | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Gln | Pro | Leu | Ser | Pro | Pro | Arg | Val | Thr | Pro | Pro | Pro | Gln | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Cys | Glu | Ala | Ala | Thr | Leu | Gln | His | Ala | Arg | Arg | His | Leu | Ser |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Pro | Arg | Val | Gln | Leu | Asp | Leu | Pro | Arg | Ala | Tyr | Ala | His | Pro | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Arg | Ala | Ala | Pro | Ser | Cys | Gly | Gln | His | Arg | His | Pro | Ser | Pro |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Pro | Val | Pro | Ala | Ala | Thr | Ala | Gly | Ile | Asn | Pro | Phe | Leu | Thr | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Ser | Ala | Cys | Gly | Gly | Gly | Ala | Pro | Pro | Pro | Arg | Thr | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Arg | Arg | Thr | Ala | Pro | Pro | Thr | Pro | Ala | Ser | Pro | Pro | Pro | Lys | Met |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Ser | Glu | Ala | Xaa | Pro | Pro | Pro | Ala | Pro | Ala | Ser | Ala | Xaa | Gln | Gly |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Pro | Tyr | Pro | Arg | Leu | Pro | Pro | Ser | Trp | Ser | Arg |     |     |     |     |     |
|     |     |     |     |     | 145 |     | 150 |     |     | 155 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2454:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 155 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..155  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503498  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Leu | Tyr | Thr | His | Pro | Pro | Val | Glu | Pro | Arg | Val | Ser | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Gln | Pro | Leu | Ser | Pro | Pro | Arg | Val | Thr | Pro | Pro | Pro | Gln | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Cys | Glu | Ala | Ala | Thr | Leu | Gln | His | Ala | Arg | Arg | His | Leu | Ser |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Pro | Arg | Val | Gln | Leu | Asp | Leu | Pro | Arg | Ala | Tyr | Ala | His | Pro | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Arg | Ala | Ala | Pro | Ser | Cys | Gly | Gln | His | Arg | His | Pro | Ser | Pro |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Pro | Val | Pro | Ala | Ala | Thr | Ala | Gly | Ile | Asn | Pro | Phe | Leu | Thr | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Ser | Ala | Cys | Gly | Gly | Gly | Ala | Pro | Pro | Pro | Arg | Thr | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Arg | Arg | Thr | Ala | Pro | Pro | Thr | Pro | Ala | Ser | Pro | Pro | Pro | Lys | Met |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Ser | Glu | Ala | Xaa | Pro | Pro | Pro | Ala | Pro | Ala | Ser | Ala | Xaa | Gln | Gly |
|     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

Val Asp Thr Leu His Pro Pro Ser Cys Arg Ala Thr Gly Leu Pro Thr  
1 5 10  
Ser Ala Thr Ala Phe Ser Ser Thr Gly Asp Pro Ser Pro Pro Ala His  
20 25 30  
Gly Leu Arg Gly Cys Asp Thr Ala Ala Cys Pro Thr Pro Ser Ile Ser  
35 40 45  
Ser Ser Arg Pro Ala Arg Pro Pro Pro Cys Leu Arg Pro Ser Leu Val  
50 55 60  
Arg Pro Arg Cys Pro Leu Met Arg Pro Thr Ser Thr Ser Leu Pro Ser  
65 70 75 80  
Pro Ser Thr Gly Cys Asn Cys Arg His Gln Pro Leu Pro His Ala Gln  
85 90 95  
Phe Ile Cys Leu Trp Arg Arg Arg Ala Ser Ser Pro His Ala Gly Leu  
100 105 110  
Ala Ser Asp Ser Ser Ser Asp Ala Ser Val Pro Ser Ser Lys Asp Asp  
115 120 125  
Glu

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

tcttcattga aaagcttattc gtaaaagkttg ttctacctga agggctcaag gatattcgaag 60  
tttcagctcc cctttccaaca cagcagcagc aagaggttaa gtattcacac cttgacattg 120  
tcggaaagacc agttgtttgct ttggagaaac ctgatgttat tccagagcat aatttgtatt 180  
tccaggttta ctacagattc aacaacatat ccttgctcag agagccggtg atgttgatta 240  
ctggtttctt cctcctctgt gtggcctgta ttgtttacat gcgtactgat atgtcaatat 300  
ccaagagctc tccttcctac ttggccaagc tgcaatggga tgaggtgcaa gcaactgttc 360  
agaaaatcca gggatctttt gagcaatgct tagcagttca tgataaactg gaggcctcat 420  
tgccgggattt gtctaggaca ggagacattc agtcttgcga ggcagctcgt

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1503508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

Leu Ile Glu Lys Leu Ile Val Lys Xaa Val Leu Pro Glu Gly Ser Lys  
1 5 10 15  
Asp Ile Glu Val Ser Ala Pro Leu Pro Thr Gln Gln Gln Gln Glu Val  
20 25 30  
Lys Tyr Ser His Leu Asp Ile Val Gly Arg Pro Val Val Val Leu Glu  
35 40 45  
Lys Pro Asp Val Ile Pro Glu His Asn Leu Tyr Phe Gln Val Tyr Tyr  
50 55 60  
Arg Phe Asn Asn Ile Ser Leu Leu Arg Glu Pro Leu Met Leu Ile Thr  
65 70 75 80  
Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr Met Arg Thr Asp  
85 90 95  
Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala Lys Leu Gln Trp  
100 105 110  
Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly Ile Phe Glu Gln  
115 120 125  
Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu Arg Asp Leu Ser  
130 135 140  
Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1503509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

Met Leu Ile Thr Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr  
1 5 10 15  
Met Arg Thr Asp Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala  
20 25 30  
Lys Leu Gln Trp Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly  
35 40 45  
Ile Phe Glu Gln Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu  
50 55 60  
Arg Asp Leu Ser Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1503510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

ttggatttga caaagatgcc agagaaggc tcttcacat gattaacaac ctgccactg  
tttatgaagt tgtgacgggg gttgctaaga agcaatcgaa agccccaac ggcacgagca

aaagcagcaa gcctaactct aaaccatcaa aactgaccaa ttctaacagt aagcccgcca 180  
mscagcccac cc

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Gly Phe Asp Lys Asp Ala Arg Arg Arg Leu Phe Thr Met Ile Asn Asn  
1 5 10 15  
Leu Pro Thr Val Tyr Glu Val Val Thr Gly Val Ala Lys Lys Gln Ser  
20 25 30  
Lys Ala Pro Asn Gly Ser Ser Lys Ser Ser Lys Pro Asn Ser Lys Pro  
35 40 45  
Ser Lys Leu Thr Asn Ser Asn Ser Lys Pro Ala Xaa Gln Pro Thr  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

Met Ile Asn Asn Leu Pro Thr Val Tyr Glu Val Val Thr Gly Val Ala  
1 5 10 15  
Lys Lys Gln Ser Lys Ala Pro Asn Gly Ser Ser Lys Ser Ser Lys Pro  
20 25 30  
Asn Ser Lys Pro Ser Lys Leu Thr Asn Ser Asn Ser Lys Pro Ala Xaa  
35 40 45  
Gln Pro Thr  
50

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

ctcgagcctg acccttacgc cttcgctcgc gccgccgcgc ccgccgccgc tacgccccgc 60  
acctcgcttc atttcgtgtc gccaaagtga cgaagcgcac taagaaggca ggaattgttg 120  
gcaaatatgg aaccagggtat ggtgctagct tgcgtaassa atcaagaaga tggagggtatc 180  
tcagcattcc aattactttt gcgagttctg tgggaagtgt gctgtgaaga ggaagaatat 240  
agcaagggtt ttgttcgcag ctatttttgt ccaatgatat tgatatt

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..46  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503523  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:  
Met Thr Lys Arg Thr Lys Lys Ala Gly Ile Val Gly Lys Tyr Gly Thr  
1 5 10 15  
Arg Tyr Gly Ala Ser Leu Arg Xaa Xaa Ser Arg Arg Trp Arg Tyr Leu  
20 25 30  
Ser Ile Pro Ile Thr Phe Ala Ser Ser Val Gly Ser Leu Leu  
35 40 45  
(2) INFORMATION FOR SEQ ID NO:2464:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503524  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:  
Met Glu Pro Gly Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly  
1 5 10 15  
Gly Ile Ser Ala Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys  
20 25 30  
Cys Glu Glu Glu Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys  
35 40 45  
Pro Met Ile Leu Ile  
50  
(2) INFORMATION FOR SEQ ID NO:2465:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..49  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503525  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:  
Met Val Leu Ala Cys Val Xaa Asn Gln Glu Asp Gly Gly Ile Ser Ala  
1 5 10 15  
Phe Gln Leu Leu Leu Arg Val Leu Trp Glu Val Cys Cys Glu Glu  
20 25 30  
Arg Met Ser Lys Val Phe Val Arg Ser Tyr Phe Cys Pro Met Ile Leu  
35 40 45  
Ile  
(2) INFORMATION FOR SEQ ID NO:2466:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..498  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503526  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:  
ctagtagaga gaaaggaaga gaagggggcg gagaagcacg tacgtcgtac atcgcccacc 60  
gccctttgccc tcgctcgcgc tcgctcgcgc tgcatactcta acagccggag ccggagccgg 120  
agccggagccc gacgcggcg ccgacaatcg ttccaactga tatggctacg acgcaaccag 180  
gattcacggg caacctgaag aaagcacttg caggctctgag aagaatcagt ttatagtggt 240  
tcgcatggcg cgtatttgat gctaagggtc aggtgctcgg gcgattggct tcccaaatag 300  
ctgttgtgct tcaaggcaag gataaaccga cctatgcacc acatgtagaa aatggagaca 360  
tgtgcattgt acctaatgca aaggatatca gtgtttacag gaaggaaaaat gacagataag 420  
attactattt ggcatacagg gtatgttgcc cattgaagg aaaggaggct caaggaccag 480  
atggagaaag acccaact  
(2) INFORMATION FOR SEQ ID NO:2467:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..65  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503527  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:  
Leu Val Glu Arg Lys Glu Glu Lys Gly Ala Glu Lys His Val Arg Arg  
1 5 10 15  
Thr Ser Pro Thr Ala Leu Cys Leu Ala Ser Pro Arg Leu Ala Cys Ile  
20 25 30  
Ser Asn Ser Arg Ser Arg Ser Arg Ser Arg Arg Arg Arg Arg  
35 40 45  
Gln Ser Phe Gln Leu Ile Trp Leu Arg Arg His Gln Asp Ser Arg Ala  
50 55 60  
Thr  
65  
(2) INFORMATION FOR SEQ ID NO:2468:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 85 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..85  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503528  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:  
Met Ala Thr Thr Pro Gly Phe Thr Gly Asn Leu Lys Lys Ala Leu  
1 5 10 15  
Ala Gly Leu Arg Arg Ile Ser Leu Asp Gly Leu Arg Trp Arg Val Phe  
20 25 30  
Asp Ala Lys Gly Gln Val Leu Gly Arg Leu Ala Ser Gln Ile Ala Val  
35 40 45  
Val Leu Gln Gly Lys Asp Lys Pro Thr Tyr Ala Pro His Val Glu Asn  
50 55 60  
Gly Asp Met Cys Ile Val Leu Asn Ala Lys Asp Ile Ser Val Tyr Arg  
65 70 75 80  
Lys Glu Asn Asp Arg

85

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Thr | Cys | Ala | Leu | Tyr | Leu | Met | Gln | Arg | Ile | Ser | Val | Phe | Thr |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Arg | Lys | Met | Thr | Asp | Lys | Ile | Tyr | Trp | His | Thr | Gly | Tyr | Val |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | His | Leu | Lys | Glu | Arg | Arg | Leu | Lys | Asp | Gln | Met | Glu | Lys | Asp | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

|            |            |            |             |             |            |     |
|------------|------------|------------|-------------|-------------|------------|-----|
| ataaccaag  | ataaccagag | tgtgctggtt | tattgcttct  | catgggttgt  | aattttcggt | 60  |
| gttttactcg | ttatgaagac | cgtatcagtg | gggaggaggga | ggttcagtcg  | agagttccag | 120 |
| ctagtgttcc | ggctgatcaa | gggtctcata | tttataactt  | ttacagccat  | cgtgggtaac | 180 |
| ctaatagcaa | tccttgccat | gacggttctg | gacatctttg  | tttgcatctc  | tgccctcatg | 240 |
| cccactggat | ggggtttgct | cctgattgcc | caagctatca  | ggcctgtgat  | tcaaaagatc | 300 |
| gggctgtggg | ggtcgatcaa | ggctcttgcc | cggggctacg  | agatccaat   | ggggcttctc | 360 |
| ctgttcacgc | ccattgcttt | ccttgctctg | ttcccgcttg  | tgctccgagtt | ccagaccagg | 420 |
| atgctgttca | accagccctt | cagcagaggt | tctgcagatc  | tcccgtatcc  | tgggagg    |     |

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Lys | Asp | Asn | Gln | Ser | Val | Leu | Val | Tyr | Cys | Phe | Ser | Trp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Ile | Phe | Val | Val | Leu | Leu | Val | Met | Lys | Thr | Val | Ser | Val | Gly | Arg |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Arg | Arg | Phe | Ser | Ala | Glu | Phe | Gln | Leu | Val | Phe | Arg | Leu | Ile | Lys | Gly |
|     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Leu | Ile | Phe | Ile | Thr | Phe | Thr | Ala | Ile | Val | Val | Ile | Leu | Ile | Ala | Ile |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |

Pro Gly Met Thr Val Leu Asp Ile Phe Val Cys Ile Leu Ala Phe Met  
65 70 75 80  
Pro Thr Gly Trp Gly Leu Leu Ile Ala Gln Ala Ile Arg Pro Val  
85 90 95  
Ile Gln Lys Ile Gly Leu Trp Gly Ser Ile Lys Ala Leu Ala Arg Gly  
100 105 110  
Tyr Glu Ile Leu Met Gly Leu Leu Leu Phe Thr Pro Ile Ala Phe Leu  
115 120 125  
Ala Trp Phe Pro Phe Val Ser Glu Phe Gln Thr Arg Met Leu Phe Asn  
130 135 140  
Gln Ala Phe Ser Arg Gly Ser Ala Asp Leu Pro Tyr Pro Gly Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1503552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Gly Cys Asn Phe Arg Cys Phe Thr Arg Tyr Glu Asp Arg Ile Ser  
1 5 10 15  
Gly Glu Glu Glu Val Gln Cys Arg Val Pro Ala Ser Val Pro Ala Asp  
20 25 30  
Gln Gly Ser His Ile Tyr Asn Phe Tyr Ser His Arg Gly Asn Pro Asn  
35 40 45  
Ser Asn Pro Trp His Asp Gly Ser Gly His Leu Cys Leu His Pro Cys  
50 55 60  
Leu His Ala His Trp Met Gly Phe Ala Pro Asp Cys Pro Ser Tyr Gln  
65 70 75 80  
Ala Cys Asp Ser Lys Asp Arg Ala Val Gly Val Asp Gln Gly Ser Cys  
85 90 95  
Pro Gly Leu Arg Asp Pro Asn Gly Ala Ser Pro Val His Ala His Cys  
100 105 110  
Phe Pro Cys Leu Val Pro Val Arg Val Arg Val Pro Asp Gln Asp Ala  
115 120 125  
Val Gln Pro Gly Leu Gln Gln Arg Phe Cys Arg Ser Pro Val Ser Trp  
130 135 140  
Glu  
145

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1503553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Lys Thr Val Ser Val Gly Arg Arg Arg Phe Ser Ala Glu Phe Gln  
1 5 10 15  
Leu Val Phe Arg Leu Ile Lys Gly Leu Ile Phe Ile Thr Phe Thr Ala  
20 25 30  
Ile Val Val Ile Leu Ile Ala Ile Pro Gly Met Thr Val Leu Asp Ile

35 40 45  
Phe Val Cys Ile Leu Ala Phe Met Pro Thr Gly Trp Gly Leu Leu Leu  
50 55 60  
Ile Ala Gln Ala Ile Arg Pro Val Ile Gln Lys Ile Gly Leu Trp Gly  
65 70 75 80  
Ser Ile Lys Ala Leu Ala Arg Gly Tyr Glu Ile Leu Met Gly Leu Leu  
85 90 95  
Leu Phe Thr Pro Ile Ala Phe Leu Ala Trp Phe Pro Phe Val Ser Glu  
100 105 110  
Phe Gln Thr Arg Met Leu Phe Asn Gln Ala Phe Ser Arg Gly Ser Ala  
115 120 125  
Asp Leu Pro Tyr Pro Gly Arg  
130 135

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

caggctcctag ctccggcctc cgcgcgcgtc tctcacctcc gtcctcccttc cctgcccccca 60  
tggcgaagcgc gacgcgccga gccgagcgcc gccgcctctc cactgtcccca ctcccacatg 120  
ggcgacacnca cggagggcctt gaccacagtc ctgacccacc cgtcccaccgc gcgctcactc 180  
cactcgcagc tcttctctcgc ctcccgcgtc ccgtgccccgc cgcggggcct cgctctcacc 240  
acgtcgtacc cgcgcctctc ctgccccgny gcctcgtctc tccgctgggc tctcgcctcc 300  
gtgttccctc cgcgcgcgcg agcctctgcc tcccgccttc gtctaggcgg tcccggtgcc 360  
ccttcaggcgc tcccgcgcgc cggctcgtgcc ctccgcgcgc atcgagccgg gcgcccagagc 420

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

Gly Pro Ser Ser Gly Leu Arg Arg Arg Leu Ser Pro Pro Leu Pro Phe  
1 5 10 15  
Pro Ala Pro Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro  
20 25 30  
Leu Thr Ser Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro  
35 40 45  
Arg Pro Asp Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu  
50 55 60  
Pro Arg Leu Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His  
65 70 75 80  
Val Val Pro Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly  
85 90 95  
Ser Arg Leu Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro  
100 105 110  
Ser Ser Trp Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Ser  
115 120 125

Cys Pro Pro Arg Pro Ser Ser Arg Ala Pro Glu  
130 135

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1503556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro Leu Thr Ser  
1 5 10 15  
Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro Arg Pro Asp  
20 25 30  
Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu Pro Arg Leu  
35 40 45  
Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His Val Val Pro  
50 55 60  
Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly Ser Arg Leu  
65 70 75 80  
Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro Ser Ser Trp  
85 90 95  
Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser Cys Pro Pro  
100 105 110  
Arg Pro Ser Ser Arg Ala Pro Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1503557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Gly Ala Xaa Thr Glu Ala Leu Thr His Val Leu Thr His Pro Ser  
1 5 10 15  
His Ala Pro Ser Leu His Ser Gln Leu Phe Leu Ala Ser Arg Val Pro  
20 25 30  
Cys Pro Pro Arg Gly Leu Gly Ser Thr Thr Ser Tyr Pro Pro Leu Leu  
35 40 45  
Cys Pro Xaa Ala Ser Leu Leu Arg Trp Ala Leu Ala Ser Val Phe Leu  
50 55 60  
Pro Arg Ala Arg Ala Ser Ala Ser Arg Pro Arg Pro Gly Gly Pro Gly  
65 70 75 80  
Ala Pro Ser Arg Leu Pro Ala Ala Gly Arg Ala Leu Arg Gly His Arg  
85 90 95  
Ala Gly Arg Pro Ser  
100

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..418  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:  
ttctggctcc tctgtcttcc tcatgatcaa gcgtgtgtcc tctgtccctg cctgtgccag 60  
gcaccacaag gcaaaagaag ctacaggtgag aatgtttgtg tggttgatcc actggaagct 120  
aagcgctcgt ctgctaaaca aatgcaagaa attagggcca aagaaaagct gaagaggcgc 180  
cgtaacagcag aagcgatcaa cggggcattg gcagtgatag gactcacggc tggattgcta 240  
gtggaggctc agacaggaaa ggacatctta gggcagctag ctggatatct gacgctatt 300  
tctagtttat ttgggcaata acactggacc atggttggag atttattttt cacgttccac 360  
ggccaggaga ggtcttatct gaactttatt tgatggatcc acccaatttt ttggggag

(2) INFORMATION FOR SEQ ID NO:2479:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 106 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..106  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:  
Phe Trp Leu Leu Leu Pro His Asp Gln Ala Cys Val Leu Cys Ser  
1 5 10 15  
Val Leu Val Gln Ala Pro Gln Gly Lys Arg Ser Ser Gly Glu Asn Val  
20 25 30  
Val Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met  
35 40 45  
Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala Glu  
50 55 60  
Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu  
65 70 75 80  
Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr  
85 90 95  
Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln  
100 105

(2) INFORMATION FOR SEQ ID NO:2480:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 73 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
    (B) LOCATION: 1..73  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:  
Met Val Asp Pro Leu Glu Ala Lys Arg Leu Ala Ala Lys Gln Met Gln  
1 5 10 15  
Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala Glu Ala  
20 25 30  
Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu Leu Val  
35 40 45  
Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly Tyr Leu  
50 55 60  
Thr Ala Ile Ser Ser Leu Phe Gly Gln

65 70  
(2) INFORMATION FOR SEQ ID NO:2481:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 59 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..59  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503572  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:  
Met Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala  
1 5 10 15  
Glu Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu  
20 25 30  
Leu Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly  
35 40 45  
Tyr Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln  
50 55

(2) INFORMATION FOR SEQ ID NO:2482:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 438 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..438  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503585  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:  
cagaggatat caatatattgg tgggtgaattc ccatacagggc atacagctga tgttcaaagt 60  
gtgtccatca actcatcaat acaaatatgt ttgtctctgg ctcatgtgat acaactgtga 120  
ggctgtggga tatcagaatt gcaagtcgag ctgttcgaac ctaccatgga catgaggatg 180  
atgttaacag tgtgaagttt ttccctgatg gccatagggt ttgtactggc tcagattatg 240  
gcacatgtag attatttgat atgagaacag ggcatacaat tcaggtgtac agtagggagc 300  
ctgatagaaa tagtaatgaa ctaccctactg ttacatctat tgcattttca atatcaggaa 360  
ggctactttt tgcctggttac tccaatgggt actgttatgt gtgggacacm ttctcgccga 420  
ggtggtaactt aattggg

(2) INFORMATION FOR SEQ ID NO:2483:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..117  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503586  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:  
Met Phe Val Ser Gly Ser Cys Asp Thr Thr Val Arg Leu Trp Asp Ile  
1 5 10 15  
Arg Ile Ala Ser Arg Ala Val Arg Thr Tyr His Gly His Glu Asp Asp  
20 25 30  
Val Asn Ser Val Lys Phe Phe Pro Asp Gly His Arg Phe Gly Thr Gly  
35 40 45  
Ser Asp Tyr Gly Thr Cys Arg Leu Phe Asp Met Arg Thr Gly His Gln  
50 55 60

Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg Asn Ser Asn Glu Leu Pro  
65 70 75 80  
Thr Val Thr Ser Ile Ala Phe Ser Ile Ser Gly Arg Leu Leu Phe Ala  
85 90 95  
Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp Asp Xaa Phe Ser Pro Arg  
100 105 110  
Trp Tyr Leu Ile Trp  
115

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

Met Arg Thr Gly His Gln Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg  
1 5 10 15  
Asn Ser Asn Glu Leu Pro Thr Val Trp Ser Ile Ala Phe Ser Ile Ser  
20 25 30  
Gly Arg Leu Leu Phe Ala Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp  
35 40 45  
Asp Xaa Phe Ser Pro Arg Trp Tyr Leu Ile Trp  
50 55

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..506
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

ttcgcgcgcg cgcgcctcgg agaagagata gaggcggcgg ctgcctcgac cccgcgccac 60  
ccccgcctcg ctccccccgg accgatcggg ttgatcgat ggcgtcgaag aggatcctga 120  
aggagttgaa ggaacctgcag aaggaccgcc ccacctcctg cagcgcrtcc tgttggtgag 180  
gacatgttcc attggcaagc gaccatcatg gggccttcgg acagcccatt tgcagggtggg 240  
gtattcttgg tgaacattca ctcccccacg gattaccctt tcaagccacc aaagggtgtet 300  
ttccgcacca aggtttttcca cccgaacatc aacagcaacg gcagcatttg ccttgacatt 360  
cttaaggaaac agtggagtcc tgctttaact atctcaagg ttctcctgtc aatctgctca 420  
ctgctcacgg acccaaaccc tgatgatcct ctgtgccctg agattgctca catgtacaat 480  
tcattcgttg gaaaacctgg aacgtg

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Phe  
1 5 10 15  
Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro  
20 25 30  
Phe Lys Pro Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn  
35 40 45  
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp  
50 55 60  
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Ser Ile Cys Ser Leu  
65 70 75 80  
Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His  
85 90 95  
Met Tyr Asn Ser Phe Val Gly Lys Pro Gly Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

Met Gly Pro Ser Asp Ser Pro Phe Ala Gly Gly Val Phe Leu Val Asn  
1 5 10 15  
Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe  
20 25 30  
Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys  
35 40 45  
Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys  
50 55 60  
Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp  
65 70 75 80  
Pro Leu Val Pro Glu Ile Ala His Met Tyr Asn Ser Phe Val Gly Lys  
85 90 95  
Pro Gly Thr

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

gtacgagcgg acgcacgcagc agcttgactt cgagttccctc gggaaacgtgc gcggcaagga 60  
gtggcgcgctg cagaccaaacg tgtacggcaa cggcagcacg gcggccggcc gggaggagcg 120  
ctacggcctc tggttcgacc ccacggaggga ctccaccgc tacgccatcc actggaccgc 180  
cgacaggatc atattctaca tcgacgcacac gccaatcatg gagatgggtc ggacggagtc 240  
aatggggcgc cagttcccggt ccaagcccat gtcgctgtac gccaccatct gggacggctc 300  
cagctggggc acctcggggg gccgctacaa ggtggactac aagtacgcgc cctacgtcgc 360  
cgaagtcgcc gacctcgccg tcc

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1503592
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:

Tyr Glu Arg Thr His Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Val  
1 5 10 15  
Arg Gly Lys Glu Trp Arg Val Gln Thr Asn Val Tyr Gly Asn Gly Ser  
20 25 30  
Thr Ala Ala Gly Arg Glu Glu Arg Tyr Gly Leu Trp Phe Asp Pro Thr  
35 40 45  
Glu Asp Phe His Arg Tyr Ala Ile His Trp Thr Arg Asp Arg Ile Ile  
50 55 60  
Phe Tyr Ile Asp Asp Thr Pro Ile Met Glu Met Val Arg Thr Glu Ser  
65 70 75 80  
Met Gly Ala Gln Phe Pro Ser Lys Pro Met Ser Leu Tyr Ala Thr Ile  
85 90 95  
Trp Asp Gly Ser Ser Trp Ala Thr Ser Gly Arg Tyr Lys Val Asp  
100 105 110  
Tyr Lys Tyr Ala Pro Tyr Val Ala Glu Phe Ala Asp Leu Ala Leu  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2490:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:

Thr Ser Gly Arg Thr Thr Ser Leu Thr Ser Ser Ser Gly Thr Cys  
1 5 10 15  
Ala Ala Arg Ser Gly Ala Cys Arg Pro Thr Cys Thr Ala Thr Ala Ala  
20 25 30  
Arg Arg Pro Ala Gly Arg Ser Ala Thr Ala Ser Gly Ser Thr Pro Arg  
35 40 45  
Arg Thr Ser Thr Ala Thr Pro Ser Thr Gly Pro Ala Thr Gly Ser Tyr  
50 55 60  
Ser Thr Ser Thr Thr Arg Gln Ser Trp Arg Trp Cys Gly Arg Ser Gln  
65 70 75 80  
Trp Ala Arg Ser Ser Arg Pro Ser Pro Cys Arg Cys Thr Pro Pro Ser  
85 90 95  
Gly Thr Ala Pro Ala Gly Pro Pro Arg Gly Ala Ala Thr Arg Trp Thr  
100 105 110  
Thr Ser Thr Arg Pro Thr Ser Pro Ser Pro Thr Ser Arg Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2491:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1503594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| actgaacatt | ctgctgtaag | attggaagcc | tgttctcaac | atcaaacaccg | ttatttatgg | 60  |
| cctgaatctt | ctttttacgc | aaccaaacga | cgaggatcct | tgaaccacg   | aagctgcagc | 120 |
| tgtccctcgt | ggcaacccaa | agatgtttga | ggcaaatgtg | aaaagagcca  | tgaccggagc | 180 |
| tagctaggcc | aacactattt | ccaaagatgc | ttggcttgat | gtgatggctt  | caagccagcg | 240 |
| ggcccatgta | tcagcaccag | cgcgcccagg | tttggaggat | ttttgtggat  | ttagggcgct | 300 |
| tctggaagca | aaggtcaaat | cggtcggtgt | tgataatgtg | atgtactccc  | tcagttcttt | 360 |
| ttatt      |            |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1503595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Asn | Ile | Leu | Arg | Glu | Asp | Trp | Lys | Pro | Val | Leu | Asn | Ile | Asn | Thr |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Val | Ile | Tyr | Gly | Leu | Asn | Leu | Leu | Phe | Thr | Gln | Pro | Asn | Asp | Glu | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Leu | Asn | His | Glu | Ala | Ala | Ala | Val | Leu | Arg | Gly | Asn | Pro | Lys | Met |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Phe | Glu | Ala | Asn | Val | Lys | Arg | Ala | Met | Thr | Gly | Ala | Thr |     |     |     |  |
|     | 50  |     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Ser | Gln | Arg | Ala | His | Val | Ser | Ala | Pro | Ala | Arg | Pro | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Glu | Asp | Phe | Cys | Gly | Phe | Arg | Ala | Leu | Glu | Ala | Lys | Val | Lys |     |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ser | Val | Val | Val | Asp | Asn | Val | Met | Tyr | Ser | Leu | Ser | Ser | Phe | Tyr |     |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1503597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:  
Met Tyr Gln His Gln Arg Ala Gln Val Trp Arg Ile Phe Val Asp Leu  
1 5 10 15  
Gly Arg Phe Trp Lys Gln Arg Ser Asn Arg Ser Leu Leu Ile Met  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..413

(D) OTHER INFORMATION: / Ceres Seq. ID 1503600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

|            |            |             |            |             |             |     |
|------------|------------|-------------|------------|-------------|-------------|-----|
| atatacgcct | ccaaacccta | gctcttccat  | tcttccccc  | cgggcgccgc  | ctccccccaga | 60  |
| cacttcgccc | cggcgaagat | gggcgcgctg  | attcgcgctc | agssaagggt  | gcgggggtccg | 120 |
| tggtcaagtc | ccataccct  | caccgcaagg  | ccctgcgcgt | tccggtccct  | cgacttcggc  | 180 |
| gagcgcaacg | ggtacctgaa | gggcgtggct  | accgacgtca | tccacgaccc  | gggcgcgggc  | 240 |
| gcgcgcgtgg | ccaaggtcac | cttcgcgccat | ccattccggt | acaagcacca  | gaaggagctg  | 300 |
| ttcgtggctg | ctgagggcct | gtacactggc  | cagttcgttt | actgcggagc  | ccgtgctaca  | 360 |
| ctctccattg | gcaacgtcct | gcgcgtcagg  | gggatccctg | aggggtgccgt | tgt         |     |

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1503601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Arg | Leu | Gly | Thr | Leu | Ala | Leu | Pro | Phe | Pro | Leu | Arg | Arg | Arg |
| 1   | 5   | 10  | 15  | 20  | 25  | 30  | 35  | 40  | 45  | 50  | 55  | 60  | 65  | 70  |
| Leu | Pro | Gln | Thr | Leu | Arg | Arg | Arg | Gln | Asp | Gly | Pro | Arg | Asp | Ser |
| 75  | 80  | 85  | 90  | 95  | 100 | 105 | 110 | 115 | 120 | 125 | 130 | 135 | 140 | 145 |
| Ser | Xaa | Lys | Gly | Ala | Gly | Ser | Val | Phe | Lys | Ser | His | Thr | His | His |
| 150 | 155 | 160 | 165 | 170 | 175 | 180 | 185 | 190 | 195 | 200 | 205 | 210 | 215 | 220 |
| Lys | Ala | Leu | Pro | Val | Pro | Val | Pro | Arg | Leu | Arg | Arg | Ala | Gln | Arg |
| 225 | 230 | 235 | 240 | 245 | 250 | 255 | 260 | 265 | 270 | 275 | 280 | 285 | 290 | 295 |
| Pro | Glu | Gly | Arg | Gly | His | Arg | Arg | His | Pro | Arg | Pro | Gly | Pro | Arg |
| 300 | 305 | 310 | 315 | 320 | 325 | 330 | 335 | 340 | 345 | 350 | 355 | 360 | 365 | 370 |
| Ala | Ala | Gly | Gln | Gly | His | Leu | Pro | Pro | Ser | Ile | Pro | Val | Gln | Ala |
| 375 | 380 | 385 | 390 | 395 | 400 | 405 | 410 | 415 | 420 | 425 | 430 | 435 | 440 | 445 |
| Glu | Gly | Ala | Val | Arg | Gly | Cys |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1503602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:  
Met Gly Arg Val Ile Arg Ala Gln Xaa Arg Val Arg Gly Pro Cys Ser  
1 5 10 15  
Ser Pro Ile Pro Ile Thr Ala Arg Pro Cys Arg Phe Arg Ser Leu Asp  
20 25 30  
Phe Gly Glu Arg Asn Gly Tyr Leu Lys Gly Val Val Thr Asp Val Ile  
35 40 45  
His Asp Pro Gly Arg Gly Ala Pro Leu Ala Lys Val Thr Phe Arg His  
50 55 60  
Pro Phe Arg Tyr Lys His Gln Lys Glu Leu Phe Val Ala Ala Glu Gly  
65 70 75 80  
Met Tyr Thr Gly Gln Phe Val Tyr Cys Gly Arg Arg Ala Thr Leu Ser  
85 90 95  
Ile Gly Asn Val Leu Pro Leu Arg Gly Ile Pro Glu Gly Ala Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

attccattcc atcgattg attgcattcc catccattc cccgctctac tcattcagat 60  
ctcgtcactc gctctccaca agcagagcac cgcagcagaa cgaggatgct ggccattctc 120  
cagaagcagg tggcgcaagc gtcsgcagga gcntcaacag cccccgcgcc ggccgctcgc 180  
ccagcaagcc cccgaacccc gacgagatcc tgcgcgactc ccacgccgcg caccggcgcg 240  
ccgcctcttc cgcctccttc ggccggcgtgc gntgctcgcc ttgcgttcgg cccctctctc 300  
gccaccgccca cctaccagcg ggatgtttct gcggccttgg accacatcta ctgcgtcttc 360  
ctcggccgcc tcgacaacct cagcggcctc atccgccagt wacggcctgt gcggccgctc 420  
ccaccaacga ggcatgctg gtcacgagg cctaccgcac gctgcg

(2) INFORMATION FOR SEQ ID NO:2499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

Ile Pro Phe His Arg Ile Gly Leu His Ser His Pro Ile Pro Arg Ser  
1 5 10 15  
Thr His Ser Asp Leu Val Thr Arg Ser Pro Gln Ala Glu His Arg Ser  
20 25 30  
Arg Thr Arg Met Leu Ala Ile Phe Gln Lys Gln Val Ala His Ala Xaa  
35 40 45  
Ala Gly Xaa Ser Thr Ala Pro Ala Pro Ala Arg Arg Pro Ala Ser Pro  
50 55 60  
Gly Thr Pro Thr Arg Ser Cys Ala Thr Ser Thr Pro Arg Thr Arg Pro  
65 70 75 80  
Pro Pro Ser Pro Pro Ser Ala Ala Cys Xaa Ala Arg Leu Ala Phe  
85 90 95  
Gly Pro Ser Ser Ala Thr Ala Thr Tyr Gln Arg Asp Val Ser Ala Ala  
100 105 110

Leu Asp His Ile Tyr Cys Val Phe Leu Gly Arg Leu Asp Asn Leu Ser  
115 120 125  
Gly Leu Ile Arg Gln Xaa Arg Pro Val Arg Pro Leu Pro Pro Thr Arg  
130 135 140  
Arg Cys Trp Ser Ser Arg Pro Thr Ala Arg Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1503617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Phe His Ser Ile Ala Leu Asp Cys Ile Pro Ile Pro Phe Pro Ala Leu  
1 5 10 15  
Leu Ile Gln Ile Ser Ser Leu Ala Leu His Lys Gln Ser Thr Ala Ala  
20 25 30  
Glu Arg Gly Cys Trp Pro Ser Ser Arg Ser Arg Trp Arg Thr Arg Xaa  
35 40 45  
Gln Glu Xaa Gln Gln Pro Pro Arg Arg Arg Val Ala Gln Gln Ala Pro  
50 55 60  
Glu Pro Arg Arg Asp Pro Ala Arg Leu Pro Arg Arg Ala Pro Gly Arg  
65 70 75 80  
Arg Leu Leu Arg Leu Leu Arg Arg Arg Ala Xaa Leu Ala Leu Arg Ser  
85 90 95  
Ala Pro Pro Pro Pro Pro Pro Thr Ser Gly Met Phe Leu Arg Pro  
100 105 110  
Trp Thr Thr Ser Thr Ala Ser Ser Ser Ala Ala Ser Thr Thr Ser Ala  
115 120 125  
Ala Ser Ser Ala Ser Xaa Gly Leu Cys Gly Arg Ser His Gln Arg Gly  
130 135 140  
Asp Ala Gly His Arg Gly Leu Pro His Ala Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1503618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

Ser Ile Pro Ser His Trp Ile Ala Phe Pro Ser His Ser Pro Leu Tyr  
1 5 10 15  
Ser Phe Arg Ser Arg His Ser Leu Ser Thr Ser Arg Ala Pro Gln Gln  
20 25 30  
Asn Glu Asp Ala Gly His Leu Pro Glu Ala Gly Gly Ala Arg Val Xaa  
35 40 45  
Arg Ser Xaa Asn Ser Pro Arg Ala Gly Ala Ser Pro Ser Lys Pro Arg  
50 55 60  
Asn Pro Asp Glu Ile Leu Arg Asp Phe His Ala Ala His Pro Ala Ala  
65 70 75 80  
Ala Phe Ser Ala Ser Phe Gly Gly Val Xaa Cys Ser Pro Cys Val Arg

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |
| Pro | Leu | Leu | Arg | His | Arg | His | Leu | Pro | Ala | Gly | Cys | Phe |
|     |     |     | 100 |     |     |     | 105 |     |     |     | Cys | Gly |
| Gly | Pro | His | Leu | Leu | Arg | Leu | Pro | Arg | Pro | Arg | Gln | Pro |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 | Gln |
| Pro | His | Pro | Pro | Xaa | Thr | Ala | Cys | Ala | Ala | Ala | Pro | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 | Asn |
| Met | Leu | Val | Ile | Glu | Ala | Tyr | Arg | Thr | Leu |     |     | Glu |
|     |     |     | 145 |     |     |     | 150 |     |     |     |     | Ala |

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..403

(D) OTHER INFORMATION: / Ceres Seq. ID 1503621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| agtgtcggtg | tggcggttg  | cgagtggcga  | ctggcgactt | ctctgcctcg | tccctccccg | 60  |
| ttttcccttc | cgctccagc  | ckgcgcgac   | gccaccacgc | acctagccgc | ggantccgag | 120 |
| gcgcagatcc | aatccagcga | tggcgctccac | ggcgcgagg  | cggttgcggg | aaatgcaggc | 180 |
| ccagacgggg | aacaagacct | gcgtggactg  | cgcgcrssta | acccgcagtg | ggcgagcgct | 240 |
| tcctacggcg | tggtcatgtg | cctcgagtg   | tcyggcaagc | accggggcct | cgcgctgcac | 300 |
| atcagtttgc | tgcgctcggt | caccatggac  | tcctggaccg | agggccasst | ccgcaagatg | 360 |
| gaggccggcg | gcaacgacgc | cctcaacgcc  | ttcctcacag | cgc        |            |     |

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1503622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Val | Gly | Val | Gly | Val | Glu | Trp | Arg | Leu | Ala | Thr | Ser | Leu | Pro |
|     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Pro | Ser | Pro | Phe | Ser | Pro | Pro | Arg | Pro | Ala | Xaa | Arg | Asp | Ala |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  | Thr |
| Thr | His | Leu | Ala | Ala | Xaa | Ser | Glu | Ala | Gln | Ile | Gln | Ser | Ser | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| Val | His | Gly | Gly | Glu | Ala | Val | Ala | Gly | Xaa | Ala | Gly | Pro | Asp | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Gln | Asp | Leu | Arg | Gly | Leu | Arg | Xaa | Xaa | Asn | Pro | Gln | Trp | Ala | Ser |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Ser | Tyr | Gly | Val | Phe | Met | Cys | Leu | Glu | Cys | Xaa | Gly | Lys | His | Arg |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Gly | Val | His | Ile | Ser | Phe | Val | Arg | Ser | Val | Thr | Met | Asp | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 | Trp |
| Thr | Glu | Ala | Xaa | Xaa | Arg | Lys | Met | Glu | Ala | Gly | Gly | Asn | Asp | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |
| Asn | Ala | Phe | Leu | Thr | Ala |     |     |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..72  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503623  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:  
Cys Arg Cys Arg Arg Trp Arg Val Ala Thr Gly Asp Phe Ser Ala Ser  
1                  5                  10                  15  
Ser Leu Pro Val Phe Pro Ser Ala Ser Ser Xaa Ala Arg Arg His His  
                  20                  25                  30  
Ala Pro Ser Arg Gly Xaa Arg Gly Ala Asp Pro Ile Gln Arg Trp Arg  
                  35                  40                  45  
Pro Arg Arg Arg Gly Gly Cys Gly Xaa Cys Arg Pro Arg Arg Gly Thr  
50                  55                  60  
Arg Pro Ala Trp Thr Ala Arg Xaa  
65                  70

(2) INFORMATION FOR SEQ ID NO:2505:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 88 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..88  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503624  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:  
Met Ala Ser Thr Ala Ala Arg Arg Leu Arg Xaa Xaa Gln Ala Gln Thr  
1                  5                  10                  15  
Gly Asn Lys Thr Cys Val Asp Cys Ala Xaa Xaa Thr Arg Ser Gly Arg  
                  20                  25                  30  
Ala Ser Pro Thr Ala Cys Ser Cys Ala Ser Ser Ala Xaa Ala Ser Thr  
                  35                  40                  45  
Gly Ala Ser Ala Cys Thr Ser Val Ser Cys Ala Arg Ser Pro Trp Thr  
50                  55                  60  
Pro Gly Pro Arg Arg Xaa Ser Ala Arg Trp Arg Pro Ala Ala Thr Thr  
65                  70                  75                  80  
Ala Ser Thr Pro Ser Ser Gln Arg  
85

(2) INFORMATION FOR SEQ ID NO:2506:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 389 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..389  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503662  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:  
actcgcgcac agsstccaat ttctccacc tcccgaacc taccggcggc gcmagcattc 60  
acaaccacca ccgaagatg gtgaagtttc tgaagcccg caggccgcta atcctcctcc 120  
agggcagatt ccgcggcctg aagsgggtga tcgtgcgcgt gttcgaggag ggcaccgcgg 180  
accgtcccta tgggcactgc ctgcgcgcgc gctcggccaa gtaccaccaag aaggtgatcc 240  
gcaagactcc gccaaagaag cggccaagaa gtcccgcgtc aagtgtctca tcaagctcat 300  
caatttcact caccctatgc ccaccgccta caccctcgac gtgcacttca aggacgtcgc 360

(2) INFORMATION FOR SEQ ID NO:2507:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

[illegible]

(2) INFORMATION FOR SEO ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Val | Lys | Phe | Leu | Lys | Pro | Gly | Lys | Ala | Val | Ile | Leu | Leu | Gln | Gly |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Arg | Phe | Ala | Gly | Arg | Lys | Xaa | Val | Ile | Val | Arg | Val | Phe | Glu | Glu | Gly |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Thr | Arg | Asp | Arg | Pro | Tyr | Gly | His | Cys | Leu | Val | Ala | Gly | Leu | Ala | Lys |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Tyr | Pro | Lys | Lys | Val | Ile | Arg | Lys | Thr | Pro | Pro | Arg | Arg | Arg | Pro | Arg |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Pro | Ala | Ser | Ser | Ala | Ser | Ser | Ser | Ser | Ser | Ile | Ser | Leu | Thr | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Cys | Pro | Pro | Ala | Thr | Pro | Ser | Thr | Ser | Thr | Ser | Arg | Thr | Ser | Pro | Arg |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Gly | Gly | Pro | Thr | Arg | Ser | Pro | Pro |     |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     | 100 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| atttgtcggt | gcacaccac  | tcctgagaat | gctaagtac  | gtgacctga  | actcncatt  | 60  |
| gcangtgcgc | ttctgaatac | catatgatta | agtaccttcc | ggcatgttaa | tttcatctcc | 120 |
| aaaagtcttt | atacgagcgc | gcagcaactt | ggattatata | tccttagtgc | tgcgtccacg | 180 |
| cgggtgcggt | cgccgagcgc | gacgcccacg | ccgccacctc | ctccggcgcg | gccgcggtgg | 240 |
| tgctcttggc | cggggcgcta | ccgctccccc | cggagcttcc | cttggttttc | cggcggttgg | 300 |
| acttcttggt | aacggcgggg | aggtcctggc | atgtgcccca | ggcgctcgtc | cggnccgact | 360 |
| tgctcctgct | cttgcggttc | tttcgggttt | gcaacaagag | gaggatgaag | atcgaagacc | 420 |

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Ile | Ser | Ser | Pro | Lys | Val | Leu | Ile | Arg | Gly | Arg | Ser | Asn | Leu |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Asp | Tyr | Ile | Ser | Leu | Val | Val | Val | His | Gly | Gly | Cys | Gly | Arg | Arg | Arg |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Arg | Arg | Arg | Arg | His | Leu | Leu | Arg | Arg | Gly | Arg | Gly | Gly | Val | Leu |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Gly | Arg | Gly | Ala | Thr | Ala | Pro | Leu | Gly | Ala | Ser | Leu | Val | Phe | Pro | Ala |
| Val | Gly | Leu | Leu | Gly | Asn | Gly | Gly | Glu | Val | Leu | Ala | Cys | Arg | Arg | Gly |
| Val | Val | Ala | Xaa | Arg | Leu | Val | Leu | Leu | Leu | Ala | Val | Leu | Ser | Gly | Leu |
| Gln | Gln | Glu | Glu | Asp | Glu | Asp | Arg | Arg |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEO ID NO:2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..475  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

|             |             |             |            |            |             |     |
|-------------|-------------|-------------|------------|------------|-------------|-----|
| tatctattct  | gttgcttttg  | tgtatggttg  | cogtggggcg | agactatagc | acataggctg  | 60  |
| agcttttgct  | agatggttgt  | tccctattga  | gactcaaggc | aaccacattg | tgcgaaggct  | 120 |
| gcattttgatg | ctggagaaga  | tggactttga  | aaaaattgtc | attctcttaa | gaagggtctg  | 180 |
| gattgtctgg  | ctgcacataaa | ataattttgat | gcacattctc | caaacctcac | tgggtgtatg  | 240 |
| gagacaattg  | agaactctgtg | tgtgtttgat  | ggaggagatc | attgggtcct | ttgttaaacat | 300 |
| caagactctg  | gaacdggttt  | agcagaagta  | agggcgctca | ggagcgctac | tgtttctctt  | 360 |
| atctgtacag  | ttgcaaacata | tgtgatttgt  | ttttactgct | actctctata | ggatggggaa  | 420 |
| katagagaag  | gaagtaaaagc | ttaactggaat | tctcagaagg | ggqgctttga | tggctc      |     |

(2) INFORMATION FOR SEO ID NO:2513

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..495

(D) OTHER INFORMATION: / Ceres Seq. ID 1503703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| aaagcagagt | ctgcccctcc | cgcgcgcgtt | ctttttggtt | ccccagtc    | cgccgcgcgc | 60  |
| gaaacccgca | gatggaggtc | gtcgtcgccg | cgamssagaa | ggcgaagaaa  | cacatacacc | 120 |
| tcttctactg | ctcagaatgc | gaggagctcg | ccctcaagat | cgccgcgcgc  | tccgacgcca | 180 |
| tcgagctcca | atccatcaac | tggcggasst | tcgacgacgg | gttcgccgaac | ctattcatcg | 240 |
| cctcattcac | gctcgtgctg | ccattctctc | ccacgggctc | attcgagcgc  | gttgaggagg | 300 |
| agggcgatgt | cgccaccgcg | ttcaccctcg | cgcgcattct | ctcgatgac   | cccaagtcgc | 360 |
| gcggcgggcc | taccagcgct | gtcactcaag | acatccacgc | gctccaggag  | aggttttact | 420 |
| tcggggacga | tgtctgccat | gttcgagac  | agggatcccc | ctctcgtcgc  | agcgctcccg | 480 |
| ccagctcccg | gaecg      |            |            |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Glu | Ser | Ala | Pro | Pro | Arg | Ala | Val | Leu | Phe | Gly | Ser | Pro | Val |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Ala | Ala | Ala | Glu | Thr | Arg | Arg | Trp | Arg | Ser | Ser | Ser | Pro | Arg | Xaa |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Arg | Arg | Asn | Thr | Tyr | Thr | Ser | Ser | Thr | Ala | Gln | Asn | Ala | Arg |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | Ser | Pro | Ser | Arg | Ser | Pro | Pro | Ala | Pro | Thr | Pro | Ser | Ser | Ser | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Ser | Thr | Gly | Gly | Xaa | Ser | Thr | Thr | Gly | Ser | Arg | Thr | Tyr | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Pro | His | Ser | Arg | Ser | Cys | Cys | His | Ser | Ser | Pro | Arg | Ala | His | Ser | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Leu | Arg | Arg | Arg | Ala | Met | Ser | Pro | Pro | Arg | Ser | Pro | Ser | Arg | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1503705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

Ser Arg Val Cys Pro Ser Pro Arg Arg Ser Phe Trp Phe Pro Ser Pro  
1 5 10 15  
Arg Arg Arg Arg Asn Pro Gln Met Glu Val Val Val Ala Ala Xaa Xaa  
20 25 30  
Lys Ala Lys Lys His Ile His Leu Phe Tyr Cys Ser Glu Cys Glu Glu  
35 40 45  
Leu Ala Leu Lys Ile Ala Ala Ser Ser Asp Ala Ile Glu Leu Gln Ser  
50 55 60  
Ile Asn Trp Arg Xaa Phe Asp Asp Gly Phe Pro Asn Leu Phe Ile Ala  
65 70 75 80  
Ser Phe Thr Leu Val Leu Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg  
85 90 95  
Val Glu Glu Glu Gly Asp Val Ala Thr Ala Phe Thr Leu Ala Arg Ile  
100 105 110  
Leu Ser Met Ile Pro Lys Ser Arg Gly Gly Pro Thr Ser Val Val Ile  
115 120 125  
Tyr Asp Ile His Ala Leu Gln Glu Arg Phe Tyr Phe Gly Asp Asp Val  
130 135 140  
Cys His Ala Ser Arg Gln Gly Ser Arg Ser Cys Cys Ser Ala Ser Ala  
145 150 155 160  
Ser Ser Arg Thr

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1503706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

Met Glu Val Val Val Ala Ala Xaa Xaa Lys Ala Lys Lys His Ile His  
1 5 10 15  
Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala  
20 25 30  
Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Xaa Phe Asp  
35 40 45  
Asp Gly Phe Pro Asn Leu Phe Ile Ala Ser Phe Thr Leu Val Leu Pro  
50 55 60  
Phe Phe Pro Thr Gly Ser Phe Glu Arg Val Glu Glu Gly Asp Val  
65 70 75 80  
Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu Ser Met Ile Pro Lys Ser  
85 90 95  
Arg Gly Gly Pro Thr Ser Val Val Ile Tyr Asp Ile His Ala Leu Gln  
100 105 110  
Glu Arg Phe Tyr Phe Gly Asp Asp Val Cys His Ala Ser Arg Gln Gly  
115 120 125  
Ser Arg Ser Cys Cys Ser Ala Ser Ala Ser Ser Arg Thr  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 474 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1503714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

| acattctaacg | gcctctctctc | ccttcctcgc  | catcgccgtc  | gctgggggcgc  | cctatacaatt | 160 |
|-------------|-------------|-------------|-------------|--------------|-------------|-----|
| caaaatggct  | gcctaccgaca | tcgcacatggc | tatagaaacat | gtcttcacac   | cctacatacgt | 170 |
| cccatcccgcc | ccctctcccat | ccctcccccct | cgggctccgc  | ctctccgccctc | aacctccctat | 180 |
| tttctgctgt  | ctcccgccgcc | gcctctctcc  | atgttcccaca | agccgcctcc   | tgggacgaat  | 240 |
| cgctcccgc   | aggaatggtg  | agatcgccgag | gaattccggtg | ccgcttgggga  | cgacagaggac | 300 |
| gaggacgaga  | agccgcggcc  | cgagccgggt  | ctctctccctc | agttccagtt   | ctcgccgccca | 360 |
| ccgacgggct  | acgtcgcagcc | cctcgckkkt  | gcgcagagcta | ccgcgcgaat   | ccccaaaga   | 420 |
| ctgtgcggcg  | gcgtacgaat  | ctctctaacg  | gcccggcctc  | agccgcgaga   | catt        |     |

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEO ID NO:2519:

Phe Thr Gly Leu Leu Leu Leu Pro Val His Ar

[illegible]

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Ala | Ser | Ser | Ser | Phe | Pro | Ser | Ile | Ala | Val | Ala | Gly | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Tyr | Asn | Phe | Lys | Met | Ala | Ala | Thr | Ala | Leu | Ala | Met | Ala | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Xaa | Ser | Pro | Ala | Ala | Pro | Ile | Pro | Ser | Ala | Pro | Phe | Pro | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Pro | Leu | Gly | Leu | Arg | Leu | Arg | Pro | Gln | Pro | Leu | Leu | Phe | Ala | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |

Arg Arg Arg Leu Pro Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile  
65 70 75 80  
Arg Pro Pro Arg Met Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly  
85 90 95  
Thr Thr Arg Thr Arg Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro  
100 105 110  
Pro Ser Ser Ser Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg  
115 120 125  
Xaa Phe Asp Glu Leu Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala  
130 135 140  
Tyr Glu Ser Leu Tyr Gly Pro Ala Phe Ser Gly Glu Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2521:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

Met Ala Ala Thr Ala Leu Ala Met Ala Ile Ala Thr Xaa Ser Pro Ala  
1 5 10 15  
Ala Pro Ile Pro Ser Ala Pro Phe Pro Ser Leu Pro Leu Gly Leu Arg  
20 25 30  
Leu Arg Pro Gln Pro Leu Leu Phe Ala Ala Ser Arg Arg Arg Leu Pro  
35 40 45  
Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile Arg Pro Pro Arg Met  
50 55 60  
Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly Thr Thr Arg Thr Arg  
65 70 75 80  
Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro Ser Ser Ser Ser  
85 90 95  
Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg Xaa Phe Asp Glu Leu  
100 105 110  
Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Tyr Glu Ser Leu Tyr  
115 120 125  
Gly Pro Ala Phe Ser Gly Glu Thr  
130 135

(2) INFORMATION FOR SEQ ID NO:2522:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..412  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

agagcagcca agcgccacac acacgccgac gcgaaccaac caaccagctg gtagtaggtt 60  
cgccgcggcg ccgcgctgac gatgatgcct cgccgcggccc ttctcttcgc cgcggtgctc 120  
ctcgcggcct ccgcgcgcgc gttctcgggt ttcaactcgg cggggacgag agcggtctctc 180  
tgagggggtg gctcgcgcgc ctcgcgcagc kgtccgaggg cgtggacgcc gctcgtctcg 240  
cgctgcgccca ctacaacaag aaccaggggc ccgctttgga gtttactagg gtgctcaaat 300  
ccaagcggca ggtgggtgacc gggaccctgc atgacctgat actggaggca cctgatgctg 360  
gaaaaaagag tgtgtacaga gcaaagggtt ggggtgaagcg tgggaagatt tc

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ser | Gln | Ala | Pro | His | Thr | Arg | Arg | Arg | Glu | Pro | Thr | Asn | Gln | Leu |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Val | Gly | Ser | Pro | Arg | Arg | Arg | Ala | Asp | Asp | Asp | Ala | Ser | Pro | Arg |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Pro | Ser | Leu | Arg | Arg | Gly | Ala | Pro | Arg | Gly | Leu | Arg | Arg | Ala | Val | Ser |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Gly | Phe | His | Leu | Gly | Gly | Asp | Glu | Ser | Gly | Leu | Val | Arg | Gly | Val | Leu |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ala | Ala | Leu | Arg | Ser | Xaa | Ser | Glu | Ala | Val | Asp | Ala | Ala | Arg | Phe | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Val | Ala | His | Tyr | Asn | Lys | Asn | Gln | Gly | Ala | Ala | Leu | Glu | Phe | Thr | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Val | Leu | Lys | Ser | Lys | Arg | Gln | Val | Val | Thr | Gly | Thr | Leu | His | Asp | Leu |  |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Leu | Glu | Ala | Ala | Asp | Ala | Gly | Lys | Lys | Ser | Val | Tyr | Arg | Ala | Lys |  |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     |     | 125 |     |     |  |
| Val | Trp | Val | Lys | Arg | Gly | Lys | Ile |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

|             |            |            |            |            |             |     |
|-------------|------------|------------|------------|------------|-------------|-----|
| ccccacacac  | tgcacgcnc  | cgccgggtcc | tcctagggtt | tcgccgcgat | gtcgtccgg   | 60  |
| ccgagcgagc  | gggagcagat | cggaagggc  | aactacaagc | agacggtgga | cgccggaggag | 120 |
| agccgcgcgc  | gccgcgaggg | ccagatgatg | gacatgcgca | aggccaagcg | cgaggaaaat  | 180 |
| ctccagaaga  | agcgctgcga | tgggtttccc | gcctccgcgc | ccggtgtgcc | gccgatgggc  | 240 |
| cactccaccg  | cgctccagca | gaagtccccc | aatcgaagag | gtgatcagca | caggagtgtg  | 300 |
| gtcgcgattc  | attgagtttc | ttacacgtga | ggaccatccc | caactccagt | ttgaggctgc  | 360 |
| atgggcactc  | accaacattg | catcaggcac | atcagagaa  | actaaggtgg | tcgttgagag  | 420 |
| tggctgctgtg | cgctctgtgc | catctttgtc | aagctactca | actccctcaa | gcgaggatgt  | 480 |
| tc          |            |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1503721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Pro His Thr Ala Arg Xaa Arg Arg Val Leu Leu Gly Phe Arg Arg Asp  
1 5 10 15  
Val Ala Pro Ala Glu Arg Ala Gly Ala Asp Ala Glu Gly Gln Leu Gln  
20 25 30  
Ala Asp Gly Gly Arg Gly Gly Glu Pro Pro Pro Arg Gly Pro Asp  
35 40 45  
Asp Gly His Ala Gln Gly Gln Ala Arg Gly Lys Ser Pro Glu Glu Ala  
50 55 60  
Leu Arg Trp Val Ser Arg Leu Arg Arg Arg Cys Ala Ala Asp Gly Pro  
65 70 75 80  
Leu His Arg Ala Pro Ala Glu Val Pro Gln Ser Lys Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1503722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

Met Ser Leu Arg Pro Ser Glu Arg Glu Gln Met Arg Lys Gly Asn Tyr  
1 5 10 15  
Lys Gln Thr Val Asp Ala Glu Glu Ser Arg Arg Arg Arg Glu Gly Gln  
20 25 30  
Met Met Asp Met Arg Lys Ala Lys Arg Glu Glu Ser Leu Gln Lys Lys  
35 40 45  
Arg Cys Asp Gly Phe Pro Ala Ser Ala Ala Gly Val Pro Pro Met Gly  
50 55 60  
His Ser Thr Ala Leu Gln Gln Lys Ser Pro Asn Arg Arg Gly Asp Gln  
65 70 75 80  
His Arg Ser Gly Val Ala Ile His  
85

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1503723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

Met Gly Phe Pro Pro Pro Pro Val Cys Arg Arg Trp Ala Thr Pro  
1 5 10 15  
Pro Arg Ser Ser Arg Ser Pro Pro Ile Glu Glu Val Ile Ser Thr Gly  
20 25 30  
Val Val Ser Arg Phe Ile Glu Phe Leu Thr Arg Glu Asp His Pro Gln  
35 40 45  
Leu Gln Phe Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr  
50 55 60  
Ser Glu Asn Thr Lys Val Val Val Glu Ser Gly Ala Val Arg Leu Cys  
65 70 75 80  
Pro Ser Leu Ser Ser Tyr Ser Thr Pro Ser Ser Glu Asp Val

85

90

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

|            |             |            |            |            |             |     |
|------------|-------------|------------|------------|------------|-------------|-----|
| agataacagg | aaaggctctg  | caacacggct | tgagttcaaa | caaaggctct | caatagctat  | 60  |
| tggggcagct | aaagggttga  | atcatctgca | cagttctgat | cctcctttga | tacacaagga  | 120 |
| cttcaagaca | aacaatgtgc  | tggttgatga | aaatttcatt | gcaaagggtg | ctgatgctgg  | 180 |
| acttgtagg  | tttaattagag | gatctgacga | tgccggccca | tcgcgtgggt | tcagttaaacg | 240 |
| tgtttaccaa | gatccagagag | tacagtcgat | gactcagttc | tctgaaagca | gtgatgttta  | 300 |
| cagcttggag | tttttctttt  | ggagctaatt | actggcaggg | aagcagcttc | cttgatacct  | 360 |
| acagagtcca | gagaatattt  | ggcacactgg | atggaagcgc | atttcagttc | aaatgaactg  | 420 |
| attgacccaa | gattagccgg  | caacttcact | gcagaaggtg | tgaaggagct | t           |     |

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1503729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Asn | Arg | Lys | Gly | Ser | Ala | Thr | Arg | Leu | Glu | Phe | Lys | Gln | Arg | Leu |
| 1   |     | 5   |     | 10  |     | 15  |     | 20  |     | 25  |     | 30  |     | 35  |     |
| Ser | Ile | Ala | Ile | Gly | Ala | Ala | Lys | Gly | Leu | Asn | His | Leu | His | Ser | Leu |
|     |     | 20  |     | 25  |     | 30  |     | 35  |     | 40  |     | 45  |     | 50  |     |
| Asp | Pro | Pro | Leu | Ile | His | Lys | Asp | Phe | Lys | Thr | Asn | Asn | Val | Leu | Val |
|     |     | 35  |     | 40  |     | 45  |     | 50  |     | 55  |     | 60  |     | 65  |     |
| Asp | Glu | Asn | Phe | Ile | Ala | Lys | Val | Ala | Asp | Ala | Gly | Leu | Val | Arg | Leu |
|     |     | 50  |     | 55  |     | 60  |     | 65  |     | 70  |     | 75  |     | 80  |     |
| Ile | Arg | Gly | Ser | Asp | Asp | Ala | Gly | Pro | Ser | Arg | Gly | Phe | Ser | Asn | Ser |
|     |     | 65  |     | 70  |     | 75  |     | 80  |     | 85  |     | 90  |     | 95  |     |
| Val | Tyr | Gln | Asp | Pro | Glu | Val | Gln | Ser | Met | Thr | Gln | Phe | Ser | Glu | Ser |
|     |     | 85  |     | 90  |     | 95  |     | 100 |     | 105 |     | 110 |     | 115 |     |
| Ser | Asp | Val | Tyr | Ser | Leu | Glu | Phe | Phe | Trp | Ser |     |     |     |     |     |
|     |     | 100 |     | 105 |     | 110 |     | 115 |     | 120 |     | 125 |     | 130 |     |

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..469

(D) OTHER INFORMATION: / Ceres Seq. ID 1503734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

|             |            |            |            |           |            |            |     |
|-------------|------------|------------|------------|-----------|------------|------------|-----|
| atctctttggc | aaccgaactg | gttttggtg  | gtg        | ccacctctc | tctcttccat | gggatatggc | 60  |
| agggacggaa  | tccagatgag | gatgaactcg | tggcaggacg | gcgtcaagg | caccaactgc |            | 120 |

ccctccctc cggatgga cttggacct gagttccag tcaaggacca gatcgccagc 180  
ttcttctact tcccgctcgt cggcctccag cgaagctgcc gcggggttcg ccccatcacc 240  
gtcaacaacc gcgcaccgt gccnntcccc ttcgaccagc ctcattggcg catcacccctg 300  
ttcatcgggg actggtacac caagggccac gttgtaagag cttgtttttt ctgtttctgt 360  
caatgcaaat ctagctagat gtttgcctct ttgttttcag atcgagatat atagccaggg 420  
aaaaatactg cgcttttccc ttgattctcag tgaactggat ttactgag

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

Ile Leu Trp Gln Pro Asn Trp Phe Gly Val Pro Thr Ser Leu Ser Ser  
1 5 10 15  
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln  
20 25 30  
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp  
35 40 45  
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe  
50 55 60  
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr  
65 70 75 80  
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly  
85 90 95  
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val  
100 105 110  
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

Pro Leu Ala Thr Glu Leu Val Trp Cys Ala His Leu Ser Leu Phe His  
1 5 10 15  
Gly Ile Trp Gln Gly Arg Asn Pro Asp Glu Asp Glu Leu Val Ala Gly  
20 25 30  
Arg Arg His Gly His Gln Leu Pro His Pro Ser Arg Met Glu Leu Asp  
35 40 45  
Leu Arg Val Pro Ala Gln Gly Pro Asp Arg Gln Leu Leu Leu Pro  
50 55 60  
Val Ala Arg Pro Pro Ala Ser Cys Arg Arg Val Arg Pro His His Arg  
65 70 75 80  
Gln Gln Pro Arg His Arg Ala Xaa Pro Leu Arg Pro Ala Ser Trp Arg  
85 90 95  
His His Pro Val His Arg Gly Leu Val His Gln Gly Pro Arg Cys Lys  
100 105 110  
Ser Phe Val Phe Leu Phe Leu Ser Met Gln Ile

115 120  
(2) INFORMATION FOR SEQ ID NO:2533:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..109  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503737  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:  
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln  
1 5 10 15  
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp  
20 25 30  
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe  
35 40 45  
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr  
50 55 60  
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly  
65 70 75 80  
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val  
85 90 95  
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:2534:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503743  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:  
aattctttca ctcaactctcc agatccgggtg cttgtgggag cctaacacgc cccccgcctc 60  
cctctccgcc gtcgcgcgagt cctctgcggg cttaccctgt cgctggcgaa ggcaactccgg 120  
cgtggacgc

(2) INFORMATION FOR SEQ ID NO:2535:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..42  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503744  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:  
Ile Leu Ser Leu Thr Leu Gln Ile Arg Cys Leu Trp Glu Pro Asn Thr  
1 5 10 15  
Pro Pro Ala Ser Leu Ser Ala Val Ala Glu Ser Leu Ala Gly Leu Pro  
20 25 30  
Arg Arg Trp Arg Arg His Ser Gly Val Asp  
35 40  
(2) INFORMATION FOR SEQ ID NO:2536:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..42  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503745  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:  
Phe Phe His Ser Leu Ser Arg Ser Gly Ala Cys Gly Ser Leu Thr Arg  
1                    5                    10                    15  
Pro Pro Pro Pro Pro Ser Pro Ser Pro Ser Pro Ser Pro Ala Tyr Pro  
                    20                    25                    30  
Val Ala Gly Glu Gly Thr Pro Ala Trp Thr  
                    35                    40

(2) INFORMATION FOR SEQ ID NO:2537:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 409 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
    (A) NAME/KEY: -  
    (B) LOCATION: 1..409  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503746  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:  
ctagccgcgcg ccagaccatt cgtttctcgc gagccatcct tctgtaattc tcaggcatcc 60  
ggaagaaatg gccaaagtgcg agaaccacac ggcgcacaac cagtcgttca aggcgcacaa 120  
gaacggcatt aagaaccaca agcgccaccg ccagacctcc accaaggggg tggaccccaa 180  
gttcctgagg aacctgaggt attctaggaa gggcaacaaa aagagtgggt aggcgtgaagc 240  
tgaggagtag gaaggaaagc atggctttgt ggtaatgtgc tgctgtgggg gtccattagt 300  
atgaagagga agacgctgct ggcgcggagt cttttctct ttattagtat ttgtgttaaa 360  
actatgtatg accgaatggt ggtatttatt tgtgtcatcc ttgactctc

(2) INFORMATION FOR SEQ ID NO:2538:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 43 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..43  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503747  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:  
Leu Ala Ala Ala Arg Pro Phe Val Ser Arg Glu Pro Ser Phe Cys Asn  
1                    5                    10                    15  
Ser Gln Ala Ser Gly Arg Asn Gly Gln Val Glu Glu Pro His Gly Ala  
                    20                    25                    30  
Gln Pro Val Val Gln Gly Ala Gln Glu Arg His  
                    35                    40

(2) INFORMATION FOR SEQ ID NO:2539:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 60 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1503748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala  
1 5 10 15  
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr  
20 25 30  
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys  
35 40 45  
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1503749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

Met Lys Arg Lys Thr Leu Leu Ala Arg Ser Leu Phe Leu Phe Ile Ser  
1 5 10 15  
Ile Leu Phe Lys Thr Met Tyr Asp Arg Met Val Val Phe Ile Cys Val  
20 25 30  
Ile Leu Asp Ser  
35

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1503769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

aaaatgatcg agtgggctcc catgtgattt tgcataccta gtgacagaaa tttttccctt 60  
ttttttttct caagctcaca acactctctt gctgtgattc cagatggagc gaactttcat 120  
tgccatcaag ccgacgcgcg tccaagagag cctgatttct gagattgtga accgatttga 180  
gagaaaaagc tacaagcttg ttgccatcaa gctgattgtc ccatccaaag gattcgctga 240  
gaagcaactac catgatctca aggaaaagcc ttcttcaac gggttgtgtg acttccctag 300  
ctctggccct gtacttgcaa tggtttggga aggagagggg gtcatacaag atggggagaa 360  
actaatttgt gccacagacc cacagaaatc tgaaccagga accatcaggg gcgactcttg 420  
cgttgtttgt ggaagaacaa tcattcatgg

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503770  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:  
Met Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly  
1 5 10 15  
Leu Ile Ser Glu Ile Val Asn Arg Phe Glu Arg Lys Gly Tyr Lys Leu  
20 25 30  
Val Ala Ile Lys Leu Ile Val Pro Ser Lys Gly Phe Ala Glu Lys His  
35 40 45  
Tyr His Asp Leu Lys Glu Arg Pro Phe Phe Asn Gly Leu Cys Asp Phe  
50 55 60  
Leu Ser Ser Gly Pro Val Leu Ala Met Val Trp Glu Gly Glu Gly Val  
65 70 75 80  
Ile Lys Tyr Gly Arg Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser  
85 90 95  
Glu Pro Gly Thr Ile Arg Gly Asp Leu Gly Val Val Val Gly Arg Asn  
100 105 110  
Ile Ile His  
115

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1503775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

tgattattttg cacaaaaagc aatctggcgg tcaaggtcag tatggacgag tttgtgggta 60  
cattgagcct ctaccttcag gttctgatgg taaattcgaa tttgataaca tgattatttg 120  
acaagcaatt ccttcaaaact ttataccagc aatagagaag ggttttaagg aagcttgcaa 180  
ttcaggctcg ttgattggtc atctctgttg aaatttaaga attgatttga ctgatggggc 240  
ttcacatcag gtggattcca gtgaacttgc ttttaagcta gctgctatct atgcttttct 300  
acagtgtcac actcttgcca aacctgtaat attagaacct gtgatgaagg tggaaactcaa 360  
atttccaact gagtttcagg gcacagtaac tgggtgatatg aacaagagaa aagggatcat 420  
tgttggaat gaggaggaag gtgacgacac cattgtagtt tgccatgtcc gctaaacaat 480  
atgtttggat atgcacagc

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

Asp Tyr Leu His Lys Lys Gln Ser Gly Gly Gln Gly Gln Tyr Gly Arg  
1 5 10 15  
Val Cys Gly Tyr Ile Glu Pro Leu Pro Ser Gly Ser Asp Gly Lys Phe  
20 25 30  
Glu Phe Asp Asn Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile  
35 40 45  
Pro Ala Ile Glu Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu  
50 55 60  
Ile Gly His Pro Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala  
65 70 75 80

Ser His Gln Val Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile  
85 90 95  
Tyr Ala Phe Arg Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu  
100 105 110  
Pro Val Met Lys Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr  
115 120 125  
Val Thr Gly Asp Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu  
130 135 140  
Gln Glu Gly Asp Asp Thr Ile Val Val Cys His Val Arg  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile Pro Ala Ile Glu  
1 5 10 15  
Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu Ile Gly His Pro  
20 25 30  
Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala Ser His Gln Val  
35 40 45  
Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile Tyr Ala Phe Arg  
50 55 60  
Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu Pro Val Met Lys  
65 70 75 80  
Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr Val Thr Gly Asp  
85 90 95  
Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu Gln Glu Gly Asp  
100 105 110  
Asp Thr Ile Val Val Cys His Val Arg  
115 120

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

ttgattacat tatcatgga gatgatcctt gtcttctacc tgatggcact gatgcatatg 60  
cgctacgaag aaggtcgggc gttacaagca aatcaagcga acagaagggt tctcgagcac 120  
tgacatagtt gggaggatat tgctaacatt caggcagaaa gatgctggca ctgatttaag 180  
tgttgtcgtt gctgagaagt ctggagagaa atcaaatgat gaagtgaaaa gtcagctatc 240  
tcatttctct ccaacttctc gccggatcat gcagttttca aatgggcagg ctcccttgcc 300  
aggtgctcgt gttgtctatg tagatggcac attgatcctt ttccacgctg gccatgttga 360  
gttcctcagg agtgccagac aacttggtga ctctctctt gtccgtatct atgacgacga 420  
gtctcatcag gatagaagag cgtgccgtcc tataatgcac ctccatgagc g

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..41  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503779  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:  
Asp Tyr Ile Ile His Gly Asp Asp Pro Cys Leu Leu Pro Asp Gly Thr  
1 5 10 15  
Asp Ala Tyr Ala Leu Arg Arg Arg Ser Gly Val Thr Ser Lys Ser Ser  
20 25 30  
Glu Gln Lys Val Ser Arg Ala Leu Thr  
35 40  
(2) INFORMATION FOR SEQ ID NO:2548:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 67 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..67  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503780  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:  
Met Gln Phe Ser Asn Gly Gln Ala Pro Ser Pro Gly Ala Arg Val Val  
1 5 10 15  
Tyr Val Asp Gly Thr Phe Asp Leu Phe His Ala Gly His Val Glu Phe  
20 25 30  
Leu Arg Ser Ala Arg Gln Leu Gly Asp Phe Leu Leu Val Gly Ile Tyr  
35 40 45  
Asp Asp Glu Ser Ile Arg Asp Arg Gly Cys Arg Pro Ile Met His  
50 55 60  
Leu His Glu  
65  
(2) INFORMATION FOR SEQ ID NO:2549:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..43  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503781  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:  
Met Ala His Leu Ile Phe Ser Thr Leu Ala Met Leu Ser Ser Ser Gly  
1 5 10 15  
Val Pro Asp Asn Leu Val Thr Phe Phe Leu Ser Val Ser Met Thr Thr  
20 25 30  
Ser Leu Ser Gly Ile Glu Glu Ala Ala Val Leu  
35 40  
(2) INFORMATION FOR SEQ ID NO:2550:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1503796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| cacattaatt  | aaacattttt | tgtgtttctt  | tttatacctt | aatttttttc | tttccctttt | 60  |
| tctctataag  | tatctgactc | tactctgtct  | gttgcagaat | cattcgagat | atcattcaga | 120 |
| atcattttact | gcaggttttc | tgtttgggtg  | caatggaaaa | gcctgtctcc | cttaagcctg | 180 |
| agcacatcag  | agatkagaaa | gtcaagggtc  | tgcaatctgt | gaacctatt  | aagcctgaag | 240 |
| aggtagtctt  | tgggcaatac | gatggctctac | aaggatgacc | ctacagtgc  | agatgacttg | 300 |
| aatactccaa  | cttttgcatc | tgttgttctt  | cgggtacaca | atgaaagatg | ggaaggtgtt | 360 |
| cccttcattc  | ttaaagctgg | taaagcattg  | agttc      |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Ile | Lys | His | Phe | Leu | Cys | Phe | Phe | Leu | Tyr | Leu | Asn | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Ser | Leu | Phe | Leu | Tyr | Lys | Tyr | Leu | Thr | Leu | Leu | Leu | Leu | Gln |     |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asn | His | Ser | Arg | Tyr | His | Ser | Glu | Ser | Phe | Thr | Ala | Gly | Phe | Leu | Phe |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Cys | Asn | Gly | Lys | Ala | Cys | Leu | Pro |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1503798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Pro | Val | Ser | Leu | Lys | Pro | Glu | His | Ile | Arg | Asp | Xaa | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Val | Leu | Gln | Ser | Val | Asn | Pro | Ile | Lys | Pro | Glu | Glu | Val | Val |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Leu | Gly | Gln | Tyr | Asp | Gly | Leu | Gln | Gly |     |     |     |     |     |     |     |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1503799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

Met Val Tyr Lys Asp Asp Pro Thr Val Pro Asp Asp Leu Asn Thr Pro  
1 5 10 15  
Thr Phe Ala Ser Val Val Leu Arg Val His Asn Glu Arg Trp Glu Gly  
20 25 30  
Val Pro Phe Ile Leu Lys Ala Gly Lys Ala Leu Ser  
35 40

(2) INFORMATION FOR SEQ ID NO:2554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1503810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

gaagtgttcgg cggcggcgta ggtagcggcg gttgtgcttgt gatctcaatc tcaaccccgag 60  
gcgagctcgg ctcgggtcac ccgtcgatcc acgcaaccat gtcgaggagg aagaccaggg 120  
agcccaagga ggagaaagctt ccctctggac ccactgtccg tgaaggagag ttgtctctttg 180  
gtgttgctca catctttgca tcttccaatg acactctcat tgtgagtgtc atagtctttt 240  
ccctgtggat gggccctttc attatctttc ccattgtaac tgtgatgggt taatatgcag 300  
catgtcactg atttgcctgg gagggaacct ttggttcgga tcaactgggtg catgaaggtt 360  
aaggctgacg gtgatgagtc gtcctcttat gctgctatgc ttgctgccca agagtgttgc 420  
cagcgttgca aggagctcgg tatcacagcg ctgcacatta agctctcgtc cactggaggc 480  
aacaagacca atgacccctg gacct

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1503811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Ser Phe Gly Gly Gly Val Gly Ser Gly Gly Val Leu Val Ile Ser Ile  
1 5 10 15  
Ser Thr Pro Gly Glu Leu Gly Ser Gly His Pro Ser Ile His Ala Thr  
20 25 30  
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu  
35 40 45  
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile  
50 55 60  
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser  
65 70 75 80  
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val  
85 90 95

(2) INFORMATION FOR SEQ ID NO:2556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Arg | Arg | Lys | Thr | Arg | Glu | Pro | Lys | Glu | Glu | Asn | Val | Thr | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Pro | Thr | Val | Arg | Glu | Gly | Glu | Phe | Val | Phe | Gly | Val | Ala | His | Ile |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Ala | Ser | Phe | Asn | Asp | Thr | Phe | Ile | Val | Ser | Ala | Ile | Cys | Phe | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Trp | Met | Gly | Leu | Phe | Ile | Ile | Phe | Pro | Ile | Val | Thr | Val | Met | Val |  |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1503813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | His | Val | Thr | Asp | Leu | Ser | Gly | Arg | Glu | Thr | Leu | Val | Arg | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Gly | Gly | Met | Lys | Val | Lys | Ala | Asp | Arg | Asp | Glu | Ser | Ser | Pro | Tyr |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ala | Ala | Met | Leu | Ala | Ala | Gln | Asp | Val | Ala | Gln | Arg | Cys | Lys | Glu | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Gly | Ile | Thr | Ala | Leu | His | Ile | Lys | Leu | Arg | Ala | Thr | Gly | Gly | Asn | Lys |  |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Asn | Asp | Pro | Trp | Thr |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1503822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| gcnkccgcgcg | ccatacaacag | gtgccccagg | tcttcgctgc | gccattcgc   | agcgacgagc  | 60  |
| accacaacagc | atggtaaac   | gcaatgacct | catgtactgg | attgtcgcgg  | cactctgatg  | 120 |
| tggttgcckc  | ckckgkgcac  | cagaagtgtg | tggggctctt | gaacaacaac  | gaggkactca  | 180 |
| tgtttgggg   | ggttgtggca  | ckgttcaacg | aggtcgtgac | aaatttggtta | ctacaggggtg | 240 |
| ccctggaaac  | tttcgacgca  | tactctgtta | aagcagaaaa | tataacagtt  | gttagtgctc  | 300 |
| ctgggaagctt | tgaagtctct  | ataacgkac  | aaaagcttgg | gaaactctgga | aaatttgatg  | 360 |
| caattctgtg  | cattggagct  | gtgattagag | gtgacacaca | ccactatgat  | gccgttgcaa  | 420 |
| actcagctgc  | atcaggtgta  | ctcaatgctg | gattat     |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..151  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503823  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:  
Xaa Arg Arg Leu Gln Gln Val Pro Gln Val Phe Ala Ala Pro Phe Ala  
1 5 10 15  
Ser Asp Glu His Pro Thr Ala Trp Ser Thr Ala Met Thr Ser Cys Thr  
20 25 30  
Gly Leu Ser Arg His Ser Asp Val Val Ala Xaa Xaa Xaa His Gln Lys  
35 40 45  
Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu Met Phe Gly Val Val  
50 55 60  
Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Gln Gly Ala  
65 70 75 80  
Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val  
85 90 95  
Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu  
100 105 110  
Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile  
115 120 125  
Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser  
130 135 140  
Gly Val Leu Asn Ala Gly Leu  
145 150  
(2) INFORMATION FOR SEQ ID NO:2560:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 124 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..124  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503824  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:  
Met Thr Ser Cys Thr Gly Leu Ser Arg His Ser Asp Val Val Ala Xaa  
1 5 10 15  
Xaa Xaa His Gln Lys Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu  
20 25 30  
Met Phe Gly Val Val Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu  
35 40 45  
Leu Leu Gln Gly Ala Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala  
50 55 60  
Glu Asn Ile Thr Val Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile  
65 70 75 80  
Thr Xaa Gln Lys Leu Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys  
85 90 95  
Ile Gly Ala Val Ile Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala  
100 105 110  
Asn Ser Ala Ala Ser Gly Val Leu Asn Ala Gly Leu  
115 120  
(2) INFORMATION FOR SEQ ID NO:2561:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 102 amino acids  
        (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..102  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503825  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:  
Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu Met Phe Gly Val Val Val  
1          5          10          15  
Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Leu Gln Gly Ala Leu  
          20          25          30  
Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val Val  
          35          40          45  
Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu Gly  
          50          55          60  
Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile Arg  
65          70          75          80  
Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser Gly  
          85          90          95  
Val Leu Asn Ala Gly Leu  
          100  
(2) INFORMATION FOR SEQ ID NO:2562:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 392 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..392  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503826  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:  
gaagtgcgag tcaatgctat catgatcacc agcacagtta ttgtgttctt attcagcaca          60  
atggtttttcgc gcctkctgac gaagccgctg ctcagttctcc tcaatcccacc aaggactgga          120  
ctgaacacgt cgtctctgct ctcaagccag tctatgtctgg acccactcct tactagcatg          180  
atggggctctg actttgatgt agggcagatc aactcccctc aatacaacct ccagttcatg          240  
ctcacccgcgc caastcgcct cgtccatcgc ctttgkycaa gtttgacgat cggtttcatg          300  
cgcccggtgt tcggggggcg aggtttcgtc cctttgtgct ctggttcgcc ktkkkagagk          360  
agtgtccctg aatctcacct gggcactgtg ac  
(2) INFORMATION FOR SEQ ID NO:2563:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 130 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..130  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503827  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:  
Glu Val Arg Val Asn Ala Ile Met Ile Thr Ser Thr Val Ile Val Val  
1          5          10          15  
Leu Phe Ser Thr Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser  
          20          25          30  
Leu Leu Ile Pro Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser  
          35          40          45  
Ser Gln Ser Met Leu Asp Pro Leu Leu Thr Ser Met Gly Ser Asp  
50          55          60

Phe Asp Val Gly Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile  
65 70 75 80  
Leu Thr Ala Pro Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr  
85 90 95  
Ile Gly Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe  
100 105 110  
Val Pro Gly Ser Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly  
115 120 125  
Thr Val  
130

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val Phe  
1 5 10 15  
Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg Thr  
20 25 30  
Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met Leu Asp Pro  
35 40 45  
Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile Asn  
50 55 60  
Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Xaa Arg Ser  
65 70 75 80  
Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met Arg Pro Val  
85 90 95  
Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Xaa Xaa Xaa  
100 105 110  
Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val  
115 120

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro  
1 5 10 15  
Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met  
20 25 30  
Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly  
35 40 45  
Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro  
50 55 60  
Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met  
65 70 75 80  
Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser

85 90 95  
Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2566:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 464 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..464  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503869  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:  
gtagtgggaa ggggtacgtt agcktttgck gcgcgtmrac tcccacgcga aagccgccgc 60  
cgttccctct cgcttccccc agttccccta cgcggtaaat cccacgtcct atcagccgnc 120  
gatccagcct tgcttccatc catccatcca tccatccatc catctcgtcg cttctctctg 180  
ttccgcgtgc gatcgagtgc atcaaaaggga ggaggaggat ggcgaggagt tcgttcaagt 240  
tggagcacc cttcgaaagg aggcgaagctg aggctaaccg catcaggagg aaataccctg 300  
acagataccc tgtcattgtt gagaaggccg agaggagtga catcccagac attgacaaga 360  
aaaagtaact tgttcctgcc gacctcacag tcggacagtt tgtgtatgtg gtacggaaagc 420  
ggatcaagct aagcgctgag aaggcaatct tcattctcgt aaag

(2) INFORMATION FOR SEQ ID NO:2567:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 65 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..65  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503870  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:  
Ser Gly Lys Gly Tyr Val Ser Xaa Cys Xaa Ala Xaa Thr Pro His Ala  
1 5 10 15  
Lys Pro Pro Pro Phe Pro Leu Val Phe Pro Ser Ser Pro Thr Pro Val  
20 25 30  
Ile Pro Arg Pro Ile Ser Xaa Arg Ser Ser Leu Ala Ser Ile His Pro  
35 40 45  
Ser Ile His Pro Ser Ile Ser Ser Leu Leu Ser Val Pro Arg Ala Ile  
50 55 60  
Glu  
65

(2) INFORMATION FOR SEQ ID NO:2568:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 82 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..82  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503871  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:  
Met Ala Arg Ser Ser Phe Lys Leu Glu His Pro Phe Glu Arg Gln  
1 5 10 15  
Ala Glu Ala Asn Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val  
20 25 30

Ile Val Glu Lys Ala Glu Arg Ser Asp Ile Pro Asp Ile Asp Lys Lys  
35 40 45  
Lys Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val  
50 55 60  
Val Arg Lys Arg Ile Lys Leu Ser Ala Glu Lys Ala Ile Phe Ile Phe  
65 70 75 80  
Val Lys

(2) INFORMATION FOR SEQ ID NO:2569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

|         |         |        |        |        |       |        |        |        |       |        |     |
|---------|---------|--------|--------|--------|-------|--------|--------|--------|-------|--------|-----|
| cccagtc | atgcacc | gcga   | tccatg | agat   | cgtcg | agaca  | agggtc | agat   | ccaac | agatg  | 60  |
| ctttcg  | gaag    | ctcag  | ccaca  | acgatg | gcgg  | cgcgg  | agtg   | g      | atagg | cttc   | 120 |
| tgctc   | ctgt    | gtgcg  | gttc   | tcactg | tggt  | ggcgt  | ctctc  | atcccc | ctct  | ttgggt | 180 |
| catctc  | gttc    | gtcgg  | gagca  | ccatgt | ggg   | cttctc | ctct   | ttgtg  | ctgc  | ggctct | 240 |
| catctc  | agca    | ttgtag | gctc   | gtcaat | accc  | ttgtg  | gaggc  | gggtt  | gtctg | actac  | 300 |
| cctctc  | cttt    | ggtctg | gctt   | tcgtct | ggata | tggtc  | ttgtc  | actgc  | ctct  | cctcg  | 360 |
| aacaat  | ggcc    | caaac  | agtc   | aaaa   | agtgc | gagat  | cagga  | tatct  | ttgt  | tgac   | 420 |
| caaatg  | gatg    | ctagg  | agcac  | catata | tcag  | atagc  | acggc  | tcggat | tagt  | gcgtg  |     |

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Val | Met | Met | His | Pro | Ile | His | Glu | Ile | Val | Glu | Thr | Arg | Phe | Arg |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ser | Asn | Arg | Cys | Phe | Arg | Lys | Leu | Ser | His | Asn | Asp | Gly | Gly | Ala | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Trp | Ile | Gly | Leu | His | Xaa | Xaa | Ala | Val | Leu | Val | Val | Ala | Val | Leu | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Val | Ala | Ser | Phe | Ile | Pro | Phe | Phe | Gly | Ser | Phe | Ile | Ser | Phe | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Gly | Ser | Thr | Met | Trp | Arg | Phe | Ser | Pro | Leu | Cys | Cys | Arg | Leu | Ser | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ile | Ser | Ala | Leu |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1503875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg Ser Asn  
1 5 10 15  
Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu Trp Ile  
20 25 30  
Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr Val Val  
35 40 45  
Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val Gly Ser  
50 55 60  
Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser Ile Ser  
65 70 75 80  
Ala Leu

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1503876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

Met Leu Ser Glu Ala Gln Pro Gln Arg Trp Arg Arg Gly Val Asp Arg  
1 5 10 15  
Leu Ala Arg Xaa Xaa Cys Pro Arg Gly Gly Gly Pro His Cys Gly Gly  
20 25 30  
Val Leu His Pro Leu Leu Trp Val Leu His Leu Val Arg Arg Glu His  
35 40 45  
His Val Ala Leu Leu Ser Phe Val Leu Pro Ala Leu Phe His Leu Ser  
50 55 60  
Ile Val Gly Ser Ser Ile Pro Leu Trp Arg Arg Val Ala Gly Leu Arg  
65 70 75 80  
His Pro Ser Leu Trp Ser Gly Phe Arg Trp Ile Trp Ser Cys His Cys  
85 90 95  
Ser Leu Leu Ala Leu Asn Asn Gly Pro Asn Ser Gln Lys Ser Ala Glu  
100 105 110  
Ile Arg Ile Ser Cys Asp Asp Xaa Ser Gln Met Asp Ala Arg Ser Thr  
115 120 125  
Ile Tyr Gln Ile Ala Arg Leu Gly Leu Val Arg Asp  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1503886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

aaaccttccc accacctcct cccctcctc ccaacagtc ccaacgtcgca ctaccgagcc  
atgtcctccg ctaccacact ccgtttattg tcgtggggact gcgccgagga cccgctggat  
ttcggtgcgt tcgcgcgac cgcgtttctc ccgctccagc

60  
120

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:

Lys Pro Ser His His Leu Leu Pro Leu Leu Pro Thr Val Thr Thr Ser  
1 5 10 15  
His Tyr Arg Ala Met Ser Ser Ala Thr Asn Leu Arg Leu Leu Ser Trp  
20 25 30  
Asp Cys Ala Glu Asp Pro Leu Asp Phe Gly Ala Phe Ala Asp Thr Ala  
35 40 45  
Phe Leu Pro Leu Gln  
50

(2) INFORMATION FOR SEQ ID NO:2575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:

Asn Leu Pro Thr Thr Ser Ser Pro Ser Ser Gln Gln Ser Pro Arg Arg  
1 5 10 15  
Thr Thr Glu Pro Cys Pro Pro Leu Pro Thr Ser Val Tyr Cys Arg Gly  
20 25 30  
Thr Ala Pro Arg Thr Arg Trp Ile Ser Val Arg Ser Pro Thr Pro Arg  
35 40 45  
Phe Ser Arg Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:2576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:

Thr Phe Pro Pro Pro Pro Pro Pro Pro Asn Ser His His Val Ala  
1 5 10 15  
Leu Pro Ser His Val Leu Arg Tyr Gln Pro Pro Phe Ile Val Val Gly  
20 25 30  
Leu Arg Arg Gly Pro Ala Gly Phe Arg Cys Val Arg Arg His Arg Val  
35 40 45  
Ser Pro Ala Pro  
50

(2) INFORMATION FOR SEQ ID NO:2577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: -
  - (B) LOCATION: 1..338
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1503890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

|            |             |              |             |             |             |     |
|------------|-------------|--------------|-------------|-------------|-------------|-----|
| agctcgctct | ggagagaggtt | aatggcgaggca | agtcctccagc | tgcgcatattt | catgtccgcc  | 60  |
| gccatcgcg  | tcgggttcgg  | cggcgctccag  | gcgcggcgcg  | cgcasstgtg  | cagcgagtac  | 120 |
| tacgacggga | cgtgccccgt  | cgtgcaccgg   | gtcgtgcggc  | gggtgctgaa  | gaaggcgcac  | 180 |
| gagtcggacg | tccgcattcta | cgccagcctc   | acccgcctcc  | acttccacga  | ctgcttcgtg  | 240 |
| caaggctcgc | acggctccat  | cctgctggac   | aacagctcca  | gcactggtgc  | ggagaaagttc | 300 |
| gccacgcccc | acaacaactc  | ggcgcgcggg   | tacccegt    |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Ser | Leu | Trp | Glu | Arg | Leu | Met | Ala | Ala | Ser | Leu | Gln | Leu | Ala | Ile |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |     |     |  |
| Phe | Met | Ser | Ala | Ala | Ile | Ala | Leu | Gly | Phe | Gly | Gly | Val | Gln | Ala | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |
| Ala | Ala | Xaa | Xaa | Cys | Ser | Glu | Tyr | Tyr | Asp | Arg | Thr | Cys | Pro | Val | Val |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| His | Arg | Val | Val | Arg | Arg | Val | Leu | Lys | Lys | Ala | His | Glu | Ser | Asp | Val |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Arg | Ile | Tyr | Ala | Ser | Leu | Thr | Arg | Leu | His | Phe | His | Asp | Cys | Phe | Val |  |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     | 80  |     |     |     |  |
| Gln | Gly | Cys | Asp | Gly | Ser | Ile | Leu | Leu | Asp | Asn | Ser | Ser | Ser | Ile | Val |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |  |
| Ser | Glu | Lys | Phe | Ala | Thr | Pro | Asn | Asn | Asn | Ser | Ala | Arg | Gly | Tyr | Pro |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Ala | Leu | Gly | Glu | Val | Asn | Gly | Gly | Lys | Ser | Pro | Ala | Arg | His | Phe |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |
| His | Val | Arg | Arg | His | Arg | Ala | Arg | Val | Arg | Arg | Arg | Pro | Gly | Arg | Arg |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Gly | Ala | Xaa | Val | Gln | Arg | Val | Leu | Arg | Pro | Asp | Val | Pro | Arg | Arg | Ala |  |

35 40 45  
Pro Gly Arg Ala Ala Gly Ala Glu Glu Gly Ala Arg Val Arg Arg Pro  
50 55 60  
His Leu Arg Gln Pro His Pro Pro Pro Leu Pro Arg Leu Leu Arg Ala  
65 70 75 80  
Arg Leu Arg Arg Leu His Pro Ala Gly Gln Gln Leu Gln His Arg Val  
85 90 95  
Gly Glu Val Arg His Ala Gln Gln Gln Leu Gly Ala Arg Val Pro Arg  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1503893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met Ala Ala Ser Leu Gln Leu Ala Ile Phe Met Ser Ala Ala Ile Ala  
1 5 10 15  
Leu Gly Phe Gly Val Gln Ala Gly Ala Ala Xaa Xaa Cys Ser Glu  
20 25 30  
Tyr Tyr Asp Arg Thr Cys Pro Val Val His Arg Val Val Arg Val  
35 40 45  
Leu Lys Lys Ala His Glu Ser Asp Val Arg Ile Tyr Ala Ser Leu Thr  
50 55 60  
Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Ile  
65 70 75 80  
Leu Leu Asp Asn Ser Ser Ser Ile Val Ser Glu Lys Phe Ala Thr Pro  
85 90 95  
Asn Asn Asn Ser Ala Arg Gly Tyr Pro  
100 105

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

aggggttttt gccaaagtgc cgccgtcgct ctgcccgcat tcccttccac aacaccgaga 60  
cgccaggatg acggcgcgaga ctgcggagga gctcgccacc cagatcgagc agcagaagct 120  
cgaggagcag aagaccgagg cgaggagggt tgtgtgtggag gatgaggagg acgacgacga 180  
tgaggacgat gaggatgatg atgaacttga cggacaagaa ggggatgccg gcggcaagtc 240  
aaagcaaacg aggagtgaga agaagagccg caaagccatg ctgaagcttg gcatgaagcc 300  
catcacttgt gtcagccgtg tcaactgtgaa gaaaagcaag aatatactgt ttgtcatctc 360  
gaagccagat gtgttcaaga gcccgaaact agacacatac gtcatattcg gcgaggccaa 420  
gatcgaggac ctacgctccc agctgcagac ccaggccgca gaacagttca aggcccccttg 480  
acttgagcca gatcacgagt ccagagactt

(2) INFORMATION FOR SEQ ID NO:2582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids

- (B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..159  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503895  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

Gly Phe Phe Ala Lys Ser Pro Pro Ser Leu Cys Pro His Ser Leu Pro  
1 5 10 15  
Gln His Arg Asp Ala Arg Met Thr Ala Gln Thr Ala Glu Glu Leu Ala  
20 25 30  
Thr Gln Ile Glu Gln Gln Lys Leu Glu Glu Lys Thr Glu Ala Glu  
35 40 45  
Glu Val Val Val Glu Asp Glu Glu Asp Asp Asp Asp Glu Asp Glu  
50 55 60  
Asp Asp Asp Glu Leu Asp Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser  
65 70 75 80  
Lys Gln Ser Arg Ser Glu Lys Lys Ser Arg Lys Ala Met Leu Lys Leu  
85 90 95  
Gly Met Lys Pro Ile Thr Gly Val Ser Arg Val Thr Val Lys Lys Ser  
100 105 110  
Lys Asn Ile Leu Phe Val Ile Ser Lys Pro Asp Val Phe Lys Ser Pro  
115 120 125  
Asn Ser Asp Thr Tyr Val Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu  
130 135 140  
Ser Ser Gln Leu Gln Thr Gln Ala Ala Glu Gln Phe Lys Ala Pro  
145 150 155

(2) INFORMATION FOR SEQ ID NO:2583:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 137 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..137  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503896  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

Met Thr Ala Gln Thr Ala Glu Glu Leu Ala Thr Gln Ile Glu Gln Gln  
1 5 10 15  
Lys Leu Glu Glu Gln Lys Thr Glu Ala Glu Glu Val Val Val Glu Asp  
20 25 30  
Glu Glu Asp Asp Asp Asp Glu Asp Asp Glu Asp Asp Asp Glu Leu Asp  
35 40 45  
Gly Gln Glu Gly Asp Ala Ser Gly Lys Ser Lys Gln Ser Arg Ser Glu  
50 55 60  
Lys Lys Ser Arg Lys Ala Met Leu Lys Leu Gly Met Lys Pro Ile Thr  
65 70 75 80  
Gly Val Ser Arg Val Thr Val Lys Lys Ser Lys Asn Ile Leu Phe Val  
85 90 95  
Ile Ser Lys Pro Asp Val Phe Lys Ser Pro Asn Ser Asp Thr Tyr Val  
100 105 110  
Ile Phe Gly Glu Ala Lys Ile Glu Asp Leu Ser Ser Gln Leu Gln Thr  
115 120 125  
Gln Ala Ala Glu Gln Phe Lys Ala Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:2584:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..459  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503899  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:

|            |             |             |            |             |            |     |
|------------|-------------|-------------|------------|-------------|------------|-----|
| acaactttac | agctaacatg  | gagacagagc  | tagataatgt | ctctgctggg  | tcaactgaat | 60  |
| ggaagggtct | tctgaaagac  | tactgggaac  | gattcagcaa | atatgtgtga  | gatgtgagta | 120 |
| aacttgatgt | cagaaaagta  | gagagaatgc  | ttgaagaaaa | atttggtcct  | atcctctttt | 180 |
| ccgatgttta | caaggattgt  | agaatttgcc  | ctagtgtgtc | tgaagggaacc | ttgagattca | 240 |
| aagttagtag | gtacggtgaa  | ggctattttg  | taggtttgtg | tgcacatcca  | aaatgcaagt | 300 |
| acattgctcg | ctcactgtca  | cagcaagaag  | atgaaactga | acccatagaa  | gaaaatgcaa | 360 |
| aatcttttga | accacaggtta | cttgggtgtca | tgcttgattc | tgatcaaaa   | gtgtttttga | 420 |
| aacaagggcc | atatggctac  | tatgttcaag  | ttggagagg  |             |            |     |

(2) INFORMATION FOR SEQ ID NO:2585:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..152  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503900  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Thr | Ala | Asn | Met | Glu | Thr | Glu | Leu | Asp | Asn | Val | Ser | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Glu | Trp | Lys | Gly | Leu | Leu | Lys | Asp | Tyr | Trp | Glu | Arg | Phe | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Cys | Ala | Asp | Val | Ser | Lys | Leu | Asp | Gly | Arg | Lys | Val | Glu | Arg |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Met | Leu | Glu | Glu | Lys | Phe | Gly | Pro | Ile | Leu | Phe | Ser | Asp | Val | Tyr | Lys |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Asp | Cys | Arg | Ile | Cys | Pro | Ser | Cys | Ser | Glu | Gly | Thr | Leu | Arg | Phe | Lys |
|     |     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     | 80  |     |
| Val | Ser | Arg | Tyr | Gly | Glu | Gly | Tyr | Phe | Val | Gly | Cys | Asp | Arg | His | Pro |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Lys | Cys | Lys | Tyr | Ile | Ala | Arg | Ser | Leu | Ser | Gln | Gln | Glu | Asp | Glu | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Pro | Ile | Glu | Glu | Asn | Ala | Lys | Ser | Phe | Glu | Pro | Arg | Leu | Leu | Gly |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Val | Met | Pro | Asp | Ser | Asp | Gln | Lys | Val | Phe | Leu | Lys | Gln | Gly | Pro | Tyr |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |
| Gly | Tyr | Tyr | Val | Gln | Val | Gly | Glu |     |     |     |     |     |     |     |     |
|     |     |     |     | 145 |     |     | 150 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2586:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..147  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:

Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly Ser Thr Glu Trp Lys  
1 5 10 15  
Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser Lys Tyr Cys Ala Asp  
20 25 30  
Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg Met Leu Glu Lys  
35 40 45  
Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys Asp Cys Arg Ile Cys  
50 55 60  
Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys Val Ser Arg Tyr Gly  
65 70 75 80  
Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro Lys Cys Lys Tyr Ile  
85 90 95  
Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr Glu Pro Ile Glu Glu  
100 105 110  
Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly Val Met Pro Asp Ser  
115 120 125  
Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr Gly Tyr Val Gln  
130 135 140  
Val Gly Glu  
145

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1503902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys  
1 5 10 15  
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys  
20 25 30  
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro  
35 40 45  
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr  
50 55 60  
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly  
65 70 75 80  
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr  
85 90 95  
Gly Tyr Tyr Val Gln Val Gly Glu  
100

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 444 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1503924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

cggaagaatt ttgatatttg ggggtcagtg ggcaggtctt cactcagcgt cacagcttta 60  
ctctgttgat ccaactgaag aaaakccgcac ctggagaata ttgaatatct ctgtgcgtcc 120

tcccgctttc gcttggggcc acagcacctg tgttgttggg ggaacaaaagg cgatagtgc 180  
tgggtggacaa actgggagaag agtggatgct tacagaaaata catgagcttt ctttgggtcag 240  
ccgctcagtt tgagttcttg aatggtttgt agtcatgttc cttgcaaat agatgcggct 300  
tttatgcaa cctgaagttt gattgccgtc ttcagaagaa ctagaagaat gaatgctggg 360  
catactgaat ctcttggcag ctacotggcg gacttgggaag atgaatggc atcgactggt 420  
ttgctcgctt tgtgtagaaa aggg

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

Gly Arg Ile Leu Ile Phe Gly Gly Ser Val Ala Gly Leu His Ser Ala  
1 5 10 15  
Ser Gln Leu Tyr Leu Leu Asp Pro Thr Glu Glu Xaa Pro Thr Trp Arg  
20 25 30  
Ile Leu Asn Ile Pro Gly Arg Pro Pro Arg Phe Ala Thr Gly His Ser  
35 40 45  
Thr Cys Val Val Gly Gly Thr Lys Ala Ile Val Leu Gly Gly Gln Thr  
50 55 60  
Gly Glu Glu Trp Met Leu Thr Glu Ile His Glu Leu Ser Leu Val Ser  
65 70 75 80  
Arg Ser Val

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

tctgtgcac ttaaatatgg gggacagtag agctgtgctt gcttccatgc catatgtaga 60  
aaatggtgct ttgaaggcta ctcaactgac agagacccac tcgcttgaaa atcctttgga 120  
gtaccaaaaa cttttagctg aacatcccaa tgattcttca gttgtcaggg gtaacaaaaa 180  
aaaaggaaag ctgaaggtta ctctgtcttt tggagtggcg tatctgaagc agaggaaagt 240  
caacgatgca ctcatgggca ttctgcgagt ccgcgatttg agcagccctc catatgttta 300  
cacaaatcca cacacattga gccacaaaag tacagaagat gatttatttg ttgtgcttgg 360  
tagtgatggc ttatttgatt ttcttcagcaa tgatgaagtt gttcggttgg ttatcaatt 420  
tatgcatgat aatccaatgg gggatcctgc aaaatatctt attgagcaac ttatactca 480  
aagcagccaa gggagcagct ctaacagccg

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1503927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Cys | Ile | Leu | Asn | Met | Gly | Asp | Ser | Arg | Ala | Val | Leu | Ala | Ser | Met |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Tyr | Val | Glu | Asn | Gly | Ala | Leu | Lys | Ala | Thr | Gln | Leu | Thr | Glu | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Ser | Leu | Glu | Asn | Pro | Leu | Glu | Tyr | Gln | Lys | Leu | Leu | Ala | Glu | His |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Pro | Asn | Asp | Ser | Ser | Val | Val | Arg | Gly | Asn | Lys | Ile | Lys | Gly | Lys | Leu |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys | Val | Thr | Arg | Ala | Phe | Gly | Val | Gly | Tyr | Leu | Lys | Gln | Arg | Lys | Phe |  |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Asn | Asp | Ala | Leu | Met | Gly | Ile | Leu | Arg | Val | Arg | Asp | Leu | Ser | Ser | Pro |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Pro | Tyr | Val | Tyr | Thr | Asn | Pro | His | Thr | Leu | Ser | His | Lys | Val | Thr | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Asp | Leu | Phe | Val | Val | Leu | Gly | Ser | Asp | Gly | Leu | Phe | Asp | Phe | Phe |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Asn | Asp | Glu | Val | Val | Arg | Leu | Val | Tyr | Gln | Phe | Met | His | Asp | Asn |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Met | Gly | Asp | Pro | Ala | Lys | Tyr | Leu | Ile | Glu | Gln | Leu | Tyr | Thr | Gln |  |
|     |     |     |     | 145 |     | 150 |     |     | 155 |     |     |     |     |     | 160 |  |
| Ser | Ser | Gln | Gly | Ser | Ser | Ser | Asn | Ser |     |     |     |     |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1503928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Asp | Ser | Arg | Ala | Val | Leu | Ala | Ser | Met | Pro | Tyr | Val | Glu | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Ala | Leu | Lys | Ala | Thr | Gln | Leu | Thr | Glu | Thr | His | Ser | Leu | Glu | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Leu | Glu | Tyr | Gln | Lys | Leu | Leu | Ala | Glu | His | Pro | Asn | Asp | Ser | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Val | Val | Arg | Gly | Asn | Lys | Ile | Lys | Gly | Lys | Leu | Lys | Val | Thr | Arg | Ala |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Gly | Val | Gly | Tyr | Leu | Lys | Gln | Arg | Lys | Phe | Asn | Asp | Ala | Leu | Met |  |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Ile | Leu | Arg | Val | Arg | Asp | Leu | Ser | Ser | Pro | Pro | Tyr | Val | Tyr | Thr |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Asn | Pro | His | Thr | Leu | Ser | His | Lys | Val | Thr | Glu | Asp | Asp | Leu | Phe | Val |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Leu | Gly | Ser | Asp | Gly | Leu | Phe | Asp | Phe | Phe | Ser | Asn | Asp | Glu | Val |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Val | Arg | Leu | Val | Tyr | Gln | Phe | Met | His | Asp | Asn | Pro | Met | Gly | Asp | Pro |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ala | Lys | Tyr | Leu | Ile | Glu | Gln | Leu | Tyr | Thr | Gln | Ser | Ser | Gln | Gly | Ser |  |
|     |     |     |     | 145 |     | 150 |     |     | 155 |     |     |     |     |     | 160 |  |
| Ser | Ser | Asn | Ser |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..154
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1503929
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Tyr | Val | Glu | Asn | Gly | Ala | Leu | Lys | Ala | Thr | Gln | Leu | Thr | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | His | Ser | Leu | Glu | Asn | Pro | Leu | Glu | Tyr | Gln | Lys | Leu | Leu | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Pro | Asn | Asp | Ser | Ser | Val | Val | Arg | Gly | Asn | Lys | Ile | Lys | Gly | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Val | Thr | Arg | Ala | Phe | Gly | Val | Gly | Tyr | Leu | Lys | Gln | Arg | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Asp | Ala | Leu | Met | Gly | Ile | Leu | Arg | Val | Arg | Asp | Leu | Ser | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Pro | Tyr | Val | Tyr | Thr | Asn | Pro | His | Thr | Leu | Ser | His | Lys | Val | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Asp | Asp | Leu | Phe | Val | Val | Leu | Gly | Ser | Asp | Gly | Leu | Phe | Asp | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Ser | Asn | Asp | Glu | Val | Val | Arg | Leu | Val | Tyr | Gln | Phe | Met | His | Asp |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Pro | Met | Gly | Asp | Pro | Ala | Lys | Tyr | Leu | Ile | Glu | Gln | Leu | Tyr | Thr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Ser | Ser | Gln | Gly | Ser | Ser | Asn | Ser |     |     |     |     |     |     |     |
| 145 |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2594:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 161 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| accgcaccca  | gaggaggcaa | ggagcccatc | cacatccacc | tggtctgctc | ctcaccacac | 60  |
| cgccgcgccca | attggggctc | gcggcagcac | cgccgcggct | tcccgctggt | cccgctcctg | 120 |
| ctctccctcc  | tgccgcggcc | cgcgtaacgc | cgccctcatc | c          |            |     |

(2) INFORMATION FOR SEQ ID NO:2595:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Pro | Arg | Gly | Gly | Lys | Glu | Pro | Ile | His | Ile | His | Leu | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Leu | Ser | Pro | His | Arg | Arg | Ala | Asn | Trp | Gly | Ser | Arg | Gln | His | Arg | Arg |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Phe | Pro | Leu | Val | Pro | Leu | Leu | Leu | Ser | Leu | Leu | Ala | Ala | Ala | Ala |

35 40 45  
Tyr Gly Arg Leu Ile  
50  
(2) INFORMATION FOR SEQ ID NO:2596:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503936  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:  
Pro His Pro Glu Ala Arg Ser Pro Ser Thr Ser Thr Trp Ser Cys  
1 5 10 15  
Ser His His Thr Ala Ala Pro Ile Gly Ala Arg Gly Ser Thr Ala Ala  
20 25 30  
Ala Ser Arg Trp Ser Arg Ser Cys Ser Pro Ser Trp Pro Pro Arg  
35 40 45  
Thr Ala Ala Ser Ser  
50

(2) INFORMATION FOR SEQ ID NO:2597:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 53 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..53  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503937  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:  
Arg Thr Gln Arg Arg Gln Gly Ala His Pro His Pro Pro Gly Pro Ala  
1 5 10 15  
Leu Thr Thr Pro Pro Arg Gln Leu Gly Leu Ala Ala Ala Pro Arg  
20 25 30  
Leu Pro Ala Gly Pro Ala Pro Ala Leu Pro Pro Gly Arg Arg Val  
35 40 45  
Arg Pro Pro His Leu  
50

(2) INFORMATION FOR SEQ ID NO:2598:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 435 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..435  
(D) OTHER INFORMATION: / Ceres Seq. ID 1503942  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:  
gaaccacttc acagaagaag tgctttacc caccgcgcc caccgcgcgtt agttcggttc 60  
acacagtcac agtcacagac cagtcgtttc tcccttctct ccccggggcc cggagaggag 120  
aggatggccg gccggagcag cctctccatg gtcgcgtcgc accggtcttc caccgcgcgtc 180  
aaccagtggt gcggcgccga ccacggcggt ggagctcgac gaggcgcacg tcattggggg 240  
cggcgggcgc ggatacccg cgtcgtcttc accgctcgtc tcgcccgttc tgtctccgcg 300  
ggtcgaccgc tacgcgcggt cgccgcgcgtt ggccgcgcgc tcacaagcaga agccgcggtg 360

ggtggtggcc ggcgctccgg ggcggcgcta cggtgcccg caacatcccg gactggtcca 420  
agatccctggg cgcgcg

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Leu | His | Arg | Ser | Ala | Leu | Pro | Ser | Pro | Ala | Pro | Arg | Ala |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Val | Arg | Ser | Thr | Gln | Ser | Gln | Ser | Gln | Thr | Ser | Arg | Phe | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     | Leu |
| Leu | Ser | Pro | Gly | Pro | Gly | Glu | Glu | Arg | Met | Ala | Gly | Arg | Ser | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Leu |
| Ser | Met | Val | Ala | Ser | His | Arg | Leu | Phe | Thr | Pro | Val | Asn | Pro | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | Gly |
| Gly | Ala | Asp | His | Gly | Val | Gly | Ala | Arg | Arg | Gly | Arg | Arg | His | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | Gly |
| Arg | Arg | Arg | Arg | Ile | Pro | Gly | Val | Val | Leu | Thr | Val | Val | Val | Ala |
|     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | Val |
| Pro | Val | Leu | Arg | Gly | Arg | Pro | Val | Arg | Ala | Val | Ala | Ala | Gly | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     | Arg |
| Ala | Val | Gln | Ala | Glu | Ala | Ala | Trp | Gly | Gly | Arg | Arg | Ser | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gly | Val | Arg | Cys | Pro | Ser | Thr | Ser | Arg | Thr | Gly | Pro | Arg | Ser | Trp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     | Ala |
| Pro |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Ser | Gln | Lys | Lys | Cys | Phe | Thr | Leu | Thr | Arg | Pro | Thr | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Ser | Phe | Asp | Thr | Val | Thr | Val | Thr | Asp | Gln | Ser | Phe | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     | Ser |
| Leu | Pro | Arg | Ala | Arg | Arg | Gly | Glu | Asp | Gly | Arg | Pro | Glu | Gln | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     | Leu |
| His | Gly | Arg | Val | Ala | Pro | Ala | Leu | His | Ala | Gly | Gln | Pro | Ser | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     | Arg |
| Arg | Arg | Pro | Arg | Arg | Gly | Ser | Ser | Thr | Arg | Pro | Thr | Ser | Ser | Gly |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | Ala |
| Ala | Ala | Ala | Asp | Thr | Arg | Arg | Arg | Pro | His | Arg | Arg | Arg | Arg | Ser |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Cys | Pro | Pro | Arg | Ser | Thr | Arg | Thr | Arg | Gly | Arg | Arg | Arg | Trp | Pro |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     | Arg |
| Arg | Pro | Ser | Arg | Ser | Arg | Val | Gly | Trp | Trp | Pro | Ala | Leu | Arg | Gly |

115 120 125  
Arg Thr Val Pro Val Asn Ile Pro Asp Trp Ser Lys Ile Leu Gly Ala  
130 135 140

(2) INFORMATION FOR SEQ ID NO:2601:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1503945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Met Ala Gly Arg Ser Ser Leu Ser Met Val Ala Ser His Arg Leu Phe  
1 5 10 15  
Thr Pro Val Asn Pro Val Gly Gly Ala Asp His Gly Val Gly Ala Arg  
20 25 30  
Arg Gly Arg Arg His Leu Gly Arg Arg Arg Arg Ile Pro Gly Val Val  
35 40 45  
Leu Thr Val Val Val Ala Val Pro Val Leu Arg Gly Arg Pro Val Arg  
50 55 60  
Ala Val Ala Ala Gly Gly Arg Ala Val Gln Ala Glu Ala Ala Trp Gly  
65 70 75 80  
Gly Gly Arg Arg Ser Gly Ala Gly Val Arg Cys Pro Ser Thr Ser Arg  
85 90 95  
Thr Gly Pro Arg Ser Trp Ala Pro  
100

(2) INFORMATION FOR SEQ ID NO:2602:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 494 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1503946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

tgttcagttg caagaagtgt tacggggctg tgatgttttc cttgtgcac cgtcgtgtcc 60  
tcacgcaaat gaaaatctta tggagcttct gatcatgatt gatgctctga ggagagcacc 120  
tgctaaagat atcactgcag ttatccctta ttttggttat gcaagggtcg acaggaaagtc 180  
ccagggcagg gaactctatag ctgcaaaact tgtagctaat atgattaccg aagctggtgc 240  
caacgtgtcc ttgttttgta tcttcattct agtcaagcaa tgggatactt tgacatccca 300  
gtagatcacg tttatggcca gcctgtttatt cttgattacc tcgccagcaa gacaatatgt 360  
tcagatgact tggtagttgt atctcctgat gttggagggt ttgccagggc acgtgccttt 420  
gccaaaaagc tgtcagatgc acctctagct attgtagata aaagaaggca aggacataat 480  
gtcgtctgagg tgat

(2) INFORMATION FOR SEQ ID NO:2603:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1503947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

```
Val Gln Leu Gln Glu Ser Val Arg Gly Cys Asp Val Phe Leu Val Gln
1      5      10      15
Pro Ser Cys Pro Pro Ala Asn Glu Asn Leu Met Glu Leu Leu Ile Met
20      25      30
Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys Asn Ile Thr Ala Val Ile
35      40      45
Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg Lys Ser Gln Gly Arg Glu
50      55      60
Ser Ile Ala Ala Lys Leu Val Ala Asn Met Ile Thr Glu Ala Gly Ala
65      70      75      80
Asn Val Ser Leu Phe Val Ile Phe Ile Leu Val Lys Gln Trp Asp Thr
85      90      95
Leu Thr Ser Gln
100
```

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

```
Met Glu Leu Leu Ile Met Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys
1      5      10      15
Asn Ile Thr Ala Val Ile Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg
20      25      30
Lys Ser Gln Gly Arg Glu Ser Ile Ala Ala Lys Leu Val Ala Asn Met
35      40      45
Ile Thr Glu Ala Gly Ala Asn Val Ser Leu Phe Val Ile Phe Ile Leu
50      55      60
Val Lys Gln Trp Asp Thr Leu Thr Ser Gln
65      70
```

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1503949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

```
Met Gly Tyr Phe Asp Ile Pro Val Asp His Val Tyr Gly Gln Pro Val
1      5      10      15
Ile Leu Asp Tyr Leu Ala Ser Lys Thr Ile Cys Ser Asp Asp Leu Val
20      25      30
Val Val Ser Pro Asp Val Gly Gly Val Ala Arg Ala Arg Ala Phe Ala
35      40      45
Lys Lys Leu Ser Asp Ala Pro Leu Ala Ile Val Asp Lys Arg Arg Gln
50      55      60
Gly His Asn Val Ala Glu Val
65      70
```

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| gattttgaaa | ggggtttcat | atgcgctgag | gtaatgaagt | ttgaagatct | gaaagaactg | 60  |
| ggcagtgaa  | ctgctgtaaa | ggctgctgga | aaatacaagc | aggaggggaa | aacctatgtg | 120 |
| gtccaggacg | gggacatcat | ctttttcaaa | tcaacactgt | ctggtggcgg | gaagaagtga | 180 |
| ataatgtatg | aagatggtag | catcaacagt | gtttacgtc  | ttaccccgaa | ttctcattc  | 240 |
| aacagtgttt | acaccttgcc | ccgtatttcc | acatttttga | ggtcgcttcc | cagtagctct | 300 |
| aggttcgggt | atcgaaaact | tgtacaacaa | ggctccagac | cgttgaagga | ttgtattaa  | 360 |
| taacatgcac | aattgtatgg | cttgtgcttg | agctctcgct | gttaccagaa | gcttagaatc | 420 |
| gtttgagttc | tgtgg      |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Phe | Glu | Arg | Gly | Phe | Ile | Cys | Ala | Glu | Val | Met | Lys | Phe | Glu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Lys | Glu | Leu | Gly | Ser | Glu | Ser | Ala | Val | Lys | Ala | Ala | Gly | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Gln | Glu | Gly | Lys | Thr | Tyr | Val | Val | Gln | Asp | Gly | Asp | Ile | Ile | Phe |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Phe | Asn | Val | Ser | Gly | Gly | Lys | Lys |     |     |     |     |     |     |
|     |     |     | 50  |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Glu | Asp | Leu | Lys | Glu | Leu | Gly | Ser | Glu | Ser | Ala | Val | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ala | Gly | Lys | Tyr | Lys | Gln | Glu | Gly | Lys | Thr | Tyr | Val | Val | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Asp | Ile | Ile | Phe | Phe | Lys | Phe | Asn | Val | Ser | Gly | Gly | Lys | Lys |     |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2609:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 58 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..58  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1503972  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:  
Met Tyr Glu Asp Gly Ser Ile Asn Ser Val Leu Arg Leu Thr Pro Asn  
1           5           10           15  
Phe Ser Phe Asn Ser Val Tyr Thr Leu Pro Arg Ile Ser Thr Phe Leu  
          20           25           30  
Arg Ser Leu Pro Ser Ser Ser Arg Phe Arg Tyr Arg Lys Leu Val Gln  
          35           40           45  
Gln Gly Ser Arg Pro Leu Lys Asp Leu Tyr  
50           55  
(2) INFORMATION FOR SEQ ID NO:2610:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 506 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..506  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503989  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:  
accgcgccct gatccactct ccgcttcccg ctccgatgca cctgtccctt cccccacc 60  
gagcccatgg cggaccagct caccgacgac cagatcgccg agttcaagga ggccttcagc 120  
ctcttcgaca aggacgggga tggttgcac acgaccaagg agctggggac tgtcatgccc 180  
tcgctggggc aaaatcctac agaggctgag ctccaggaca tgatcaacga ggctgatgct 240  
gatggcaacg gcaccatcga ttctccagag ttctcaacc ttatggctcg caagatgaag 300  
gacaccgact ctgaggaaga gctcaaggag gccttcctgt tgttgacaa ggaccagaac 360  
ggcttcactc cgccgcgcca gctccgccat gtcatgacaa atcttggtga gaagctaact 420  
gatgaggagg tggacgagat gatccgtgag gctgatgctg atgggtgatg ccagatcaac 480  
tacgaggagt ttgtcaaggt catgat  
(2) INFORMATION FOR SEQ ID NO:2611:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 146 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..146  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1503990  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:  
Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala  
1           5           10           15  
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu  
          20           25           30  
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu  
          35           40           45  
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile  
50           55           60  
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Asn | Glu | Val | Asp | Ala | Asp | Gly | Asn | Gly | Thr | Ile | Asp | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Phe | Leu | Asn | Leu | Met | Ala | Arg | Lys | Met | Lys | Asp | Thr | Asp | Ser | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Glu | Leu | Lys | Glu | Ala | Phe | Arg | Val | Phe | Asp | Lys | Asp | Gln | Asn | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Ile | Ser | Ala | Ala | Glu | Leu | Arg | His | Val | Met | Thr | Asn | Leu | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Leu | Thr | Asp | Glu | Glu | Val | Asp | Glu | Met | Ile | Arg | Glu | Ala | Asp | Glu |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gly | Asp | Gly | Gln | Ile | Asn | Tyr | Glu | Glu | Phe | Val | Lys | Val | Met |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

|             |            |            |            |             |            |     |
|-------------|------------|------------|------------|-------------|------------|-----|
| tcaacgcaca  | tctccaccgt | cgctccgcgc | cgccgaagac | ggaaggagaa  | gagggtacgg | 60  |
| ccgtctctctc | gcccccatgg | cccacagaaa | gaagctgtcc | aaccgcgatgc | gggagatcaa | 120 |
| gggtgcagaag | ctcgtctcca | atatctcgt  | cggggagagc | ggcgaccgtc  | tcacccggcg | 180 |
| cgcaaaagtg  | ctcgagcagc | tcagcggcca | gaccccgtc  | ttctccaaag  | gtgagtactg | 240 |
| agttctcggc  | gtctcgttcc | atgccttcg  | ctgacggggg | gcttcctctc  | gcctgctggc | 300 |
| gggtgtgggt  | cgctctgcag | cgaggtacac | ggtgcggtcg | ttcggcatcc  | ggcgtaacga | 360 |
| gaagatcgcc  | tgtctactca | cggtgagggg | cgagaaggcc | atgcagctgc  | ttgagagcgg | 420 |
| ccctcaagtc  | aaggagtag  | agctgctcag | gaggaacttc | agcgacaccg  | ggtgctttg  |     |

(2) INFORMATION FOR SEQ ID NO:2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Thr | His | Ile | Ser | Thr | Val | Val | Arg | Arg | Arg | Arg | Arg | Lys | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Val | Arg | Pro | Ser | Pro | Arg | Pro | His | Gly | Pro | Arg | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Val | Gln | Pro | Asp | Ala | Gly | Asp | Gln | Gly | Ala | Glu | Ala | Arg | Pro | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Arg | Arg | Gly | Glu | Arg | Arg | Pro | Ser | His | Pro | Arg | Arg | Lys | Gly |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Arg | Ala | Ala | Gln | Arg | Pro | Asp | Pro | Arg | Leu | Leu | Gln | Gly |     |     |
|     |     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Arg | Thr | Ser | Pro | Pro | Ser | Ser | Ala | Ala | Glu | Asp | Gly | Arg | Arg |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Arg | Gly | Tyr | Gly | Arg | Leu | Leu | Ala | Pro | Met | Ala | His | Glu | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |
| Ser | Asn | Pro | Met | Arg | Glu | Ile | Lys | Val | Gln | Lys | Leu | Val | Leu | Asn |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Ser | Val | Gly | Glu | Ser | Gly | Asp | Arg | Leu | Thr | Arg | Ala | Ala | Lys | Val |

50 55 60  
Glu Gln Leu Ser Gly Gln Thr Pro Val Phe Ser Lys Gly Glu Tyr  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1504004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | His | Leu | His | Arg | Arg | Pro | Pro | Pro | Pro | Lys | Thr | Glu | Gly | Glu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Gly | Thr | Ala | Val | Ser | Ser | Pro | Pro | Trp | Pro | Thr | Arg | Arg | Ser | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Thr | Arg | Cys | Gly | Arg | Ser | Arg | Cys | Arg | Ser | Ser | Ser | Ser | Ile | Ser |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Pro | Ser | Gly | Arg | Ala | Ala | Thr | Val | Ser | Pro | Ala | Pro | Gln | Arg | Cys | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |
| Ser | Ser | Ser | Ala | Ala | Arg | Pro | Pro | Ser | Ser | Pro | Arg | Val | Ser | Thr | Glu |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Phe | Ser | Arg | Leu | Arg | Phe | Met | Pro | Ser | Ala | Asp | Gly | Val | Leu | Pro | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Cys | Trp | Arg | Cys | Trp | Phe | Val | Leu | Gln | Arg | Gly | Thr | Arg | Cys | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Ser | Ala | Ser | Gly | Val | Thr | Arg | Arg | Ser | Pro | Ala | Thr | Ser | Arg |     |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1504016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

|             |             |             |             |            |             |     |
|-------------|-------------|-------------|-------------|------------|-------------|-----|
| atcgagacac  | acacagaact  | tctcctgtcg  | gcctactaat  | acagctagct | agctgccctc  | 60  |
| ttaggtatgc  | tgtgatggcc  | acaaccttgt  | ctccacagt   | agtagttgca | cttggtgacc  | 120 |
| tctctctcttg | ctccttgttaa | cgtgtggctc  | gtgcgcgagg  | ccggtgagct | ttaacgcctc  | 180 |
| cgacctcacc  | gccgatcccg  | gctgggatgc  | tgccagggcc  | acctgttacg | gtgcgcccac  | 240 |
| cggcgcggcc  | ctgatgacga  | cgttgtgtcc  | tgtggattca  | agaacgtgaa | tctgccgccc  | 300 |
| ttctcgcaaa  | tgaagctctg  | cggaacagag  | cccctgttca  | aggacggcaa | gggctcgggc  | 360 |
| tccctgtacc  | agatacagtg  | ccaaaaccac  | ccggcctgct  | ccggcaacc  | agagacgggtg | 420 |
| atcatcactg  | acatgaacta  | ctaccccggtg | gccaaagtacc | acttcgacct | yagcggc     |     |

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1504017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Arg Asp Thr His Arg Thr Ser Pro Val Gly Leu Leu Ile Gln Leu Ala  
1 5 10 15  
Ser Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Thr Leu Ser Ser Thr  
20 25 30  
Val Val Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

Met Thr Ser Cys Gly Asn Glu Pro Leu Phe Lys Asp Gly Lys Gly Cys  
1 5 10 15  
Gly Ser Cys Tyr Gln Ile Arg Cys Gln Asn His Pro Ala Cys Ser Gly  
20 25 30  
Asn Pro Glu Thr Val Ile Ile Thr Asp Met Asn Tyr Tyr Pro Val Ala  
35 40 45  
Lys Tyr His Phe Asp Xaa Ser Gly  
50 55

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1504025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

catgtgggttg tgggcactgt gaaagctctt tggccactca cagaagccct agaataagaa 60  
tatttgctaat gatgagaagt aactaaaaca atatcataca attgcagtgc tctctccaat 120  
agtttggagg gtatgctcct tggagattt ttggtaggaa cagggatggg attgggtcca 180  
ccagtagctt cactttatat aacggaggtt tctccttcta cagtggaggg tacatatggt 240  
agccttggtc agattgcaac ctgaccttga attatagtat cactactcat tggtagacct 300  
gtcaaagata ttgatagatg gtggagagtg tgtttctggg ttgccgttat cccagcaact 360  
ttacaagctc tcggtatgga gttttgtgct gagagccctc agtggcttta taagtgtgga 420  
aaaataagtg

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1504026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Met Leu Leu Gly Arg Phe Leu Val Gly Thr Gly Met Gly Leu Gly Pro

1 5 10 15  
Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser Pro Ser Thr Val Arg  
20 25 30  
Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr Cys Leu Gly Ile Ile  
35 40 45  
Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp Ile Asp Arg Trp Trp  
50 55 60  
Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala Thr Leu Gln Ala Leu  
65 70 75 80  
Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp Leu Tyr Lys Cys Gly  
85 90 95  
Lys Ile Ser

(2) INFORMATION FOR SEQ ID NO:2623:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..88  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met Gly Leu Gly Pro Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser  
1 5 10 15  
Pro Ser Thr Val Arg Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr  
20 25 30  
Cys Leu Gly Ile Ile Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp  
35 40 45  
Ile Asp Arg Trp Trp Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala  
50 55 60  
Thr Leu Gln Ala Leu Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp  
65 70 75 80  
Leu Tyr Lys Cys Gly Lys Ile Ser  
85

(2) INFORMATION FOR SEQ ID NO:2624:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 462 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..462  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

tattatcaga gaacaacagag ctgtgcttct ctgttgcttc attgctctgg cagaagctca 60  
tagcttctcc tgaaatgcag atgtctgcag aaagtacatc agctcaccaa ggatggagga 120  
aggttgttga tgcactttgt gatgtcgttt cagcctcacc aaccaaggca tcagctgtcta 180  
tcgttctcca gcccgagaag gacttgcagc ctgtgattgc tagagatgac gaacaaggctc 240  
agaagatgtg gagagtcac cagcgtatag tgaagcttat agctgagctt atgaggaacc 300  
atgacagccc tgaagcgttg gtgatactcg ctagtgcctc cgaccttcta ctctgtgcta 360  
ccgatggaa gctcgtcgat ggtgaagctt gtactttgcc acagcttgag ctcttggaag 420  
tgaccgctcg ggcgtccat ctatcatcg aatggggaga tc

(2) INFORMATION FOR SEQ ID NO:2625:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504037  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Leu Ser Glu Lys Gln Glu Leu Cys Phe Ser Val Val Ser Leu Leu Trp  
1 5 10 15  
Gln Lys Leu Ile Ala Ser Pro Glu Met Gln Met Ser Ala Glu Ser Thr  
20 25 30  
Ser Ala His Gln Gly Trp Arg Lys Val Val Asp Ala Leu Cys Asp Val  
35 40 45  
Val Ser Ala Ser Pro Thr Lys Ala Ser Ala Ala Ile Val Leu Gln Ala  
50 55 60  
Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg Asp Asp Glu Gln Gly Gln  
65 70 75 80  
Lys Met Trp Arg Val Asn Gln Arg Ile Val Lys Leu Ile Ala Glu Leu  
85 90 95  
Met Arg Asn His Asp Ser Pro Glu Ala Leu Val Ile Leu Ala Ser Ala  
100 105 110  
Ser Asp Leu Leu Leu Arg Ala Thr Asp Gly Met Leu Val Asp Gly Glu  
115 120 125  
Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu Glu Val Thr Ala Arg Ala  
130 135 140  
Val His Leu Ile Ile Glu Trp Gly Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:2626:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..129  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met Gln Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys  
1 5 10 15  
Val Val Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala  
20 25 30  
Ser Ala Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile  
35 40 45  
Ala Arg Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg  
50 55 60  
Ile Val Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu  
65 70 75 80  
Ala Leu Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Leu Arg Ala Thr  
85 90 95  
Asp Gly Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu  
100 105 110  
Leu Leu Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly  
115 120 125  
Asp

(2) INFORMATION FOR SEQ ID NO:2627:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: peptide
  - (B) LOCATION: 1..127
  - (D) OTHER INFORMATION: / Ceres Seq. ID 1504039
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys Val Val  
1 5 10 15  
Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala Ser Ala  
20 25 30  
Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg  
35 40 45  
Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg Ile Val  
50 55 60  
Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu Ala Leu  
65 70 75 80  
Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Leu Arg Ala Thr Asp Gly  
85 90 95  
Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu  
100 105 110  
Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly Asp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:2628:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

aaatctctct ctctctctcg cctcgcttg gtgttcacgc cgtcgctagc gcctgckcct 60  
gccssggcka asttctctgcc ctcccgcgcg ccgggctcgg gtcgtcgctcg gccaggaaga 120  
tggtctggcg cttcagggta ctgcatctgg tcaggccttt tctggtcttc ttgccatakk 180  
ttgcagagcg cggatagkaa gatacgcgtt agagaaaaag ttatctacac tgttatttcc 240  
ctcttcattt tcttggtctg cagccagctc ccactctatg gcattcattc aacaactgga 300  
gctgatcctt tctactggat gcgtgttatc ctgcgatcaa accgtggcac tgtgatggag 360  
ttgggtatta ctccaattgt gacactctgg atggtaatgc aacttcttgt tggatcgaa 420  
atcatttgaa gtgacaaca gtgtgagaca ggtcgtgct ctg

(2) INFORMATION FOR SEQ ID NO:2629:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 142 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

Lys Ser Leu Ser Ser Pro Arg Leu Ala Leu Val Phe Thr Pro Ser Leu  
1 5 10 15  
Ala Pro Xaa Pro Ala Xaa Xaa Xaa Phe Leu Pro Ser Pro Ala Pro Gly  
20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Gly | Arg | Arg | Arg | Pro | Gly | Arg | Trp | Leu | Ala | Ala | Ser | Gly | Tyr | Cys |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ile | Trp | Ser | Gly | Leu | Phe | Trp | Leu | Ser | Cys | His | Xaa | Leu | Gln | Ser | Ala |  |
|     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Asp | Xaa | Lys | Ile | Pro | Phe | Arg | Glu | Lys | Val | Ile | Tyr | Thr | Val | Ile | Ser |  |
|     | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Leu | Phe | Ile | Phe | Leu | Val | Cys | Ser | Gln | Leu | Pro | Leu | Tyr | Gly | Ile | His |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Ser | Thr | Thr | Gly | Ala | Asp | Pro | Phe | Tyr | Trp | Met | Arg | Val | Ile | Leu | Ala |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Asn | Arg | Gly | Thr | Val | Met | Glu | Leu | Gly | Ile | Thr | Pro | Ile | Val | Thr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser | Gly | Met | Val | Met | Gln | Leu | Leu | Val | Gly | Ser | Lys | Ile | Ile |     |     |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

|             |            |             |            |            |            |     |
|-------------|------------|-------------|------------|------------|------------|-----|
| atctgaagga  | tatggcttat | catggagtat  | ttttaagag  | ggacatttgt | taagtgggtc | 60  |
| tgaacgatgct | caaatttgct | tgtgggacat  | taaagcaaat | agtagaaaca | aaagtcttga | 120 |
| cgcttgcag   | atttttaagc | atcatgatgg  | tgtcgttgaa | gatgttgctt | ggcacttgag | 180 |
| gcacgatgac  | ttatttgggt | cagttgggtga | cgattatcat | cttttgattt | gggacctgcg | 240 |
| gtctcccgcc  | ctactaaac  | ctgttcagtc  | agtgggtggc | caccagggtg | aggtgaactg | 300 |
| ccctggctttt | aacccgttca | acgaatgggt  | tgttgcaact | gggtctactg | acaagactgt | 360 |
| caaatatttt  | gatcttagga | agattgatac  | ttctctgcac | acctttgact | gtcacaaaga | 420 |
| ggaagttttt  | caagttggat | ggagtcacaa  | gaatgaaact | gtacttgcat | cctgttgtct | 480 |
| gggcagaagg  | ctcatggtct | gg          |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Glu | Gly | Tyr | Gly | Leu | Ser | Trp | Ser | Ile | Phe | Lys | Glu | Gly | His | Leu |  |
|     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Ser | Gly | Ser | Asp | Ala | Gln | Ile | Cys | Leu | Trp | Asp | Ile | Lys | Ala |     |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Asn | Ser | Arg | Asn | Lys | Ser | Leu | Asp | Ala | Leu | Gln | Ile | Phe | Lys | His | His |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asp | Gly | Val | Val | Glu | Asp | Val | Ala | Trp | His | Leu | Arg | His | Glu | Tyr | Leu |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Gly | Ser | Val | Gly | Asp | Asp | Tyr | His | Leu | Leu | Ile | Trp | Asp | Leu | Arg |  |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ser | Pro | Ala | Pro | Thr | Lys | Pro | Val | Gln | Ser | Val | Val | Ala | His | Gln | Gly |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Glu | Val | Asn | Cys | Leu | Ala | Phe | Asn | Pro | Phe | Asn | Glu | Trp | Val | Val | Ala |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

Thr Gly Ser Thr Asp Lys Thr Val Lys Leu Phe Asp Leu Arg Lys Ile  
115 120 125  
Asp Thr Ser Leu His Thr Phe Asp Cys His Lys Glu Val Phe Gln  
130 135 140  
Val Gly Trp Ser Pro Lys Asn Glu Thr Val Leu Ala Ser Cys Cys Leu  
145 150 155 160  
Gly Arg Arg Leu Met Val Trp  
165

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

|             |             |            |            |             |             |     |
|-------------|-------------|------------|------------|-------------|-------------|-----|
| attccgttcc  | gagagccaaa  | aactccactg | ctttcatcaa | ctccggcgac  | ttggagaaga  | 60  |
| cgaaktccag  | aatccgatcg  | gaagtttggt | gctcgcgcct | tgacggattg  | atttcggtgc  | 120 |
| gccgatgggg  | caggcgttcc  | gcaagctgtt | cgattccttc | tccggcaccac | gcgagatgag  | 180 |
| ggttgatgat  | cttggctctgg | atgctgccgg | taaaaccacc | atattgtaca  | agctgcata   | 240 |
| cggggaggtt  | ttgtcgactg  | ttcccacgat | tggtttcaac | gtcgagaaaag | tccaatacaca | 300 |
| gaatgtgat   | tttactgtgt  | ggagttgttg | tgcccaagaa | aagttgaggg  | tgactacctc  | 360 |
| cgcaaaggag  | atgagtttgg  | gtatttctcc | tttggaggga | gtacagtgat  | attcgctcttc | 420 |
| gagaaaggacg | ccatccaatt  | tgacgctgat | ctcgtggcaa | acagcgaaaag | gtcactggag  | 480 |
| accaagtccc  | ggatctgcag  | aaagtctcgc | tcgg       |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Gln | Ala | Phe | Arg | Lys | Leu | Phe | Asp | Ser | Phe | Phe | Gly | Thr | Ser |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |  |
| Glu | Met | Arg | Val | Val | Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ile | Leu | Trp | Lys | Leu | His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Gly | Phe | Asn | Val | Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Val | Trp | Asp | Val | Gly | Gly | Gln | Glu | Lys | Leu | Arg | Val | Thr | Thr | Ser | Ala |  |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Glu | Met | Ser | Lys | Gly | Ile | Ser | Pro | Leu | Glu | Gly | Val | Gln |     |     |  |
|     |     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..77  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Val | Val | Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr | Ile |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Tyr | Lys | Leu | His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr | Ile |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Phe | Asn | Val | Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr | Val |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Trp | Asp | Val | Gly | Gly | Gln | Glu | Lys | Leu | Arg | Val | Thr | Thr | Ser | Ala | Lys |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Glu | Met | Ser | Leu | Gly | Ile | Ser | Pro | Leu | Glu | Gly | Val | Gln |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2635:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 73 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..73  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Gly | Leu | Asp | Ala | Ala | Gly | Lys | Thr | Thr | Ile | Leu | Tyr | Lys | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| His | Ile | Gly | Glu | Val | Leu | Ser | Thr | Val | Pro | Thr | Ile | Gly | Phe | Asn | Val |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Lys | Val | Gln | Tyr | Lys | Asn | Val | Met | Phe | Thr | Val | Trp | Asp | Val | Gly |  |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |  |
| Gly | Gln | Glu | Lys | Leu | Arg | Val | Thr | Thr | Ser | Ala | Lys | Glu | Met | Ser | Leu |  |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |  |
| Gly | Ile | Ser | Pro | Leu | Glu | Gly | Val | Gln |     |     |     |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2636:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 460 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..460  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

|            |            |            |            |            |            |  |     |
|------------|------------|------------|------------|------------|------------|--|-----|
| atatatactc | ctgttgcgta | gaatcggcac | aagggtgcac | gttcaggagg | agctctcgtg |  | 60  |
| gcgtcctagt | ctgtggaagg | tccaaagaag | aagatggacg | gcgagatgga | cgaggacgtt |  | 120 |
| ctcacggaga | tctcgcgag  | gctgccgtgc | aggtcgctgg | cgcgattcca | gtcgtgttc  |  | 180 |
| acgtcgtgcg | gcgcacatc  | tccagcgact | acctccgcgc | ccggtgcgcg | ctcatcacgt |  | 240 |
| cggcgctgtc | ctaccacgat | ggtggcagga | ggcagcagtc | gtacacgtac | gcgtgcgcgt |  | 300 |
| caggcgcgcg | cggcgcgccg | ggcgcattgg | cggaggccgc | ggacatgcgc | ttcttccgcg |  | 360 |
| gccacgagac | gtccaccatc | atcgacggct | gcaacgggct | gctgtcttac | tacgcgtccc |  | 420 |
| gcccgcgcg  | ttccagctcg | tgaagccgac | cacgcggcgg |            |            |  |     |

(2) INFORMATION FOR SEQ ID NO:2637:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..153  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504103  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Tyr Ile Leu Leu Leu Arg Arg Ile Gly Thr Arg Val His Val Gln Glu  
1 5 10 15  
Glu Leu Ser Trp Arg Pro Ser Leu Trp Lys Val Gln Arg Arg Arg Trp  
20 25 30  
Thr Ala Arg Trp Thr Arg Thr Phe Ser Arg Arg Ser Ser Arg Gly Cys  
35 40 45  
Arg Ala Gly Arg Trp Arg Gly Ser Ser Ala Cys Pro Arg Arg Ala Ala  
50 55 60  
His His Leu Gln Arg Leu Pro Pro Pro Ala Ala Ala His His Val  
65 70 75 80  
Gly Arg Ala Leu Pro Arg Trp Trp Gln Glu Ala Ala Val Val His Val  
85 90 95  
Arg Val Arg Val Arg Arg Arg Arg Arg Arg Arg Ile Gly Gly Gly  
100 105 110  
Arg Gly His Ala Leu Leu Pro Ala Pro Arg Asp Val His His His Arg  
115 120 125  
Arg Leu Gln Arg Pro Ala Ala Leu Leu Arg Val Pro Gly Ala Phe  
130 135 140  
His Val Val Ser Pro Thr Thr Arg Arg  
145 150

- (2) INFORMATION FOR SEQ ID NO:2638:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 146 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504104  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

Ile Tyr Ser Cys Cys Val Glu Ser Ala Gln Gly Cys Thr Phe Arg Arg  
1 5 10 15  
Ser Ser Arg Gly Val Leu Val Cys Gly Arg Ser Lys Glu Glu Asp Gly  
20 25 30  
Arg Arg Asp Gly Arg Gly Arg Ser His Gly Asp Pro Arg Glu Ala Ala  
35 40 45  
Val Gln Val Ala Gly Ala Val Pro Val Arg Val His Val Val Arg Arg  
50 55 60  
Ile Ile Ser Ser Asp Trp Leu Arg Arg Arg Leu Pro Leu Ile Thr Ser  
65 70 75 80  
Gly Val Leu Tyr His Asp Gly Gly Arg Arg Gln Gln Ser Tyr Thr Tyr  
85 90 95  
Ala Cys Ala Ser Gly Gly Gly Gly Gly Gly Ala Leu Ala Glu Ala  
100 105 110  
Ala Asp Met Arg Phe Phe Pro Arg His Glu Thr Ser Thr Ile Ile Asp  
115 120 125  
Gly Cys Asn Gly Leu Leu Leu Tyr Tyr Ala Ser Arg Pro Ala Arg Ser  
130 135 140  
Thr Ser  
145

- (2) INFORMATION FOR SEQ ID NO:2639:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..122  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504105  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:  
Met Asp Gly Glu Met Asp Glu Asp Val Leu Thr Glu Ile Leu Ala Arg  
1 5 10 15  
Leu Pro Cys Arg Ser Leu Ala Arg Phe Gln Cys Val Ser Thr Ser Cys  
20 25 30  
Gly Ala Ser Ser Pro Ala Thr Thr Ser Ala Ala Gly Cys Arg Ser Ser  
35 40 45  
Arg Arg Ala Cys Ser Thr Thr Met Val Ala Gly Gly Ser Ser Arg Thr  
50 55 60  
Arg Thr Arg Ala Arg Gln Ala Ala Ala Ala Ala His Trp Arg  
65 70 75 80  
Arg Pro Arg Thr Cys Ala Ser Ser Arg Ala Thr Arg Arg Pro Pro Ser  
85 90 95  
Ser Thr Ala Ala Thr Ala Cys Cys Ser Thr Thr Arg Pro Ala Arg Arg  
100 105 110  
Val Pro Arg Arg Glu Pro Asp His Ala Ala  
115 120  
(2) INFORMATION FOR SEQ ID NO:2640:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 469 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..469  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504107  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:  
aactgcggct gtgcgcttcg ttcagttcag ttcattccgtg ttcttggttg cgaggctcga 60  
agagactgag agaggatgct gtgctgcgga ggcaactcgc ggtgcggctc cggtgcgaag 120  
tgccggcaacg gtgcgggagg gtgcagcaag atgtaccgcg gaagtgggta tcgacctcgt 180  
cgccggtggg aggaataaga agaccaagcg cactgcgcc aagtctgacg atgtctacct 240  
caagctctct gtcaagctct acogtttctt ggtcaggagg accaagagca atttcaacgc 300  
tgtcattctc aagaggcttt tcatgagtaa aaccaaccga ccaccaatct ccatgcgcc 360  
ccttgtaacg tttatgggaag gaaaggagaa gaacattgct gtcattgttg gcacagtcac 420  
agatgacaaa aggatccagg aggtccagc aatgaaggtt actgccttg  
(2) INFORMATION FOR SEQ ID NO:2641:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..156  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504108  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:  
Thr Ala Ala Val Arg Phe Val Gln Phe Ser Ser Ser Val Phe Leu Phe  
1 5 10 15  
Ala Arg Ser Arg Glu Thr Glu Arg Gly Cys Arg Ala Ala Glu Ala Thr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
|     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |  |  |  |  |
| Ala | Gly | Ala | Ala | Pro | Ala | Ala | Ser | Ala | Ala | Thr | Ala | Ala | Glu | Gly | Ala |  |  |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |  |  |
| Ala | Arg | Cys | Thr | Arg | Arg | Met | Gly | Ile | Asp | Leu | Val | Ala | Gly | Gly | Arg |  |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |  |
| Asn | Lys | Lys | Thr | Lys | Arg | Thr | Ala | Pro | Lys | Ser | Asp | Asp | Val | Tyr | Leu |  |  |  |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |  |
| Lys | Leu | Leu | Val | Lys | Leu | Tyr | Arg | Phe | Leu | Val | Arg | Arg | Thr | Lys | Ser |  |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Asn | Phe | Asn | Ala | Val | Ile | Leu | Lys | Arg | Leu | Phe | Met | Ser | Lys | Thr | Asn |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |
| Arg | Pro | Pro | Ile | Ser | Met | Arg | Arg | Leu | Val | Lys | Phe | Met | Glu | Gly | Lys |  |  |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |  |  |
| Glu | Lys | Asn | Ile | Ala | Val | Ile | Val | Gly | Thr | Val | Thr | Asp | Asp | Lys | Arg |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |  |  |  |
| Ile | Gln | Glu | Val | Pro | Ala | Met | Lys | Val | Thr | Ala | Leu |     |     |     |     |  |  |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1504109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Leu | Arg | Leu | Cys | Ala | Ser | Phe | Ser | Ser | Val | His | Pro | Cys | Ser | Cys | Leu |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |  |  |  |  |
| Arg | Gly | Arg | Glu | Arg | Leu | Arg | Glu | Asp | Val | Val | Leu | Arg | Arg | Gln | Leu |  |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |  |  |
| Arg | Val | Arg | Leu | Arg | Leu | Gln | Val | Arg | Gln | Arg | Leu | Arg | Arg | Val | Gln |  |  |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |  |  |
| Gln | Asp | Val | Pro | Ala | Glu | Trp | Val | Ser | Thr | Ser | Ser | Pro | Val | Gly | Gly |  |  |  |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |  |  |  |
| Ile | Arg | Arg | Pro | Ser | Ala | Leu | Arg | Pro | Ser | Leu | Thr | Met | Ser | Thr | Ser |  |  |  |  |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |  |  |  |  |
| Ser | Ser | Ser | Ser | Ser | Ser | Thr | Val | Ser | Trp | Ser | Gly | Gly | Pro | Arg | Ala |  |  |  |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Ile | Ser | Thr | Leu | Ser | Phe | Ser | Arg | Gly | Phe | Ser |     |     |     |     |     |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1504110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Met | Gly | Ile | Asp | Leu | Val | Ala | Gly | Gly | Arg | Asn | Lys | Lys | Thr | Lys | Arg |  |  |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |  |  |  |  |
| Thr | Ala | Pro | Lys | Ser | Asp | Asp | Val | Tyr | Leu | Lys | Leu | Leu | Val | Lys | Leu |  |  |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |  |  |  |  |
| Tyr | Arg | Phe | Leu | Val | Arg | Arg | Thr | Lys | Ser | Asn | Phe | Asn | Ala | Val | Ile |  |  |  |  |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |  |

Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met  
50 55 60  
Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val  
65 70 75 80  
Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala  
85 90 95  
Met Lys Val Thr Ala Leu  
100

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..437  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| acatcaccag | cgcacagctt | tctcatcg   | ggcccagtc  | ctgctctgat | ggcgaccgac | 60  |
| gtggctgaga | ctccccgcgc | gttggtgat  | gcggcccctg | aggcgcccgc | ggacaccccg | 120 |
| gcggcgctgc | tgttgacgcg | amscggccaa | ggccaagaag | gccacagcgc | cgaagaagcg | 180 |
| cgccassccg | accatctcgc | cgtacgccga | gatggctctg | gaggcgatcg | cgtcgtctaa | 240 |
| ggagaggacg | gggtccagca | gctttgctat | tgccaagtcc | ttggaggaca | agcacaagga | 300 |
| caagctcccg | cccaacttcc | gcaagcttct | gaacgttcag | ctcaagaagc | tcgtcgcccg | 360 |
| cggaagctg  | accaagtgta | agaactcgta | caagctgtcg | tccgccacca | agccaaaagg | 420 |
| ccgccccgaa | gaagacc    |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ser | Pro | Ala | His | Ser | Phe | Pro | His | Arg | Gly | Pro | Ser | Pro | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Ala | Thr | Asp | Val | Ala | Glu | Thr | Pro | Ala | Pro | Leu | Val | Asp | Ala | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Pro | Glu | Ala | Pro | Ala | Asp | Thr | Pro | Ala | Ala | Leu | Leu | Leu | Thr | Arg | Xaa |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Gly | Gln | Glu | Gly | His | Ser | Ala | Glu | Glu | Ala | Arg | Xaa | Xaa | Asp |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ser | Ala | Val | Arg | Arg | Asp | Gly | Leu | Gly | Gly | Asp | Arg | Val | Ala | Gln |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Glu | Asp | Gly | Val | Gln | Gln | Leu | Cys | Tyr | Cys | Gln | Val | Leu | Gly | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gln | Ala | Gln | Gly | Gln | Ala | Pro | Ala | Gln | Leu | Pro | Gln | Ala | Ser | Glu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ser | Ala | Gln | Glu | Ala | Arg | Arg | Arg | Arg | Gln | Ala | Asp | Gln | Gly | Glu | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Gln | Ala | Val | Val | Arg | His | Gln | Ala | Lys | Arg | Pro | Pro | Arg | Arg |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

Arg  
145

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 129 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..129  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1504113  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:  
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala  
1                    5                    10                    15  
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa  
                    20                    25                    30  
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp  
                    35                    40                    45  
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln  
                    50                    55                    60  
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly  
65                    70                    75                    80  
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg  
                    85                    90                    95  
Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu  
                    100                    105                    110  
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg  
                    115                    120                    125  
Arg

(2) INFORMATION FOR SEQ ID NO:2647:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 75 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..75  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1504114  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:  
Met Val Ser Glu Ala Ile Ala Ser Leu Lys Glu Arg Thr Gly Ser Ser  
1                    5                    10                    15  
Ser Phe Ala Ile Ala Lys Phe Leu Glu Asp Lys His Lys Asp Lys Leu  
                    20                    25                    30  
Pro Pro Asn Phe Arg Lys Leu Leu Asn Val Gln Leu Lys Lys Leu Val  
                    35                    40                    45  
Ala Gly Gly Lys Leu Thr Lys Val Lys Asn Ser Tyr Lys Leu Ser Ser  
                    50                    55                    60  
Ala Thr Lys Pro Lys Gly Arg Pro Glu Glu Asp  
65                    70                    75

(2) INFORMATION FOR SEQ ID NO:2648:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 257 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1504119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:  
caccctaaag cgagagscgn gggctggtgg ctgctgacca aaacgaatcc ctgcgcgcgcg 60  
cttccccgaaa tcccccaaat ccggagcgcaa tgccgcgcgc cctcccacc ccggcgccac 120  
ncaaaactat cgccgacttc ttccgcgcgc ccgcgaagcg cctgtgcgtg ccccgccgcg 180  
ctccctctcc tccaactcct ctccctcctc gctgtgcgcg gagcagcgcc gtcgcgscga 240  
caccacactg gcgctcg

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

His Pro Lys Ala Arg Xaa Xaa Gly Trp Trp Leu Leu Thr Lys Thr Asn  
1 5 10 15  
Pro Ser Pro Pro Leu Pro Glu Ile Pro Gln Ile Arg Ser Gln Cys Arg  
20 25 30  
Arg Pro Leu Pro Pro Arg Arg His Xaa Lys Leu Ser Pro Thr Ser Ser  
35 40 45  
Arg Ala Pro Pro Ser Ala Cys Ala Cys Pro Gly Arg Leu Pro Leu Leu  
50 55 60  
Gln Leu Leu Ser Leu Leu Ala Val Ala Gly Ala Ala Pro Ser Xaa Arg  
65 70 75 80  
His Gln Pro Gly Ala  
85

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Pro Lys Ser Glu Xaa Xaa Gly Leu Val Ala Ala Asp Gln Asn Glu Ser  
1 5 10 15  
Leu Ala Ala Ala Ser Arg Asn Pro Pro Asn Pro Glu Pro Met Pro Pro  
20 25 30  
Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp Phe Phe Ala  
35 40 45  
Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro Ser Pro Pro  
50 55 60  
Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val Ala Xaa Thr  
65 70 75 80  
Pro Thr Trp Arg Ser  
85

(2) INFORMATION FOR SEQ ID NO:2651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..56  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1504122  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:  
Met Pro Pro Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp  
1                    5                    10                    15  
Phe Phe Ala Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro  
                    20                    25                    30  
Ser Pro Pro Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val  
                    35                    40                    45  
Ala Xaa Thr Pro Thr Trp Arg Ser  
50                    55

(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| acgcgcctcc  | tctgccectc | gctccgcgcg | cgccgcgcgc | gccgcctcaw | gcaccgcgcc | 60  |
| cgcgctgcgc  | tgaggtagac | accaatccgc | cgccatgddg | ssatgacaca | gcccgcgagg | 120 |
| ctggaggaaac | tgagcgggtg | ggccnccgcg | gccaaagtta | cctgttcgct | acggtgttgt | 180 |
| ttaccctagt  | ccagagtggt | tatcttcgtt | cgctctcggt | ttgttggtgc | ccatctgtgt | 240 |
| ttttgattga  | aggtcgctct | gtgtcagttg | ttagtgtgtg | gttcatectc | ggctccagca | 300 |
| gacccatgca  | tcaaccagca | tggactgcgg | atcgatgggt | gctgttaacc | ccgtcagcgt | 360 |
| tattctaagt  | taaatcctaa | ggaaaaaaat | ggtgcttctt | ggtgctgcga | aatggttgtg | 420 |
| ctcatg      |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro His Xaa  
1                    5                    10                    15  
Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Xaa  
                    20                    25                    30  
Xaa Xaa Cys Thr Ala Ala Gly Thr Gly Gly Thr Glu Arg Trp Gly Xaa  
                    35                    40                    45  
Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln  
50                    55                    60  
Ser Val Tyr Leu Arg Ser Ser Arg Val Cys Cys Cys Pro Ser Val Phe  
65                    70                    75  
Leu Ile Glu Gly Arg Ser Val Ser Val Val Ser Ala Val Phe Ile Leu  
                    85                    90                    95  
Gly Ser Ser Arg Pro Met His Gln Pro Ala Trp Thr Ala Asp Arg Trp  
                    100                    105                    110  
Val Leu Leu Pro Pro Ser Ala Leu Phe

115 120  
(2) INFORMATION FOR SEQ ID NO:2654:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..194  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504170  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:  
accacacccca tccaaggccc tcccaaaagtc ccaaaggccg ccgcccgcgc ccagcccccac 60  
atggccgcgc agtccttcct cctcgcgcgc actgccgcgc ccagtccccc gcggtcttgc 120  
ccgctcccta ttctctcgca cgcccttttc actcgggtcca cttcgctgcgc ggcccgtggg 180  
gcgccgcgcg cgcc  
(2) INFORMATION FOR SEQ ID NO:2655:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504171  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:  
Thr His Pro Ile Gln Gly Pro Pro Lys Val Pro Lys Ala Ala Ala Ala Ala  
1 5 10 15  
Arg Gln Pro Thr Met Ala Ala Gln Ser Phe Leu Leu Ala Ala Thr Ala  
20 25 30  
Ala Ala Ser Pro Pro Arg Ser Ser Pro Leu Pro Ile Pro Pro His Ala  
35 40 45  
Leu Ser Thr Arg Ser Thr Ser Ser Pro Ala Arg Gly Ala Pro Pro Pro  
50 55 60  
(2) INFORMATION FOR SEQ ID NO:2656:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..64  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504172  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:  
Pro Thr Pro Ser Lys Ala Leu Pro Lys Ser Gln Arg Pro Pro Pro Pro  
1 5 10 15  
Ala Ser Pro Pro Trp Pro Arg Ser Pro Ser Ser Ser Pro Pro Leu Pro  
20 25 30  
Pro Pro Val Pro Arg Gly Leu Arg Arg Ser Leu Phe Leu Arg Thr Pro  
35 40 45  
Phe Pro Leu Gly Pro Leu Arg Arg Arg Pro Val Gly Arg Arg Arg Arg  
50 55 60

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1504173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Pro | Pro | His | Pro | Arg | Pro | Ser | Gln | Ser | Pro | Lys | Gly | Arg | Arg | Arg | Pro |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Pro | Ala | His | His | Gly | Arg | Ala | Val | Leu | Pro | Pro | Arg | Arg | His | Cys | Arg |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Arg | Gln | Ser | Pro | Ala | Val | Phe | Ala | Ala | Pro | Tyr | Ser | Ser | Ala | Arg | Pro |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Phe | His | Ser | Val | His | Phe | Val | Ala | Gly | Pro | Trp | Gly | Ala | Ala | Ala | Ala |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1504178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| tagcaaaata | tggtttaagt | gatgatacag | tggatttcat | tggacatgca | cttgctcttc | 60  |
| atagagatga | tcgctatctt | gatgaaccgg | cacttgatac | agtgaaaagg | atgaaactat | 120 |
| attcagagtc | tcttgcgcg  | tttcaaggag | gctcgccata | tatctatcca | wtgtatggtc | 180 |
| ygggt      |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1504179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ala | Lys | Tyr | Gly | Leu | Ser | Asp | Asp | Thr | Val | Asp | Phe | Ile | Gly | His | Ala |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Ala | Leu | His | Arg | Asp | Asp | Arg | Tyr | Leu | Asp | Glu | Pro | Ala | Leu | Asp |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Thr | Val | Lys | Arg | Met | Lys | Leu | Tyr | Ser | Glu | Ser | Leu | Ala | Arg | Phe | Gln |  |
|     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |  |
| Gly | Gly | Ser | Pro | Tyr | Ile | Tyr | Pro | Xaa | Tyr | Gly | Xaa | Gly |     |     |     |  |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..509  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:  
caattccaat cccaatccca ccagtggtcca gtgctcgggg aacgacacag ctcctcagca 60  
gagaagccag cagcacaagc ccgatcagca gacagcaggc atggcgctcg cggaggccga 120  
cgacggcgcg gtggtcttcg gcgaggagca ggaggcgctg gtgctcaagt cgtgggccgt 180  
catgaagaag gacgcccaca acctggggcct ccgctctctc ctcaaggctc tcgagatcgc 240  
gccgtcgga gacgatgttc tcgttccctgc gcgactccga cgtgccgctg gagaagaacc 300  
ccaagctcaa gacgcacgcc atgtccgtct tcgtcatgac ctgcgaggcg gcgcgcgast 360  
tccgcaaggc cggaaggtc accgtgagga gaccacgctc aagaggctgg gcgccacgca 420  
cttgaggtag gcgctgcgag atggacactt cgagggtgac ggggttcgcgc tgcttgagac 480  
gatcaaggag gcgctcccg ctgacatgt

(2) INFORMATION FOR SEQ ID NO:2661:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:  
Gln Phe Gln Ser Gln Ser His Gln Cys Pro Val Leu Gly Glu Arg His  
1 5 10 15  
Ser Ser Ser Ala Glu Lys Pro Ala Arg Gln Ala Arg Ser Ala Asp Ser  
20 25 30  
Arg His Gly Ala Arg Gly Gly Arg Arg Arg Gly Gly Leu Arg Arg  
35 40 45  
Gly Ala Gly Gly Ala Gly Ala Gln Val Val Gly Arg His Glu Glu Gly  
50 55 60  
Arg Arg Gln Pro Gly Pro Pro Leu Leu Pro Gln Gly Leu Arg Asp Arg  
65 70 75 80  
Ala Val Gly Ser Arg Cys Ser Arg Ser Cys Ala Thr Pro Thr Cys Arg  
85 90 95  
Trp Arg Arg Thr Pro Ser Ser Arg Arg Thr Pro Cys Pro Ser Ser Ser  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2662:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 169 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..169  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:  
Asn Ser Asn Pro Asn Pro Thr Ser Val Gln Cys Ser Gly Asn Asp Thr  
1 5 10 15  
Ala Pro Gln Gln Arg Ser Gln His Asp Lys Pro Asp Gln Gln Thr Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Gly | Met | Ala | Leu | Ala | Glu | Ala | Asp | 40  | Asp | Gly | Ala | Val | Val | 45  | Phe | Gly | Glu |  |  |
| Glu | Gln | Glu | Ala | Leu | Val | Leu | Lys | 55  | Ser | Trp | Ala | Val | Met | 60  | Lys | Lys | Asp |  |  |
| Ala | Ala | Asn | Leu | Gly | Leu | Arg | Phe | 70  | Phe | Leu | Lys | Val | Phe | 75  | Glu | Ile | Ala |  |  |
| Pro | Ser | Glu | Ala | Asp | Val | Leu | Val | 85  | Pro | Ala | Arg | Leu | Arg | 90  | Arg | Ala | Ala |  |  |
| Gly | Glu | Glu | Pro | Gln | Ala | Gln | Asp | 100 | Ala | Arg | His | Val | Arg | 105 | Leu | Arg | His |  |  |
| Asp | Leu | Arg | Gly | Gly | Gly | Ala | Xaa | 115 | Pro | Gln | Gly | Arg | Glu | 120 | Gly | His | Arg |  |  |
| Glu | Glu | Thr | Thr | Leu | Lys | Arg | Leu | 130 | Gly | Ala | Thr | His | Leu | 135 | Arg | Tyr | Gly |  |  |
| Val | Ala | Asp | Gly | His | Phe | Glu | Val | 145 | Thr | Gly | Phe | Ala | Leu | 150 | Leu | Glu | Thr |  |  |
| Ile | Lys | Glu | Ala | Leu | Pro | Ala | Asp | 165 | Met |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:2663:

### (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..491  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

```
ttagcatgcc tacaattgtt catcgagatc tgaaatctcc aaacttgctg gttgacaata    60
attggaatgt taaggtttgt gactttggac ttctgcggtt gaagcacagt acatttttgt    120
catccaaatc tacagctggw acacctgagt ggatggcacc tgaggttctg cggaatgaac    180
aatcgaatga aaagtgtgat gtttatagct ttggtgtcat cttatgggaa ctggcaacac    240
ttagaatgcc atggagtggg atgaatccaa tgcaagtgtt gggggcagtt ggtttccagg    300
atagacgggt tgatattccc aaggaaagtt atcctctggt cgcaaggata atatttgaat    360
gctggcagaa ggatccaaat ttgcgccgtt catttgaca gttacaagt gccctgaaga    420
ctgttcaaaag actagtgacc cttgtgcacc aggagaacca gagccccatg ttcaacaaga    480
aattcagtg c
```

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1504185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

```
Ser Met Pro Thr Ile Val His Arg Asp Leu Lys Ser Pro Asn Leu Leu
1      5      10      15
Val Asp Asn Asn Trp Asn Val Lys Val Cys Asp Phe Gly Leu Ser Arg
      20      25      30
Leu Lys His Ser Thr Phe Leu Ser Ser Lys Ser Thr Ala Xaa Thr Pro
      35      40      45
Glu Trp Met Ala Pro Glu Val Leu Arg Asn Glu Gln Ser Asn Glu Lys
      50      55      60
Cys Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu
      65      70      75
Arg Met Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val
      85      90      95
Gly Phe Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu
      100      105      110
Val Ala Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg
      115      120      125
Pro Ser Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu
      130      135      140
Val Thr Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys
      145      150      155
Ser Gln Cys      160
```

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1504186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

```
Met Pro Thr Ile Val His Arg Asp Leu Lys Ser Pro Asn Leu Leu Val
1      5      10      15
Asp Asn Asn Trp Asn Val Lys Val Cys Asp Phe Gly Leu Ser Arg Leu
      20      25      30
Lys His Ser Thr Phe Leu Ser Ser Lys Ser Thr Ala Xaa Thr Pro Glu
      35      40      45
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Met | Ala | Pro | Glu | Val | Leu | Arg | Asn | Glu | Gln | Ser | Asn | Glu | Lys | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Val | Tyr | Ser | Phe | Gly | Val | Ile | Leu | Trp | Glu | Leu | Ala | Thr | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Pro | Trp | Ser | Gly | Met | Asn | Pro | Met | Gln | Val | Val | Gly | Ala | Val | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Gln | Asp | Arg | Arg | Leu | Asp | Ile | Pro | Lys | Glu | Val | Asp | Pro | Leu | Val |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Arg | Ile | Ile | Phe | Glu | Cys | Trp | Gln | Lys | Asp | Pro | Asn | Leu | Arg | Pro |
|     |     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Phe | Ala | Gln | Leu | Thr | Ser | Ala | Leu | Lys | Thr | Val | Gln | Arg | Leu | Val |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Thr | Leu | Cys | His | Gln | Glu | Asn | Gln | Ser | Pro | Met | Phe | Asn | Lys | Lys | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1504187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Pro | Glu | Val | Leu | Arg | Asn | Glu | Gln | Ser | Asn | Glu | Lys | Cys | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Tyr | Ser | Phe | Gly | Val | Ile | Leu | Trp | Glu | Leu | Ala | Thr | Leu | Arg | Met |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Trp | Ser | Gly | Met | Asn | Pro | Met | Gln | Val | Val | Gly | Ala | Val | Gly | Phe |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Asp | Arg | Arg | Leu | Asp | Ile | Pro | Lys | Glu | Val | Asp | Pro | Leu | Val | Ala |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Ile | Phe | Glu | Cys | Trp | Gln | Lys | Asp | Pro | Asn | Leu | Arg | Pro | Ser |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Phe | Ala | Gln | Leu | Thr | Ser | Ala | Leu | Lys | Thr | Val | Gln | Arg | Leu | Val | Thr |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Cys | His | Gln | Glu | Asn | Gln | Ser | Pro | Met | Phe | Asn | Lys | Lys | Ser | Gln |
|     |     |     |     | 100 |     |     | 105 |     |     |     |     |     | 110 |     |     |

Cys

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1504192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| aaagctggag | tgaatccagg  | aggctgcttc | tgaaaaaaaaa | agtagcagat | gcaacgagtg | 60  |
| cactccaagt | ctgcagttac  | aatgcaatga | ccgggtttgt  | tagtgagcta | gcacgcgtcg | 120 |
| sggctcctcg | agggaacaata | atcatcgtga | catgggtgcc  | taggaacctg | gatccatccg | 180 |
| aaacctcgct | aaagcccgat  | gaactgagcc | tcctgaggag  | gatatgcgac | gcgtactacc | 240 |
| tcccggactg | gtgctcacct  | tcagactatg | tgaacattgc  | caagtcactg | tctctcgagg | 300 |

atatcaagac agctgactgg tcggagaacg tggccccggt ttggccccgc gtgataaaat 360  
cagcgctaac atggaaggcg ttacactctc tgctgacgac cggatggaag acgatcagag 420  
gcgcgatggt gatgccgcta atgatccagg gctacaagaa ggggctcatc aaattcacca 480  
tc

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1504193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Trp | Ser | Glu | Ser | Ser | Arg | Leu | Leu | Leu | Lys | Lys | Lys | Val | Ala | Asp |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Thr | Ser | Ala | Leu | Gln | Cys | Cys | Ser | Tyr | Asn | Ala | Met | Thr | Gly | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Ser | Glu | Leu | Ala | Arg | Val | Xaa | Ala | Pro | Gly | Gly | Thr | Ile | Ile | Ile |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Thr | Trp | Cys | His | Arg | Asn | Leu | Asp | Pro | Ser | Glu | Thr | Ser | Leu | Lys |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Pro | Asp | Glu | Leu | Ser | Leu | Arg | Arg | Ile | Cys | Asp | Ala | Tyr | Tyr | Leu |     |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Pro | Asp | Trp | Cys | Ser | Pro | Ser | Asp | Tyr | Val | Asn | Ile | Ala | Lys | Ser | Leu |  |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser | Leu | Glu | Asp | Ile | Lys | Thr | Ala | Asp | Trp | Ser | Glu | Asn | Val | Ala | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Trp | Pro | Ala | Val | Ile | Lys | Ser | Ala | Leu | Thr | Trp | Lys | Gly | Phe | Thr |  |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |  |
| Ser | Leu | Leu | Thr | Thr | Gly | Trp | Lys | Thr | Ile | Arg | Gly | Ala | Met | Val | Met |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Pro | Leu | Met | Ile | Gln | Gly | Tyr | Lys | Lys | Gly | Leu | Ile | Lys | Phe | Thr | Ile |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1504194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Gly | Phe | Val | Ser | Glu | Leu | Ala | Arg | Val | Xaa | Ala | Pro | Gly | Gly |  |
| 1   |     |     |     |     |     |     |     |     |     |     | 10  |     |     | 15  |     |  |
| Thr | Ile | Ile | Ile | Val | Thr | Trp | Cys | His | Arg | Asn | Leu | Asp | Pro | Ser | Glu |  |
|     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Ser | Leu | Lys | Pro | Asp | Glu | Leu | Ser | Leu | Leu | Arg | Arg | Ile | Cys | Asp |  |
|     |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala | Tyr | Tyr | Leu | Pro | Asp | Trp | Cys | Ser | Pro | Ser | Asp | Tyr | Val | Asn | Ile |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Ala | Lys | Ser | Leu | Ser | Leu | Glu | Asp | Ile | Lys | Thr | Ala | Asp | Trp | Ser | Glu |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Asn | Val | Ala | Pro | Phe | Trp | Pro | Ala | Val | Ile | Lys | Ser | Ala | Leu | Thr | Trp |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 85  |     |     |     |     |     |     | 90  |     |     |     |     |     |     | 95  |
| Lys | Gly | Phe | Thr | Ser | Leu | Leu | Thr | Thr | Gly | Trp | Lys | Thr | Ile | Arg | Gly |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |
| Ala | Met | Val | Met | Pro | Leu | Met | Ile | Gln | Gly | Tyr | Lys | Lys | Gly | Leu | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Lys | Phe | Thr | Ile |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1504201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

|            |            |             |             |             |             |     |
|------------|------------|-------------|-------------|-------------|-------------|-----|
| agcggttaga | gagagagaag | acagggagaa  | ggaggaagag  | ccgccgcgnt  | ggaccggggtg | 60  |
| atttgtcagg | gttgtcaggg | gagtcgtcag  | ggacacggcca | agctttgtac  | ggaccacaatt | 120 |
| cagcgaataa | ccgacggggg | tgcggtggaat | tgctcaccgg  | agcaaacctt  | ccgccgcccca | 180 |
| accaccatcc | ttctgagcag | cgacacgtag  | cgctccggttc | ctggacgcac  | gccgtgaact  | 240 |
| cgaagtccac | cgctctgtga | gcacaaagcg  | ccggcatcgc  | taggggtttca | cgcccccatc  | 300 |
| ccccacgggc | gccgtcgatc | ccggtcggcc  | atctcccggt  | gcctggtaac  | tgatcgttaa  | 360 |
| tttcatcgat | gggtgccgat | gaggaccgca  | gctccaagca  | ggcaggcgcg  | ggcttgggtg  | 420 |
| cccactccca | cgacgacctc | cttgtggaga  | tcctctcccg  | cgctcccgcc  | aagtcctgtc  | 480 |
| gcgggttcaa | gtgcgtgtcc | aaggcctggc  | t           |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Glu | Arg | Glu | Lys | Thr | Gly | Arg | Arg | Arg | Lys | Ser | Arg | Arg | Xaa |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Pro | Gly | Asp | Leu | Ser | Gly | Leu | Ser | Gly | Glu | Ser | Ser | Gly | His | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ala | Leu | Tyr | Ala | Thr | Asn | Ser | Ala | Asn | Asn | Arg | Arg | Gly | Cys | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Glu | Leu | Leu | Thr | Gly | Ala | Asn | Pro | Pro | Pro | Pro | Asn | His | His | Pro | Ser |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Glu | Gln | Arg | Thr | Leu | Ala | Ser | Gly | Ser | Trp | Thr | His | Ala | Val | Asn | Ser |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     | 80  |
| Lys | Ser | Thr | Ala | Leu |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1504203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

|                                                                 |       |
|-----------------------------------------------------------------|-------|
| Met Gly Ala Met Glu Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu |       |
| 1                                                               | 5 10  |
| Val Ala His Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val |       |
| 20                                                              | 25 30 |
| Pro Ala Lys Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp     |       |
| 35                                                              | 40 45 |

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1504204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

|                                                                 |         |
|-----------------------------------------------------------------|---------|
| Met Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu Val Ala His     |         |
| 1                                                               | 5 10 15 |
| Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val Pro Ala Lys |         |
| 20                                                              | 25 30   |
| Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp                 |         |
| 35                                                              | 40      |

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1504231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| cattgtcaat ttctccagg ataaatcatg gcgtgttcgt tatatggctg ccaatcagtt   | 60  |
| atatgagctc tgtgagctg ttggccctga gccacaaga gctgatttg tgccctgata     | 120 |
| tgttcgtctc ctctcgcata atgaggctga agtcggaata gcggctgctg gaaaagtaac  | 180 |
| taagtctctc cgcataattaa atccacagct ttcaatccaa catattcttc cgtgcgttaa | 240 |
| ggaattgtca tcatattcat cccagcatgt tcgttcagct tttagctcag tcattatggg  | 300 |
| aatggctctc gtactgggaa aggatgctac catggaacag cttcttccaa tttttctctc  | 360 |
| tttctgtaag gatgaatttc cagatgttcg gcttaacata atcagcaagc ttgatcaggt  | 420 |
| taatcaggtt attggc                                                  |     |

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1504232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

|                                                                 |         |
|-----------------------------------------------------------------|---------|
| Ile Val Asn Phe Ser Gln Asp Lys Ser Trp Arg Val Arg Tyr Met Val |         |
| 1                                                               | 5 10 15 |

Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu Pro Thr  
20 25 30  
Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp Asn Glu  
35 40 45  
Ala Glu Val Arg Ile Ala Ala Gly Lys Val Thr Lys Phe Cys Arg  
50 55 60  
Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys Val Lys  
65 70 75 80  
Glu Leu Ser Ser Tyr Ser Ser Gln His, Val Arg Ser Ala Leu Ala Ser  
85 90 95  
Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Met Glu  
100 105 110  
Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp  
115 120 125  
Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile  
130 135 140

Gly  
145

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1504233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Val Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu  
1 5 10 15  
Pro Thr Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp  
20 25 30  
Asn Glu Ala Glu Val Arg Ile Ala Ala Gly Lys Val Thr Lys Phe  
35 40 45  
Cys Arg Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys  
50 55 60  
Val Lys Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu  
65 70 75 80  
Ala Ser Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr  
85 90 95  
Met Glu Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe  
100 105 110  
Pro Asp Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln  
115 120 125  
Val Ile Gly  
130

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..446

(D) OTHER INFORMATION: / Ceres Seq. ID 1504239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

cgatcctttt atccgtaact atattgagga cttattgaag aacatcagaa cccaagtgc.

gctcaagctt attaaaccat atactcgaat caggataacca ttcatttcac aggaaactcaa 120  
ttttccagaa aaggatgtcg agcagctgtt ggtgtcactc attctggaca accgtatcca 180  
aggccacata gatcaggtta acaagctgct agaactgtga gaaagggtcca aggggatgag 240  
gaagtacaat gctatcgaca agtgggaatac tcagctgaag tccatttacc aaacattgtc 300  
caacagagtt tgatgaggag gatcgctgct gctgctgctg ccatgtgcaca cctagaattg 360  
ttgatagcct gttttgtgga ttgaggggca actgcaaaaga actgtctggt gacgcttgcg 420  
atagaatcct ggatctgggt aaagtt

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1504240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Asp Pro Phe Ile Arg Asn Tyr Ile Glu Asp Leu Leu Lys Asn Ile Arg  
1 5 10 15  
Thr Gln Val Leu Leu Lys Leu Ile Lys Pro Tyr Thr Arg Ile Arg Ile  
20 25 30  
Pro Phe Ile Ser Gln Glu Leu Asn Phe Pro Glu Lys Asp Val Glu Gln  
35 40 45  
Leu Leu Val Ser Leu Ile Leu Asp Asn Arg Ile Gln Gly His Ile Asp  
50 55 60  
Gln Val Asn Lys Leu Leu Glu Arg Gly Glu Arg Ser Lys Gly Met Arg  
65 70 75 80  
Lys Tyr Asn Ala Ile Asp Lys Trp Asn Thr Gln Leu Lys Ser Ile Tyr  
85 90 95  
Gln Thr Leu Ser Asn Arg Val  
100

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

gttttctctt gatcgctttg tcacttgaat ccgtgcctgc tctaacagag agcggagacg 60  
accacgacga cggcgaggcc aggcctctgc atggagcagg agccgcaccg gcccatggag 120  
ctgcccccg gcttcgcgct ccaccgcgac gacgaggagn tcatcacgca ctacctggcc 180  
cgcaaggcgc cgagccccgc ttgcgcgcgc ttgcgcgcgc cgaggccgac ctcaacaagt 240  
gcgagccctg ggacctgccg tcgctggcga ggatggggga gaaggagtgg tacttctctt 300  
gcctcaagga ccgcaagtac ccgacg

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1504255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Phe Leu Leu Ile Ala Leu Ser Leu Glu Ser Val Pro Ala Leu Thr Glu  
1 5 10 15  
Ser Gly Asp Asp His Asp Asp Gly Glu Ala Arg Leu Cys Asp Gly Ala  
20 25 30  
Gly Ala Ala Pro Ala His Gly Ala Ala Pro Gly Leu Pro Leu Pro Pro  
35 40 45  
Asp Arg Arg Gly Xaa His His Ala Leu Pro Gly Pro Gln Gly Ala Asp  
50 55 60  
Ala Arg Phe Ala Ala Leu Ala Val Ala Glu Ala Asp Leu Asn Lys Cys  
65 70 75 80  
Glu Pro Trp Asp Leu Pro Ser Leu Ala Arg Met Gly Glu Lys Glu Trp  
85 90 95  
Tyr Phe Phe Cys Leu Lys Asp Arg Lys Tyr Pro Thr  
100 105

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1504256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

Met Glu Gln Glu Pro His Arg Pro Met Glu Leu Pro Pro Gly Phe Arg  
1 5 10 15  
Phe His Pro Thr Asp Glu Glu Xaa Ile Thr His Tyr Leu Ala Arg Lys  
20 25 30  
Ala Pro Thr Pro Ala Ser Pro Arg Leu Pro Ser Pro Arg Pro Thr Ser  
35 40 45  
Thr Ser Ala Ser Pro Gly Thr Cys His Arg Trp Arg Gly Trp Gly Arg  
50 55 60  
Arg Ser Gly Thr Ser Ser Ala Ser Arg Thr Ala Ser Thr Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1504257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Met Glu Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Xaa  
1 5 10 15  
Ile Thr His Tyr Leu Ala Arg Lys Ala Pro Thr Pro Ala Ser Pro Arg  
20 25 30  
Leu Pro Ser Pro Arg Pro Thr Ser Thr Ser Ala Ser Pro Gly Thr Cys  
35 40 45  
His Arg Trp Arg Gly Trp Gly Arg Arg Ser Gly Thr Ser Ser Ala Ser  
50 55 60  
Arg Thr Ala Ser Thr Arg  
65 70

(2) INFORMATION FOR SEQ ID NO:2684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:

```
aattccctc cctgtctgc gtctccctc accgaagcc cgdttcgaa accggcgccg      60
ttcgatttgg ggatttcggc gtctcgtccc ccggaatttc ttggtatcga gtctgtccgc      120
cgtcttcgat ttgcggctgc agtgagcctg cgagttttcc ggtctgtatt tggwcggggh      180
cttcgatatt ggggatggcg tcgtctcccg tgcctactgt gtgtacagc tgcagccgct      240
tcgtgagggt atctccgtcc accgtgtctc gcccggagtg cgatggcggc ttctgggagc      300
agtttac
```

(2) INFORMATION FOR SEQ ID NO:2685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..55
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:

```
Asn Ser Pro Pro Leu Ser Ser Ser Pro Leu Thr Arg Ser Pro Xaa Ser
1          5          10          15
Lys Pro Ala Ala Phe Asp Leu Gly Ile Ser Ala Ser Arg Ser Pro Glu
20          25          30
Phe Leu Gly Ser Glu Ser Val Arg Arg Leu Arg Phe Ala Ala Val
35          40          45
Ser Leu Arg Val Phe Arg Leu
50          55
```

(2) INFORMATION FOR SEQ ID NO:2686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:

```
Ile Pro Leu Pro Cys Arg Arg Leu Pro Ser Pro Glu Ala Pro Xaa Arg
1          5          10          15
Asn Arg Arg Arg Ser Ile Trp Gly Phe Arg Arg Leu Ala Pro Arg Asn
20          25          30
Phe Leu Asp Leu Ser Leu Ser Ala Val Phe Asp Leu Arg Leu Gln
35          40          45
```

(2) INFORMATION FOR SEQ ID NO:2687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1504261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Ser | Ser | Pro | Val | Ser | Tyr | Trp | Cys | Tyr | Ser | Cys | Ser | Arg | Phe |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |  |
| Val | Arg | Val | Ser | Pro | Ser | Thr | Xaa | Val | Cys | Pro | Glu | Cys | Asp | Gly | Gly |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Phe | Leu | Glu | Gln | Phe |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1504270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

|             |             |             |            |            |            |     |
|-------------|-------------|-------------|------------|------------|------------|-----|
| actcgcgtcg  | ssccccctcca | ctgcaccacgc | gtcatggcgg | tggcctcgac | ctcgccgctg | 60  |
| tccgccaaagc | ccgccacggc  | ccctcgcgcg  | cccgctccc  | gacccgggct | cctcgctctc | 120 |
| ggcgttcgcs  | cgccccccgc  | cactgccgcg  | tggaggaggc | tccgcgtgga | ggcgatcagg | 180 |
| acgcacgcggg | agaagcagcg  | ggcggagggtg | cccgtcgagg | agtcgcggcc | cgcc       |     |

(2) INFORMATION FOR SEQ ID NO:2689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1504271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Arg | Val | Xaa | Pro | Leu | His | Cys | Thr | Ser | Val | Met | Ala | Val | Ala | Ser |  |
| 1   |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |  |
| Thr | Ser | Pro | Leu | Ser | Ala | Lys | Pro | Ala | Thr | Ala | Pro | Ser | Pro | Pro | Ala |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     | 30  |     |     |     |     |  |
| Pro | Gly | Ser | Gly | Leu | Leu | Ala | Leu | Gly | Val | Arg | Xaa | Ala | Pro | Ala | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |  |
| Ala | Ala | Trp | Arg | Arg | Leu | Arg | Val | Glu | Ala | Ile | Arg | Thr | Gln | Arg | Glu |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |  |
| Lys | Gln | Arg | Ala | Glu | Val | Pro | Val | Glu | Glu | Ser | Ala | Pro | Ala |     |     |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

Leu Ala Ser Xaa Pro Ser Thr Ala Pro Ala Ser Trp Arg Trp Pro Arg  
1 5 10 15  
Pro Arg Arg Cys Pro Pro Ser Pro Pro Arg Pro Pro Arg Arg Pro Leu  
20 25 30  
Pro Asp Pro Gly Ser Ser Leu Ser Ala Phe Xaa Arg Pro Pro Pro Leu  
35 40 45  
Pro Arg Gly Gly Gly Ser Ala Trp Arg Arg Ser Gly Arg Ser Gly Arg  
50 55 60  
Ser Ser Gly Arg Arg Cys Pro Ser Arg Ser Pro Pro Pro  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

Ser Arg Xaa Xaa Pro Pro Leu His Gln Arg His Gly Gly Gly Leu Asp  
1 5 10 15  
Leu Ala Ala Val Arg Gln Ala Arg His Gly Pro Leu Ala Ala Arg Ser  
20 25 30  
Arg Ile Arg Ala Pro Arg Ser Arg Arg Ser Xaa Gly Pro Arg His Cys  
35 40 45  
Arg Val Glu Glu Ala Pro Arg Gly Gly Asp Gln Asp Ala Ala Gly Glu  
50 55 60  
Ala Ala Gly Gly Gly Ala Arg Arg Gly Val Arg Pro Arg  
65 70 75

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1504274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| agtcggagca | gggcaggggg  | tgctgtctcag | ttcctgtgtg  | tggtgtgtga  | agctcacagg  | 60  |
| ttctctctct | tcgcgtgass  | tagctagagt  | gggatcgcca  | ggaagaagga  | tgctcgtgctg | 120 |
| cggaggcaac | tcgcgggtgcg | gcasggantg  | caagtgcggc  | assggctgcg  | gagggtgcaa  | 180 |
| gatgtaccgc | gacatggttg  | agcaggtgac  | caccaccacc  | accaccacaga | ctctcatcat  | 240 |
| gggtgtgtcg | ccatccacgg  | gccaccgcgt  | tgctccccctc | ggcagccagg  | atgacagaag  | 300 |
| taccatttct | gccgcgtgag  | aggctcttca  | agcagcaaca  | ttacttcag   | aacttgacca  | 360 |
| agcacacctc | cctgaaagcg  | gctacgagct  | gateacctcc  | gtcgccatcc  | cccttgcact  | 420 |
| cgctgcctc  |             |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..105  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504275  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:  
Val Gly Ala Gly Gln Gly Leu Arg Leu Ser Trp Leu Cys Cys Cys  
1 5 10 15  
Lys Leu Thr Gly Phe Phe Ser Ser Arg Xaa Xaa Ala Arg Val Gly Ser  
20 25 30  
Arg Gly Arg Arg Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Xaa  
35 40 45  
Xaa Cys Lys Cys Gly Xaa Gly Cys Gly Cys Lys Met Tyr Pro Asp  
50 55 60  
Met Val Glu Gln Val Thr Thr Thr Thr Thr Gln Thr Leu Ile Met  
65 70 75 80  
Gly Val Ala Pro Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln  
85 90 95  
Asp Asp Arg Ser Thr Ile Ser Ala Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:2694:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..69  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa Xaa Cys Lys Cys  
1 5 10 15  
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Val Glu Gln  
20 25 30  
Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro  
35 40 45  
Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln Asp Asp Arg Ser  
50 55 60  
Thr Ile Ser Ala Ala  
65

(2) INFORMATION FOR SEQ ID NO:2695:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..244  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

agttgatccc atcggtctcc ccttctcttt ccccgatccc ctctctcccc cgatcccatc 60  
caattccact tccacacccc gggcctcgcc gccgacgccc acgccgacgc cgccggccat 120  
gtcccaagtac ggcacatttc ccacctcttc ctcgcggggc ggaggggccc tgccccctcg 180  
cggcgcctcc cgtcgattt catctccgc gccaaaggctc gggggcgctc ggcstggggc 240  
acgc

(2) INFORMATION FOR SEQ ID NO:2696:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 amino acids  
(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..81  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504278  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:  
Val Asp Pro Ile Gly Phe Pro Phe Leu Phe Pro Asp Pro Leu Pro Pro  
1 5 10 15  
Pro Ile Pro Ser Asn Ser Thr Ser Thr Pro Arg Ala Ser Pro Pro Thr  
20 25 30  
Pro Thr Pro Thr Pro Pro Ala Met Ser Lys Tyr Gly Thr Ile Pro Thr  
35 40 45  
Ser Ser Ser Ala Gly Gly Gly Pro Val Pro Leu Gly Gly Ala Pro Arg  
50 55 60  
Ser Ile Ser Ser Pro Ala Pro Arg Leu Gly Ala Pro Arg Xaa Gly Arg  
65 70 75 80  
Arg

(2) INFORMATION FOR SEQ ID NO:2697:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..80  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504279  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:  
Leu Ile Pro Ser Ala Ser Pro Ser Ser Ser Pro Ile Pro Phe Leu Pro  
1 5 10 15  
Arg Ser His Pro Ile Pro Leu Pro His Pro Gly Pro Arg Arg Arg Arg  
20 25 30  
Arg Arg Arg Arg Arg Arg Pro Cys Pro Ser Thr Ala Pro Phe Pro Pro  
35 40 45  
Pro Pro Pro Arg Ala Glu Gly Gly Pro Cys Pro Ser Ala Ala Leu Pro Ala  
50 55 60  
Arg Phe His Leu Pro Arg Gln Gly Ser Gly Arg Leu Gly Xaa Gly Asp  
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2698:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..42  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504280  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:  
Met Ser Lys Tyr Gly Thr Ile Pro Thr Ser Ser Ser Ala Gly Gly Gly  
1 5 10 15  
Pro Val Pro Leu Gly Gly Ala Pro Arg Ser Ile Ser Ser Pro Ala Pro  
20 25 30  
Arg Leu Gly Ala Pro Arg Xaa Gly Arg Arg

35 40  
(2) INFORMATION FOR SEQ ID NO:2699:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 231 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..231  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1504299  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:  
    cctgatttcc tgaaacacag atcatcatca ttcatgggtca tggctatggc aaactcggga 60  
    acgatcctga cegtcgttct ggctctcggg ctacgcttcc tccgcgcgcg agctccggcc 120  
    tccgcgcaga actgcggctg cccgccaggc tactgctgca gcaagttcgg ttactcggcg 180  
    accagcttcg actactgcaa tgccaacacg tgccagtcgg gcccgtcgac g  
(2) INFORMATION FOR SEQ ID NO:2700:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 77 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..77  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1504300  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:  
    Pro Asp Phe Leu Lys His Arg Ser Ser Ser Phe Met Val Met Ala Met  
    1 5 10 15  
    Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu Ala Leu Gly Leu Ala  
    20 25 30  
    Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln Asn Cys Gly Cys Pro  
    35 40 45  
    Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys Gly Thr Ser Phe Asp  
    50 55 60  
    Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro Cys Thr  
    65 70 75  
(2) INFORMATION FOR SEQ ID NO:2701:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 66 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..66  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1504301  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:  
    Met Val Met Ala Met Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu  
    1 5 10 15  
    Ala Leu Gly Leu Ala Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln  
    20 25 30  
    Asn Cys Gly Cys Pro Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys  
    35 40 45  
    Gly Thr Ser Phe Asp Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro  
    50 55 60  
    Cys Thr  
    65

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Met | Ala | Asn | Ser | Ala | Thr | Ile | Leu | Thr | Val | Val | Leu | Ala | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Leu | Ala | Phe | Leu | Arg | Ala | Ala | Ala | Pro | Ala | Ser | Ala | Gln | Asn | Cys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gly | Cys | Pro | Pro | Gly | Tyr | Cys | Cys | Ser | Lys | Phe | Gly | Tyr | Cys | Gly | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Asp | Tyr | Cys | Asn | Ala | Asn | Thr | Cys | Gln | Ser | Gly | Pro | Cys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

|            |             |             |             |             |             |     |
|------------|-------------|-------------|-------------|-------------|-------------|-----|
| tacaaggcta | tttatgatat  | tccagcaata  | aaagaggatc  | caacaaagtg  | gataccgatt  | 60  |
| cttaggaaga | tctgttggtta | cttggtgcta  | gcacctcatg  | atcctatgca  | atcaagcctt  | 120 |
| ctcaatgcta | cactagagga  | taaaaacctt  | tcagaaatcc  | caaatttcag  | gtttattactg | 180 |
| aagcagctgg | tcaccatgga  | ggtgatacac  | tggaacaagtc | tgtgggaatt  | cttcaaggag  | 240 |
| gaatatgaga | aggagaagga  | tcttcttggg  | ggagctttgg  | gtgccaaagc  | ttcagaagat  | 300 |
| ttgaggctga | ggattatcga  | acataatatc  | ttggttgtat  | ccaagtacta  | tgcaagggtt  | 360 |
| accctcaaga | ggcttgccga  | tcttcttttc  | ctgactttgc  | aggaggcgaga | gaagcatctc  | 420 |
| tcagacatgg | ttaactcgaa  | atctctagtgc | gc          |             |             |     |

(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Lys | Ala | Ile | Tyr | Asp | Ile | Pro | Ala | Ile | Lys | Glu | Asp | Pro | Thr | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Trp | Ile | Pro | Ile | Leu | Arg | Lys | Ile | Cys | Trp | Tyr | Leu | Val | Leu | Ala | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| His | Asp | Pro | Met | Gln | Ser | Ser | Leu | Leu | Asn | Ala | Thr | Leu | Glu | Asp | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Asn | Leu | Ser | Glu | Ile | Pro | Asn | Phe | Arg | Leu | Leu | Leu | Lys | Gln | Leu | Val |

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 50                                                              | 55  | 60  |
| Thr Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu |     |     |
| 65                                                              | 70  | 75  |
| Glu Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys |     | 80  |
|                                                                 | 85  | 90  |
| Ala Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val |     | 95  |
|                                                                 | 100 | 105 |
| Val Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu |     | 110 |
|                                                                 | 115 | 120 |
| Leu Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val |     | 125 |
|                                                                 | 130 | 135 |
| Asn Ser Lys Ser Leu Val                                         |     | 140 |
| 145                                                             | 150 |     |

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1504305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| Met Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser |     |     |
| 1                                                               | 5   | 10  |
| Glu Ile Pro Asn Phe Arg Leu Leu Leu Lys Gln Leu Val Thr Met Glu |     | 15  |
|                                                                 | 20  | 25  |
| Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu Tyr Glu |     | 30  |
|                                                                 | 35  | 40  |
| Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala Ser Glu |     | 45  |
|                                                                 | 50  | 55  |
| Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys |     | 60  |
|                                                                 | 65  | 70  |
| Thr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu Cys Leu |     | 75  |
|                                                                 | 85  | 90  |
| Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn Ser Lys |     | 95  |
|                                                                 | 100 | 105 |
| Ser Leu Val                                                     |     | 110 |
|                                                                 | 115 |     |

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

|                                                                 |    |    |
|-----------------------------------------------------------------|----|----|
| Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu |    |    |
| 1                                                               | 5  | 10 |
| Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala |    | 15 |
|                                                                 | 20 | 25 |
| Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val |    | 30 |
|                                                                 | 35 | 40 |
| Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu |    | 45 |
|                                                                 | 50 | 55 |
|                                                                 |    | 60 |

Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn  
65 70 75 80  
Ser Lys Ser Leu Val  
85

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ctcccggtct | agacttctgc | tgcagcgcct | ccgycgcgcg | cgccgcctct | aacgcaktcc | 60  |
| ctccgcgcga | gcccgaggca | agatggttct | ccagaacgac | attgatctgc | kcaaccgcgc | 120 |
| ggcagaactc | gagaagctca | agcacaagaa | aaagagactc | gtccagctgc | ccaactcctt | 180 |
| cttcattgat | gttaagtgc  | aggggtgctt | cagcataacc | actgktktca | gccactccca | 240 |
| gactgctgnt | gkgtnvgcta | gaagctatgc | agcggatacg | ggtacattta | tcgacagtkt | 300 |
| tc         |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Pro Gly Ser Asp Phe Cys Cys Ser Ala Ser Xaa Ala Ala Ala Ala Ser |  |
| 1 5 10 15                                                       |  |
| Asn Ala Xaa Pro Pro Pro Gln Pro Glu Ala Arg Trp Phe Ser Arg Thr |  |
| 20 25 30                                                        |  |
| Thr Leu Ile Cys Xaa Thr Arg Arg Gln Asn Ser Arg Ser Ser Thr     |  |
| 35 40 45                                                        |  |
| Arg Lys Arg Asp Ser Ser Ser Arg Pro Thr Pro Ser Ser Trp Met Leu |  |
| 50 55 60                                                        |  |
| Ser Ala Arg Gly Ala Ser Ala                                     |  |
| 65 70                                                           |  |

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Val Leu Gln Asn Asp Ile Asp Leu Xaa Asn Pro Pro Ala Glu Leu |  |
| 1 5 10 15                                                       |  |
| Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser |  |
| 20 25 30                                                        |  |
| Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Xaa     |  |

35 40 45  
Phe Ser His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala  
50 55 60  
Asp Thr Gly Thr Phe Ile Asp Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Xaa Phe Ser  
1 5 10 15  
His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala Asp Thr  
20 25 30  
Gly Thr Phe Ile Asp Ser  
35

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

accacaggaaa ttcacaaaga gatactagtc cctaccacaaag catacttcct gaaacactct 60  
tgcaatccac tgagtcctgt ttgttgagac ttgagacgca tagagctagc gtcgacaagt 120  
tcgctcgtga ggcgcmssaa cgtgttcgac cccttctcga tggacctctg ggacccttc 180  
gacaccatgt tccgctccat cgtcccgctg gcggcctcca ccaactccga gaccgccgtc 240  
ttcgccagc

(2) INFORMATION FOR SEQ ID NO:2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro  
1 5 10 15  
Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr  
20 25 30  
His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Xaa Arg Val  
35 40 45  
Arg Pro Leu Leu Asp Gly Pro Leu Gly Pro Leu Arg His His Val Pro  
50 55 60  
Leu His Arg Pro Val Gly Gly Leu His Gln Leu Arg Asp Arg Arg Leu

65

70

75

80

Arg Gln

(2) INFORMATION FOR SEQ ID NO:2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Leu | Val | Arg | Arg | Xaa | Asn | Val | Phe | Asp | Pro | Phe | Ser | Met | Asp |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Trp | Asp | Pro | Phe | Asp | Thr | Met | Phe | Arg | Ser | Ile | Val | Pro | Ser | Ala |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Ala | Ser | Thr | Asn | Ser | Glu | Thr | Ala | Val | Phe | Ala | Ser |     |     |     |     |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

|             |            |            |             |            |            |     |
|-------------|------------|------------|-------------|------------|------------|-----|
| cagaataaag  | ataaaaaata | tggaactgga | aattaggcgt  | agggaatcaa | caggatcagg | 60  |
| ctctaacaca  | tatgttgaaa | ctgagactct | tgcaaagttt  | gagttgatgg | atggctgctc | 120 |
| tgtgagaggt  | gaatctattc | cagtgaggct | gttcttgaca  | ccctatgagt | tgaaccgcac | 180 |
| ttaccgcgaac | ataaacaaca | aattcagcgt | caagtatatac | ctgaactcgg | tccttgtgga | 240 |
| cgaggaagat  | cggaggtact | tcaagcagca | agagatcaca  | atgtaccgtc | tccaagaatc | 300 |
| tcacctgcgc  | tcctagatcc | caacctgttg | catcatgttc  | actctccagg | ttttgtacaa | 360 |
| gtggacgctg  | aggttagagc | aatgtcctgt | atataaacta  | aaatccagaa | gagcgccaca | 420 |
| gctggttact  | gcatggcca  | tgcacgtgc  | actgtcgtgt  | tcatt      |            |     |

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ile | Lys | Ile | Lys | Asn | Met | Glu | Leu | Glu | Ile | Arg | Arg | Arg | Glu | Ser |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Thr | Gly | Ser | Gly | Ser | Asn | Thr | Tyr | Val | Glu | Thr | Glu | Thr | Leu | Ala | Lys |  |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Glu | Leu | Met | Asp | Gly | Ala | Pro | Val | Arg | Gly | Glu | Ser | Ile | Pro | Val |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Arg | Leu | Phe | Leu | Thr | Pro | Tyr | Glu | Leu | Thr | Pro | Thr | Tyr | Arg | Asn | Ile |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |

Asn Asn Lys Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp  
65 70 75 80  
Glu Glu Asp Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg  
85 90 95  
Leu Gln Glu Ser Pro Pro Ala Ser  
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1504335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Glu Leu Glu Ile Arg Arg Arg Glu Ser Thr Gly Ser Gly Ser Asn  
1 5 10 15  
Thr Tyr Val Glu Thr Glu Thr Leu Ala Lys Phe Glu Leu Met Asp Gly  
20 25 30  
Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe Leu Thr Pro  
35 40 45  
Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys Phe Ser Val  
50 55 60  
Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp Arg Arg Tyr  
65 70 75 80  
Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu Ser Pro Pro  
85 90 95  
Ala Ser

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1504336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met Asp Gly Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe  
1 5 10 15  
Leu Thr Pro Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys  
20 25 30  
Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp  
35 40 45  
Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu  
50 55 60  
Ser Pro Pro Ala Ser  
65

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..466

(D) OTHER INFORMATION: / Ceres Seq. ID 1504370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2718:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| ctactacgcc  | tgccctctcca | tcattgtcgt  | ggatgatcctc | ctgccccttcg | ccatcgcccat | 60  |
| ggagggggccc | aaggtgtggg  | cggcggggctg | gcagacagca  | gtcgcccgaga | tccgttcccaa | 120 |
| ctctgtctgg  | tggtgtggcgg | cgcagagcgt  | gttctaccac  | ctgtacaacc  | aggtgtccca  | 180 |
| catgtccctg  | gacgagatct  | cgcgcgtcac  | cttctccatc  | ggcaacacca  | tgaagcgcgt  | 240 |
| ctcgcctcatc | gtcgcgtcca  | tcattcatctt | ccagacgccc  | gtccagccca  | tcaacgcgct  | 300 |
| cggggccgccc | atcgccatcc  | tcggaacctt  | catctactcc  | caggccaagc  | agtagccgccc | 360 |
| cttggsccg   | cgtctggctc  | tcaggcctca  | gttcagttca  | ccgcggaatc  | agctcggcgc  | 420 |
| tcgaagatat  | aacagattat  | ataacttttt  | gaggatatct  | acctag      |             |     |

(2) INFORMATION FOR SEQ ID NO:2719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1504371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2719:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Arg | Leu | Pro | Leu | His | His | Val | Ala | Gly | Asp | Pro | Pro | Ala | Leu |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Arg | His | Arg | His | Gly | Gly | Ala | Gln | Gly | Val | Gly | Gly | Gly | Leu | Ala | Asp |
|     |     |     |     | 20  |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ser | Ser | Arg | Arg | Asp | Arg | Ser | Gln | Leu | Arg | Leu | Val | Gly | Gly | Gly | Ala |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Glu | Arg | Val | Leu | Pro | Pro | Val | Gln | Pro | Gly | Val | Leu | His | Val | Pro | Gly |
|     |     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Asp | Leu | Ala | Ala | His | Leu | Leu | His | Arg | Gln | His | His | Glu | Ala | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Leu | Arg | His | Arg | Arg | Val | His | His | His | Leu | Pro | Asp | Ala | Arg | Pro | Ala |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| His | Gln | Arg | Ala | Arg | Gly | Arg | His | Arg | His | Pro | Arg | Asn | Leu | His | Leu |
|     |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |
| Leu | Pro | Gly | Gln | Ala | Val | Ala | Ala | Leu | Xaa | Arg | Ala | Ser | Gly | Ser | Gln |
|     |     |     |     | 115 |     |     |     |     |     | 120 |     |     |     | 125 |     |
| Ala | Ser | Val | Gln | Phe | Thr | Ala | Glu | Ser | Ala | Arg | Arg | Ser | Lys | Ile |     |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1504372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2720:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Tyr | Ala | Cys | Leu | Ser | Ile | Met | Ser | Leu | Val | Ile | Leu | Leu | Pro | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Ala | Met | Glu | Gly | Pro | Lys | Val | Trp | Ala | Ala | Gly | Trp | Gln | Thr |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Ala | Val | Ala | Glu | Ile | Gly | Pro | Asn | Phe | Val | Trp | Trp | Val | Ala | Ala | Gln |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |

Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser Leu Asp  
50 55 60  
Glu Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys Arg Ile  
65 70 75 80  
Ser Val Ile Val Ala Ser Ile Ile Ile Phe Gln Thr Pro Val Gln Pro  
85 90 95  
Ile Asn Ala Leu Gly Ala Ala Ile Ala Ile Leu Gly Thr Phe Ile Tyr  
100 105 110  
Ser Gln Ala Lys Gln  
115

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Met Ser Leu Val Ile Leu Leu Pro Phe Ala Ile Ala Met Glu Gly Pro  
1 5 10 15  
Lys Val Trp Ala Ala Gly Trp Gln Thr Ala Val Ala Glu Ile Gly Pro  
20 25 30  
Asn Phe Val Trp Trp Val Ala Ala Gln Ser Val Phe Tyr His Leu Tyr  
35 40 45  
Asn Gln Val Ser Tyr Met Ser Leu Asp Glu Ile Ser Pro Leu Thr Phe  
50 55 60  
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ala Ser Ile  
65 70 75 80  
Ile Ile Phe Gln Thr Pro Val Gln Pro Ile Asn Ala Leu Gly Ala Ala  
85 90 95  
Ile Ala Ile Leu Gly Thr Phe Ile Tyr Ser Gln Ala Lys Gln  
100 105 110

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

ttagtgtata tatgttatct ggggacaagg aaagtgtctg tatgaatgtg gcttcagttg 60  
tcgggtatcca ggcagacaag gtctctgtctg aagttaaacc acatgagaaa aagaagttca 120  
tatctgaact ccagaaagag cacaaggtag tcgccatggt tggtagcggc attaagtgtg 180  
ccgcagcact agcttcagct gatgttggaa tcgcaatggg tggagggtgtt ggggcagcta 240  
gtgatgtatc ttcagttgta cttatgggca acaggttacc ccagcttacc gatgctttag 300  
agttgagtaa agagaccatg aagacgggtga agcaaaatct ttgggtggcct ttctgttata 360  
acattgttgg actaccattg ctgctgtgag cattgcttcc agctacgggg acgatactga 420  
caccatcaat agctggagct ctgatggggt nt

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504375  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:  
Ser Val Tyr Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val  
1 5 10 15  
Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys  
20 25 30  
Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys  
35 40 45  
Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala  
50 55 60  
Ser Ala Asp Val Gly Ile Ala Met Gly Gly Val Gly Ala Ala Ser  
65 70 75 80  
Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile  
85 90 95  
Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn  
100 105 110  
Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala  
115 120 125  
Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala  
130 135 140  
Gly Ala Leu Met Gly  
145

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..146  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

Met Leu Ser Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val Ala Ser Val  
1 5 10 15  
Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys Pro His Glu  
20 25 30  
Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys Val Val Ala  
35 40 45  
Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala Ser Ala Asp  
50 55 60  
Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser Asp Val Ser  
65 70 75 80  
Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile Asp Ala Leu  
85 90 95  
Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn Leu Trp Trp  
100 105 110  
Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala Gly Ala Leu  
115 120 125  
Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala Gly Ala Leu  
130 135 140  
Met Gly  
145

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..136  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504377  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:  
Met Asn Val Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala  
1 5 10 15  
Glu Val Lys Pro His Glu Lys Lys Phe Ile Ser Glu Leu Gln Lys  
20 25 30  
Glu His Lys Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala  
35 40 45  
Ala Leu Ala Ser Ala Asp Val Gly Ile Ala Met Gly Gly Gly Val Gly  
50 55 60  
Ala Ala Ser Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser  
65 70 75 80  
Gln Leu Ile Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val  
85 90 95  
Lys Gln Asn Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro  
100 105 110  
Ile Ala Ala Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro  
115 120 125  
Ser Ile Ala Gly Ala Leu Met Gly  
130 135  
(2) INFORMATION FOR SEQ ID NO:2726:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 440 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..440  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504382  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:  
accacacccca cccacagaaa ccgtaagaag cgcagagtgt gagagagaga ggagcatcaa 60  
ggacgacgtg ggcaagatga tgcaggtgtt cgtgaagacg ctggcgggga agacgatcac 120  
gctggaggtg gagggcagcg acgacgcctg nagaacgtga aggccatgat ccagggcaag 180  
gaaggcatcc gcggcgagga gcaagccctc gtcttcgcgg gcaagcagct ggacgacgac 240  
ggccgcaccc tgcccgacta cggcgctccag aaggagtcca cgctgcacct ggagctgcgc 300  
ctccgcggcg gcagcagggg cggctacccc atgggatccc gccacgcct ccgcgagctcg 360  
cgcaagaatg caacgagaac aagatggtct gccgcaagtg ctatgcgcgg cttccgccta 420  
gggcaaccaa ctgccgcaag  
(2) INFORMATION FOR SEQ ID NO:2727:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..52  
(D) OTHER INFORMATION: / Ceres Seq. ID 1504383  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:  
Pro His Pro Pro His Glu Thr Val Arg Ser Ala Glu Cys Glu Arg Glu

1 5 10 15  
Arg Ser Ile Lys Asp Asp Val Gly Lys Met Met Gln Val Phe Val Lys  
20 25 30  
Thr Leu Ala Gly Lys Thr Ile Thr Leu Glu Val Glu Gly Ser Asp Asp  
35 40 45  
Ala Xaa Arg Thr  
50

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Met Ile Gln Gly Lys Glu Gly Ile Pro Pro Glu Glu Gln Arg Leu Val  
1 5 10 15  
Phe Ala Gly Lys Gln Leu Asp Asp Asp Gly Arg Thr Leu Ala Asp Tyr  
20 25 30  
Gly Val Gln Lys Glu Ser Thr Leu His Leu Glu Leu Arg Leu Arg Gly  
35 40 45  
Gly Ser Arg Gly Gly Tyr Pro Met Gly Ser Arg Pro Ala Ser Ala Ser  
50 55 60  
Ser Arg Arg Ser Thr Thr Arg Thr Arg Trp Ser Ala Ala Ser Ala Met  
65 70 75 80  
Arg Gly Phe Arg Leu Gly Gln Pro Thr Ala Ala  
85 90

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

acatcgggaa cgccgccgac gccgcagagg agacgcacgc aggttagcac gcgaagaagc 60  
gaccatgagg gccaaagtga agaagaagcg catnaggagg ctcaagagga akccgagaaa 120  
gatgaggccag gatcccaagt aggcagatcg agatggattg tggacctgac tctcttcggt 180  
atatgtacta cctccgttct tgaatatatt taaatatnng tcgttgtcgt cggt

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Thr Ser Gly Thr Pro Pro Thr Pro Gln Arg Arg Ile Glu Val Ser  
1 5 10 15

Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu Ala His Xaa  
20 25 30  
Glu Ala Gln Glu Glu Xaa Gln Lys Asp Glu Ala Glu Ile Gln Val Gly  
35 40 45  
Arg Ser Arg Trp Ile Val Asp Leu Thr Leu Phe Val Ile Cys Thr Thr  
50 55 60  
Ser Val Leu Glu Tyr Phe  
65 70

(2) INFORMATION FOR SEQ ID NO:2731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..46

- (D) OTHER INFORMATION: / Ceres Seq. ID 1504395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

His Arg Glu Arg Arg Arg Arg Arg Gly Asp Ala Ser Arg Leu Ala  
1 5 10 15  
Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys Lys Arg Xaa Arg  
20 25 30  
Arg Leu Lys Arg Xaa Arg Arg Lys Met Arg Gln Arg Ser Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..474

- (D) OTHER INFORMATION: / Ceres Seq. ID 1504400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

cccagttgat gtggttaagt cgagaatgat gggtgactca gcctacaaaa gcaactctcga 60  
ttgtttttgtg aagactcttaa agaattgatgg ccctttggca ttttacaaag gcttcctgcc 120  
aaacttttga agactgggat ctgggaatgt gattatgttc ttgacattgg agcaggttca 180  
aaagctgttt gtgaggaaag cgacaagctg aagatagatt ttttgcagtc aggtggcgta 240  
caattgacgc acagggtttt tcttctatag acaaaagggg agaaatgaca cctccccct 300  
cgagaattgg ggaacaagga cagatctgac acctcaattg cgagaaataa aaataacagc 360  
cgacagttgc atgatccctg aacgaataaa ttcagaacta gaaacagatg tcagtaaaca 420  
acatgtgtgt aattgttgaa cttgactgct ctagtccagt gggcactctgt tggtt

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..69

- (D) OTHER INFORMATION: / Ceres Seq. ID 1504401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys  
1 5 10 15  
Ser Thr Leu Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Ala | Phe | Tyr | Lys | Gly | Phe | Leu | Pro | Asn | Phe | Ala | Arg | Leu | Gly | Ser | Trp |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Ile | Met | Phe | Leu | Thr | Leu | Glu | Gln | Val | Gln | Lys | Leu | Phe | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Lys | Ala | Thr | Ser |     |     |     |     |     |     |     |     |     |     |     |

65

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1504402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Gly | Asp | Ser | Ala | Tyr | Lys | Ser | Thr | Leu | Asp | Cys | Phe | Val | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Leu | Lys | Asn | Asp | Gly | Pro | Leu | Ala | Phe | Tyr | Lys | Gly | Phe | Leu | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Phe | Ala | Arg | Leu | Gly | Ser | Trp | Asn | Val | Ile | Met | Phe | Leu | Thr | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Glu | Gln | Val | Gln | Lys | Leu | Phe | Val | Arg | Lys | Ala | Thr | Ser |     |     |     |
|     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1504403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Ser | Ala | Tyr | Lys | Ser | Thr | Leu | Asp | Cys | Phe | Val | Lys | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Lys | Asn | Asp | Gly | Pro | Leu | Ala | Phe | Tyr | Lys | Gly | Phe | Leu | Pro | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Phe | Ala | Arg | Leu | Gly | Ser | Trp | Asn | Val | Ile | Met | Phe | Leu | Thr | Leu | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Val | Gln | Lys | Leu | Phe | Val | Arg | Lys | Ala | Thr | Ser |     |     |     |     |
|     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |